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	HEMBA1006835	1.11	1.49	3.88	5.08	7.25	4.6	*	+
	HEMBA1006843	19.27	17.89	35.47	55.34	39.67	68.17	*	+
	HEMBA1006849	5.64	4.37	11.23	10.07	11.23	10.83		
5	HEMBA1006850	31.45	33.76	60.2	44.62	53.25	45.59		
	HEMBA1006861	12.19	11.3	24.61	22.49	16.43	17.99		
	HEMBA1006865	5.42	8.35	31	33.77	33.36	34.49		
	HEMBA1006867	4.32	5.03	6.41	6.27	7.76	6.15		
	HEMBA1006873	3.14	3.59	8.87	6.5	9.26	7.75		
10	HEMBA1006877	2.52	4.03	5.87	4.03	6.26	3.68		
	HEMBA1006878	2.52	2.36	6.79	3.82	7.86	3.51		
	HEMBA1006879	6.19	5.68	8.83	11.06	15.86	17.33	*	+
	HEMBA1006884	10.11	3.17	6.59	6.15	8.42	8.78		
	HEMBA1006885	7.02	6.82	14.16	20.86	19.11	21.73	*	+
15	HEMBA1006886	20.38	17.25	26.55	29.45	29.15	40.93		
	HEMBA1006889	2.61	4.02	4.85	4.48	5.99	6.09		
	HEMBA1006896	19.11	24.76	31.7	33.67	39.11	40.41	*	+
	HEMBA1006900	6.19	5.93	20.76	16.81	23.73	18.45		
20	HEMBA1006902	1.43	2.45	3.86	4.03	6	3.98		
	HEMBA1006912	1.24	1.74	6.86	4.12	5.8	5.3		
	HEMBA1006914	6.64	6.11	18.27	14.81	18.62	15.03		
	HEMBA1006916	3.11	2.71	5.78	10.29	7.48	9.36	*	+
	HEMBA1006921	3.03	3.5	9.63	9.77	11.26	13.59		
25	HEMBA1006926	2.65	2.61	5.68	5.01	6.53	6.98		
	HEMBA1006927	3.06	2.2	5.17	3.57	5.26	5.89		
	HEMBA1006929	2.94	2.69	4.02	4.31	6.36	5.25	*	+
	HEMBA1006936	3.72	3.21	6.51	4.67	6.25	5.45		
	HEMBA1006938	1.21	2.11	6.57	2.37	3.76	3.44		
30	HEMBA1006941	9.52	8.15	12	19.26	28.62	23.74	**	+
	HEMBA1006942	5.2	2.63	6.65	10.7	10.65	11.4	**	+
	HEMBA1006945	10.07	5.91	16.81	23.73	17.09	19.91		
	HEMBA1006949	1.6	1.43	3.88	2.48	5.34	2.81		
35	HEMBA1006952	1.16	1.66	2.98	3.02	5.04	2.22		
	HEMBA1006960	2.53	2.78	7.66	5.9	8.28	8.68		
	HEMBA1006973	1.74	2.27	5.91	4.7	7.84	5.54		
	HEMBA1006974	2.49	3.44	6.76	6.09	11.01	8.14		
	HEMBA1006976	1.39	1.5	4.12	3.18	4.96	4.36		
40	HEMBA1006989	1.85	1.66	6.51	2.05	3.01	1.81		
	HEMBA1006993	2.71	2.39	6.49	6.11	7.69	8.79		
	HEMBA1006996	0.74	1.15	2.98	2.52	3.13	3.58		
	HEMBA1007001	1.91	2.47	5.12	3.98	6.37	4.76		
	HEMBA1007002	7.02	4.12	31.4	26.92	38.45	42.11		
45	HEMBA1007013	1.02	0.94	3.04	1.44	4.39	2.27		
	HEMBA1007016	2.02	1.43	5.06	3.27	5.97	5.28		
	HEMBA1007017	0.69	1.24	2.55	1.42	3.33	1.83		
	HEMBA1007018	4.02	4.52	6.54	7.65	6.1	7.07		
	HEMBA1007044	8.13	8.41	17.4	15.48	11.97	12.27		
50	HEMBA1007045	1.64	2.15	4.42	2.61	5.08	3.47		
	HEMBA1007051	2.26	2.56	4.71	3.42	4.42	3.28		
	HEMBA1007052	2.23	1.25	3.47	2.37	4.62	1.83		
	HEMBA1007053	1.83	3.14	4.03	2.64	4	2.5		
	HEMBA1007057	0.92	2.56	3.21	3.52	4.03	3.41		
55	HEMBA1007062	0.91	0.82	2.73	2.34	2.87	1.82		

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	HEMBA1007063	3.87	2.7	8.87	8.56	8.02	7.58		
	HEMBA1007066	1.72	2.03	3.62	2.2	4.39	2.71		
	HEMBA1007069	1.36	2.29	3.87	3.84	3.48	3.66		
5	HEMBA1007073	1.93	2.16	6.12	2.96	9.57	3.6		
	HEMBA1007076	1.48	2.6	5.56	4.66	7.6	3.4		
	HEMBA1007078	6.5	6.83	18.61	26.96	27.47	23.78	*	+
	HEMBA1007080	7.6	9.46	38.27	61.02	68.15	51.34	*	+
10	HEMBA1007084	1.28	1.42	4.76	3.68	6.27	4.76		
	HEMBA1007085	3.28	2.89	8.21	5.76	7.21	5.42		
	HEMBA1007087	2.6	2.88	6.31	3.96	6.92	5.63		
	HEMBA1007089	26.17	28.1	43.8	46.11	34.41	29.42		
	HEMBA1007095	75.81	62.79	111.43	134.53	48.47	121.4		
15	HEMBA1007101	2.78	3.27	8	26.73	21.52	19.57	**	+
	HEMBA1007104	1.87	1.92	3.52	2.46	4.53	2.57		
	HEMBA1007106	4.77	4.8	9.03	16.42	12.5	9.49		
	HEMBA1007112	3.01	3.07	5.16	6.39	6	4.77		
	HEMBA1007113	1.53	2.29	9.04	6.03	6.1	5.97		
20	HEMBA1007121	13.76	14	92.08	116.14	111.53	129.12	*	+
	HEMBA1007129	1.54	2.44	2.87	2.66	4.37	1.89		
	HEMBA1007147	1.68	2.88	4.4	3.96	4.76	4.06		
	HEMBA1007149	5.3	7.24	8.38	10.48	6.82	9.73		
25	HEMBA1007151	0.85	1.87	3.38	3.32	3.88	2.54		
	HEMBA1007172	1.26	1.91	4.13	2.96	4.81	3.51		
	HEMBA1007174	1.4	1.43	2.75	3.96	3.65	2.5		
	HEMBA1007176	2.58	3.95	11.7	6.7	6.78	4.52		
	HEMBA1007178	4.77	4.71	9.32	10.94	13.03	8.12		
30	HEMBA1007185	9.38	10.32	9.59	19.5	7.83	15.16		
	HEMBA1007186	1.71	2.76	4.49	4.95	5.47	3.86		
	HEMBA1007194	4.81	3.43	5.58	7.83	9.34	8.67	**	+
	HEMBA1007200	1.18	2.33	2.9	3.25	4.6	1.66		
	HEMBA1007203	1.54	3.5	5.38	6.03	6.87	5.05		
35	HEMBA1007206	1.92	2.46	5.72	7.07	7.91	5.94		
	HEMBA1007224	5.4	6.5	9.06	9.23	5.85	8.06		
	HEMBA1007226	7.19	8.07	40.61	59.31	70.51	62.19	*	+
	HEMBA1007240	10	10.96	13.45	15.35	7.71	11		
	HEMBA1007241	3.59	2.88	4.56	4.61	6.81	3.63		
40	HEMBA1007242	2.52	2.86	5.01	6.29	6.87	4.23		
	HEMBA1007243	10.23	10.91	69.57	70.17	95.69	82.75		
	HEMBA1007251	1.32	1.8	4.14	3.02	3.67	2.01		
	HEMBA1007256	1.39	1.91	3.36	3.93	5.74	3.44		
	HEMBA1007267	3.19	3.71	8.75	8.73	9.18	8.1		
45	HEMBA1007273	0.98	2.66	3.84	3.56	5.82	2.25		
	HEMBA1007279	1.55	2.25	3.52	2.95	4.35	2.02		
	HEMBA1007281	1.73	1.54	2.12	2.95	4.43	1.01		
	HEMBA1007283	2.45	3.15	6.78	6.37	6.58	5.96		
	HEMBA1007288	2.12	2.77	5.54	4.35	6.74	5.48		
50	HEMBA1007291	1.59	1.8	4.29	2.14	4.4	0.98		
	HEMBA1007299	20.39	22.25	39.67	40.95	47.97	40.26		
	HEMBA1007300	2.08	2.75	3.59	4.17	4.45	4.07	*	+
	HEMBA1007301	1.97	2.82	3.15	3.73	3.99	3.44	*	+
	HEMBA1007319	2.84	3.61	6.73	5.21	6.12	3.32		
55	HEMBA1007320	1.29	1.22	3.12	4.19	3.45	2.42		

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	HEMBA1007322	19.97	17.81	27.74	45.24	39.42	37.31	**	+
	HEMBA1007323	4.54	6.69	11.47	6	6.36	6.21		
	HEMBA1007326	4.58	3.85	13.34	8.29	8.07	9		
5	HEMBA1007327	3.37	3.98	8.91	6.14	9.31	8.98		
	HEMBA1007332	3.12	3.47	5.42	5.27	7.56	5.33		
	HEMBA1007341	1.4	2.51	3.24	2.93	3.38	3.36		
	HEMBA1007342	1.06	2.05	3.02	1.52	3.23	1.98		
	HEMBA1007347	3.39	3.24	6.34	4.55	7.34	6.32		
10	HEMBA1007353	2.43	2.22	4.99	2.68	6.9	3.01		
	HEMBA1000005	1.57	2.54	5.35	2.68	4.65	3.64		
	HEMBA1000008	2.19	2.53	5.99	3.51	6.31	3.71		
	HEMBA1000018	2.21	2.16	7.13	9.9	9.79	7.24		
15	HEMBA1000024	3.71	2.15	5.4	5.13	5.77	6.39		
	HEMBA1000025	2.11	2.09	3.55	1.68	5.13	2.62		
	HEMBA1000030	3.12	3.53	6.58	6.62	7.77	6		
	HEMBA1000036	5.3	4.76	5.04	6.95	8.19	5.93	*	+
	HEMBA1000037	4.43	3.64	4.73	4.63	8.38	5.32		
20	HEMBA1000039	1.17	0.96	3.98	2.61	4.11	2.95		
	HEMBA1000044	1.22	2.35	4.26	5.28	5.58	5.36	*	+
	HEMBA1000048	3.2	1.7	3.48	3.99	5.4	3.96		
	HEMBA1000050	2.32	1.55	3.33	2.97	3.98	2.85		
	HEMBA1000054	2.03	2.08	7.07	4.49	5.09	3.98		
25	HEMBA1000055	42.59	36.75	92.41	100.33	86.52	89.35		
	HEMBA1000059	2.5	2.65	11.34	10.96	11.52	14.73		
	HEMBA1000072	6.84	7.77	58.85	73.22	97.61	76.22	*	+
	HEMBA1000081	2.85	3.56	10.79	5.69	6.19	7.23		
30	HEMBA1000083	1.13	1.95	5.38	4.88	5.89	5.33		
	HEMBA1000089	1.14	2.53	4.54	6.03	6.73	5.43	*	+
	HEMBA1000094	4.12	4.3	8.4	4.24	5.04	6.62		
	HEMBA1000097	2.48	1.71	7.91	4.75	4.55	4.3		
	HEMBA1000099	2.69	2.07	6.27	5.18	6.75	5.64		
35	HEMBA1000103	7.19	5.28	18.55	13.99	19.26	16.16		
	HEMBA1000106	3.91	3.75	8.15	4.24	6.4	5.9		
	HEMBA1000113	1.25	1.54	3.33	1.39	4.14	2.31		
	HEMBA1000119	2.19	2.17	5.66	3.34	6.12	4.05		
	HEMBA1000133	21.01	22.21	30.57	43.5	66.13	60.69	*	+
40	HEMBA1000134	4.92	2.95	8.69	13.39	9.79	9.8		
	HEMBA1000136	7.14	8.81	29.63	23.11	26.28	28.23		
	HEMBA1000141	1.98	2.85	6.18	4.95	5.75	6.16		
	HEMBA1000144	2.05	2.59	4.85	3.09	5.36	1.38		
	HEMBA1000147	3.77	2.08	4.51	4.55	7.39	3.07		
45	HEMBA1000152	0.79	1.45	3.42	5.13	5.15	3.45		
	HEMBA1000154	0.98	-1.11	3.43	2.59	2.89	2.47		
	HEMBA1000155	0.88	0.54	3.15	3.33	4.15	1.92		
	HEMBA1000173	3.35	3.72	12.14	10.1	10.89	7.51		
	HEMBA1000175	1.85	1.32	3.39	6.06	4.09	3.86		
50	HEMBA1000176	1.48	4.03	6.12	3.43	9.75	5.03		
	HEMBA1000198	0.88	1.72	3.64	2.6	3.59	3.22		
	HEMBA1000208	1.12	1.52	3.04	1.74	3.23	2.69		
	HEMBA1000209	1.62	1.54	3.76	3.32	3.94	3.28		
	HEMBA1000212	1.88	1.03	3.26	4.37	3.93	1.98		
55	HEMBA1000215	1.61	2.13	3.8	4.67	5.49	5.32	*	+

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	HEMBB1000217	5.67	4.97	11.23	15.21	18.81	11.78	*	+
	HEMBB1000218	2.13	2.28	11.05	7.47	10.07	7.05		
	HEMBB1000226	2.63	3.26	6.02	4.02	5.86	3.41		
5	HEMBB1000230	1.39	1.83	3.73	1.95	4.31	2.58		
	HEMBB1000240	6.04	8.26	10.01	3.97	2.7	1.75	*	-
	HEMBB1000244	1.39	1.64	3.51	2.51	2.63	1.68		
	HEMBB1000250	1.17	0.99	1.12	1.94	1.25	1.12		
10	HEMBB1000258	1.71	1.94	5.8	4.38	5.63	3.27		
	HEMBB1000264	2.49	3.12	11.01	8.64	8.34	8.1		
	HEMBB1000266	2.81	2.65	5.52	3.38	5.95	3.71		
	HEMBB1000272	4.76	4.16	6.06	8.38	6.88	7.45	*	+
	HEMBB1000274	1.51	1.15	3.17	2.54	3.18	1.88		
15	HEMBB1000276	1.12	1.84	4.72	3.1	4.01	2.43		
	HEMBB1000284	0.94	1.81	2.89	2.83	3.11	1.65		
	HEMBB1000307	1.52	1.7	4.78	2.8	5.31	3.27		
	HEMBB1000309	1.43	2.73	3.07	3.09	3.56	2.19		
	HEMBB1000312	1.99	1.38	5.18	7.03	7.2	4.35		
20	HEMBB1000317	0.17	1.62	3.32	2.6	4.73	2.14		
	HEMBB1000318	1.11	2.69	3.85	2.28	4.46	1.68		
	HEMBB1000332	3.12	3.84	4.37	3.75	3.95	2.72		
	HEMBB1000335	0.77	2.35	4.66	6.16	4.66	3.44		
25	HEMBB1000336	0.99	1.11	3.59	2.09	3.52	2.29		
	HEMBB1000337	4.3	5.06	20.22	22.86	24.84	22.82		
	HEMBB1000338	2.11	1.92	5.86	7.13	8.92	4.71		
	HEMBB1000339	1.66	1.76	5.84	3.75	4.99	3.84		
	HEMBB1000341	1.4	1.91	3.68	3.06	4.77	2.83		
30	HEMBB1000343	2.51	3.15	6.96	7.24	8.68	7.46		
	HEMBB1000354	3.26	3.5	10.36	7	8.93	8.07		
	HEMBB1000358	1.09	2.11	3.82	3.43	2.83	1.93		
	HEMBB1000369	1.93	2.33	3.87	5.96	6.54	2.89		
	HEMBB1000373	1.77	2.73	3.91	2.26	6.2	2.94		
35	HEMBB1000374	3.27	4.06	9.34	9.58	13.36	6.95		
	HEMBB1000376	2.71	3.92	12.28	10.03	6.99	7.71		
	HEMBB1000383	60.87	62.14	104.01	69.28	57.52	83.25		
	HEMBB1000391	1.8	2.66	4.57	4.89	6.18	4.29		
	HEMBB1000399	2.51	3.79	3.69	3.93	5.72	3.71		
40	HEMBB1000402	1.61	2.06	3.33	2.67	5.3	1.72		
	HEMBB1000404	1.34	1.15	5.18	2.56	5.29	1.81		
	HEMBB1000407	2.2	3.36	6.76	5.57	5.75	4.66		
	HEMBB1000420	1.93	1.46	3.86	4.33	4.76	4.54	*	+
45	HEMBB1000430	38.77	36.24	61.06	51.76	34.69	50.02		
	HEMBB1000434	3.05	4.73	9.02	6.54	6.59	6.63		
	HEMBB1000438	1.13	1.83	4.16	2.23	4	1.39		
	HEMBB1000441	2.26	3	7.35	5.44	8	4.78		
	HEMBB1000447	29.84	32.01	39.91	35.88	44.02	33.55		
50	HEMBB1000449	1.3	1.31	3.72	1.51	3.04	1.54		
	HEMBB1000453	8.61	8.04	13.39	14.23	18.78	13.74		
	HEMBB1000455	1.29	1.97	3.19	3.13	5.46	3.54		
	HEMBB1000472	2.3	2.28	4.22	4.07	4.35	3.52		
	HEMBB1000480	1.9	3.59	7.03	5.71	6.63	5.87		
55	HEMBB1000486	2.15	2.98	6.93	4.82	7.86	5.9		
	HEMBB1000487	1.21	1.79	4.48	2.66	4.8	2.57		

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	HEMBB1000490	3.67	4.13	12.61	7.92	8.7	6.55	
	HEMBB1000491	1.36	2.91	5	3.83	4.78	4.42	
	HEMBB1000492	3.02	4.04	6.84	5.63	6.94	5.34	
5	HEMBB1000493	1.57	1.71	3.26	2.41	5.38	3.27	
	HEMBB1000510	1.32	1.71	4.94	4.4	5.61	4.21	
	HEMBB1000516	5.64	7.71	36.22	16.62	18.58	17.09	
	HEMBB1000518	0.88	1.22	2.63	2.21	4.27	1.73	
10	HEMBB1000523	1.32	2.78	7.41	3.33	7.74	4.1	
	HEMBB1000530	2.83	2.51	9.72	6.06	7.81	6.64	
	HEMBB1000542	3.08	4.55	9.39	8.48	14.07	9.82	
	HEMBB1000550	4.84	2.87	4.77	10.48	5.74	5.33	
	HEMBB1000554	2.14	2.26	8.65	6.43	11.59	7.19	
15	HEMBB1000556	2.64	2.68	4.48	3.1	4.67	4.6	
	HEMBB1000564	1.81	1.4	5.87	4.26	5.34	6.18	
	HEMBB1000567	1.39	1.71	3.7	2.1	3.87	3.3	
	HEMBB1000569	3.78	2.72	8.76	4.88	7.13	5.65	
	HEMBB1000573	3.48	3.44	11.31	7.33	9.55	7.56	
20	HEMBB1000575	12.42	2.7	10.57	7.16	8.38	12.35	
	HEMBB1000579	2.12	3.75	4.84	3.01	8.61	4.04	
	HEMBB1000585	0.83	1.19	3.19	2	4.1	3.35	
	HEMBB1000586	2.18	1.41	4.28	4.07	4.23	4.11	
	HEMBB1000589	2.98	1.58	3.62	3.38	3.75	3.69	
25	HEMBB1000591	2.62	2.15	3.96	4.44	5.26	4.64	* +
	HEMBB1000592	2.05	1.2	3.18	3.87	3.39	2.15	
	HEMBB1000593	10.25	5.67	51.69	53.87	82.75	77.88	* +
	HEMBB1000595	6.42	5.2	11.24	12.51	17.1	9.55	
30	HEMBB1000598	1.57	1.69	5.91	2.94	6.76	4.77	
	HEMBB1000611	0.94	1.16	2.08	1.15	2.79	1.66	
	HEMBB1000617	2.01	3.04	9.31	6.14	8.79	6.97	
	HEMBB1000623	2.51	3.08	4.64	5.58	5.83	3.9	
	HEMBB1000630	3.23	2.5	3.78	2.42	5.54	2.51	
35	HEMBB1000631	8.91	10.69	18.75	22.52	23.76	22.55	* +
	HEMBB1000632	6.77	8.77	20.85	27.2	18.4	23.31	
	HEMBB1000636	9.52	15.91	22.42	25.26	21.65	19.96	
	HEMBB1000637	6.63	9.77	19.44	17.77	24.39	20.28	
	HEMBB1000638	1.44	1.41	3.23	3.6	5.29	3.34	
40	HEMBB1000642	3.47	2.31	7.58	7.65	9.33	9.93	
	HEMBB1000643	0.71	1.87	2.71	1.62	3.54	2.12	
	HEMBB1000649	2.25	2.22	6.45	4.94	7.61	5.72	
	HEMBB1000652	1.8	2.21	5.33	5.13	5.14	4.93	
	HEMBB1000655	1.07	1.17	3.24	1.64	4.74	2.01	
45	HEMBB1000665	0.52	1.08	2.23	1.69	2.92	2.01	
	HEMBB1000668	1.85	1.46	2.76	5.07	5.42	4.1	** +
	HEMBB1000671	2.36	2.01	6.77	7.03	7.81	6.94	
	HEMBB1000673	0.75	1.27	2.92	2.84	4.63	2.43	
	HEMBB1000679	3.26	2.84	5.59	4.42	7.19	5.76	
50	HEMBB1000684	1.83	2.53	6.6	5.01	6.92	5.6	
	HEMBB1000692	0.93	2	2.46	1.77	2.5	1.09	
	HEMBB1000693	0.96	1.29	2.47	1.6	2.79	1.34	
	HEMBB1000705	2.61	2.52	4.85	4.97	8.2	6.53	
	HEMBB1000706	0.78	1.07	2.18	2.56	2.93	1.06	
55	HEMBB1000709	3.53	2.92	8.39	8.16	7.99	10.26	

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	HEMBB1000714	1.41	2.85	9.32	5.31	10.37	8.79		
	HEMBB1000725	1.61	2.22	4.35	3.04	6.22	4.72		
	HEMBB1000726	1.88	2.34	8.76	5.63	7.1	4.83		
5	HEMBB1000729	1.82	3.28	4.3	3.3	5.21	2.79		
	HEMBB1000738	1.94	2.6	5.55	3.99	5.53	6.15		
	HEMBB1000749	4.06	4.15	7.47	7.48	9.56	8.27		
	HEMBB1000763	5.81	5.56	6.21	6.65	9.9	6.61		
10	HEMBB1000770	2.76	2.06	8.8	7.73	9.62	8.83		
	HEMBB1000774	1.62	2.75	3.7	3.07	4.39	2.34		
	HEMBB1000777	5.17	5.49	7.42	6.86	4.9	7.37		
	HEMBB1000781	3.7	4.19	6.89	7.64	5.28	6.83		
	HEMBB1000788	0.87	1.79	2.45	2.65	4.88	1.35		
15	HEMBB1000789	1.91	2.22	3.01	3.1	6.55	1.86		
	HEMBB1000790	1.97	2.15	4.48	4.59	4.21	2.53		
	HEMBB1000794	1.46	1.8	2.85	2.97	3.84	2.06		
	HEMBB1000807	2.55	2.72	5.18	3.57	4	4.26		
20	HEMBB1000809	30.31	26.87	132.99	158.22	156.74	195.14	*	+
	HEMBB1000810	1.98	2.67	4.51	3.76	6.08	4.12		
	HEMBB1000821	1.98	1.93	2.98	2.05	4.45	1.79		
	HEMBB1000822	1.08	1.97	2.31	1.65	5.31	1.46		
	HEMBB1000826	1.36	1.99	3.57	3.77	6.11	3.6		
25	HEMBB1000827	2.48	2.89	5.83	2.67	5.05	2.99		
	HEMBB1000831	3.4	2.31	5.67	3.84	7.74	2.95		
	HEMBB1000835	1.76	1.94	6.2	7.59	7.62	7.47	*	+
	HEMBB1000840	1.27	2.95	6.89	4.48	7.19	3.01		
	HEMBB1000848	2.08	3.45	5.63	5.39	6.45	5.3		
30	HEMBB1000852	1.26	2.16	2.8	1.07	4.51	1.55		
	HEMBB1000857	7.65	6.49	8.13	7.01	10.69	11.53		
	HEMBB1000858	3.7	3.13	7.3	7.07	9.38	7.31		
	HEMBB1000867	2.21	1.84	4.9	3.02	5.55	4.04		
	HEMBB1000870	1.64	2.37	4.56	2.84	5.31	3.63		
35	HEMBB1000876	1.48	2.86	3.91	4.54	3.22	3.93		
	HEMBB1000881	3.35	5.56	10.5	6.12	5.88	3.85		
	HEMBB1000883	1.02	2.68	2.2	3.03	3.32	2.58		
	HEMBB1000887	16.9	14.54	43.41	67.39	61.26	59.84	*	+
	HEMBB1000888	1.03	1.67	2.39	1.63	3.92	1.86		
40	HEMBB1000890	2.93	3.36	10.85	6.01	8.62	7.68		
	HEMBB1000893	3.28	2.54	5.46	4.5	6.14	5.57		
	HEMBB1000900	1.27	1.53	2.98	2.06	2.54	1.58		
	HEMBB1000905	5.09	3.75	6.6	10.05	9.45	8.77	**	+
	HEMBB1000908	3.34	2.79	3.01	4.48	4.71	5.7	**	+
45	HEMBB1000910	1.74	2.91	2.55	2.09	3.56	2.24		
	HEMBB1000913	1.41	1.51	2.22	2.8	3.41	1.91		
	HEMBB1000915	32.08	25.6	50.05	48	58.92	51.07		
	HEMBB1000917	2.1	2.78	5.72	2.99	4.52	3.44		
50	HEMBB1000927	1.45	1.24	1.82	1.49	3.25	1.88		
	HEMBB1000932	0.66	2.06	2.74	1.81	3.41	1.61		
	HEMBB1000933	7.47	7.12	10.71	12.88	12.78	19.19		
	HEMBB1000936	1.44	1.96	2.87	3.75	6.44	3.55		
	HEMBB1000939	7.86	7.14	9.02	15.98	15.3	18.25	**	+
55	HEMBB1000941	1.53	1.86	3.17	3.99	4.46	3.52	*	+
	HEMBB1000947	3.53	3.34	4.61	4.67	6.8	5.72		

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	HEMBB1000954	1.08	1.82	2.54	1.62	4.01	3.08	
	HEMBB1000959	0.77	1.41	3.11	2.23	4.42	1.87	
	HEMBB1000973	1.21	1.12	2.6	2.07	4.47	3.2	
5	HEMBB1000975	0.9	1.28	1.55	2.48	2.86	1.7 *	+
	HEMBB1000981	1.54	0.66	1.99	1.84	3.47	2.03	
	HEMBB1000985	1.67	1.82	2.71	3.59	3.99	3.24 *	+
	HEMBB1000991	0.99	1.35	2.83	1.46	3.75	2.43	
	HEMBB1000996	4.89	3.12	6.78	6.75	6.64	11.18	
10	HEMBB1001000	1.86	1.39	4.06	3.07	5.46	3.88	
	HEMBB1001004	1.15	1.32	2.57	2.56	4.55	2.42	
	HEMBB1001008	1.48	1.79	2.75	2.44	4.6	2.88	
	HEMBB1001011	1.34	1.15	1.53	2.47	2.24	2.9 **	+
15	HEMBB1001014	1.31	1.43	2.3	2.73	4.84	4.1 *	+
	HEMBB1001020	1.17	0.75	2.77	1.77	2.67	2.26	
	HEMBB1001024	3.31	1.72	6.27	5.47	7.56	6.82	
	HEMBB1001026	5.14	4.03	5.16	5.46	7.67	5.44	
	HEMBB1001037	2	1.45	4.73	3.52	5.69	6.67	
20	HEMBB1001042	0.52	1.15	2.69	1.29	3.61	0.87	
	HEMBB1001046	1.18	1.28	2.16	1.67	3.82	0.96	
	HEMBB1001047	1.01	1.7	3.79	2.2	3.83	3.83	
	HEMBB1001048	2.5	2.34	7.02	4.34	11.02	6.93	
	HEMBB1001051	1.44	2.62	3.23	3.95	6.26	3.9	
25	HEMBB1001056	1.61	2.67	4.89	3.75	5.7	3.78	
	HEMBB1001058	1.3	1.92	4.72	2.64	6.92	2.63	
	HEMBB1001060	0.69	0.68	1.75	2.05	4.61	1.85	
	HEMBB1001063	1.23	1.83	3.52	2.43	4.21	2.9	
	HEMBB1001068	1.84	3.62	3.59	3.46	7.14	5.2	
30	HEMBB1001082	2.24	2.57	5.98	5.38	6.93	6.36	
	HEMBB1001095	6.39	7.45	11.76	14.04	14.61	13.16 *	+
	HEMBB1001096	1.3	1.91	3.05	3.21	4.12	3.49	
	HEMBB1001101	7.41	8.19	9.74	19.33	13.1	16.69 *	+
	HEMBB1001102	1.04	1.47	4.57	3.6	6.07	4.46	
35	HEMBB1001104	1.66	1.89	3.98	3.1	4.87	4.25	
	HEMBB1001105	1.57	1.59	2.13	3.11	4.82	2.71	
	HEMBB1001112	9.44	8.91	73.3	100.88	136.14	131.28 *	+
	HEMBB1001113	2.11	1.94	9.1	5.65	8.02	6.81	
	HEMBB1001114	1.88	2.27	5.18	4.16	7.06	4.82	
40	HEMBB1001115	5.78	7.88	14.52	16.77	9.5	14.78	
	HEMBB1001117	1.7	1.52	2.92	1.85	2.79	1.79	
	HEMBB1001119	1.69	1.57	4	2.29	3.74	2.28	
	HEMBB1001126	1.85	1.88	3.63	2.69	4.96	2.9	
45	HEMBB1001133	3.15	2.42	4.24	6.56	6.15	6.44 **	+
	HEMBB1001137	1.97	2.2	4.4	3.28	6.56	5.42	
	HEMBB1001142	2.96	2.68	10.51	9.2	11.69	10.38	
	HEMBB1001145	3.25	3.56	7.39	6.11	7.7	6.59	
	HEMBB1001151	5.67	6.58	9.21	12.85	7.67	7.84	
50	HEMBB1001153	2	1.89	4.57	3.79	5.37	2.9	
	HEMBB1001158	6.96	6.74	12.17	12.04	9.95	11.16	
	HEMBB1001169	1.71	2.45	4.42	2.89	4.21	2.86	
	HEMBB1001170	1	1.85	3.27	1.26	2.5	1.61	
	HEMBB1001175	1.43	1.54	5.16	3.39	6.36	4.14	
55	HEMBB1001177	3.63	2.4	7.54	5.8	6.94	6.69	

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	HEMBB1001182	2.6	3.69	4.89	3.89	6.54	3.87	
	HEMBB1001192	3.3	3.09	16.1	15.27	20.06	15.75	
	HEMBB1001199	1.16	2.27	1.91	1.43	3.96	1.15	
5	HEMBB1001200	1.86	1.66	3.14	2.43	5.38	2.29	
	HEMBB1001208	2.02	2.04	4.56	2.96	6.19	2.74	
	HEMBB1001209	2.98	2.28	5.75	5.22	6.56	4.92	
	HEMBB1001210	5.14	4.28	7.8	11.05	6.08	10.33	
	HEMBB1001215	9.57	10.46	17.69	17.91	15.75	16.96	
10	HEMBB1001217	1.78	2.13	4.39	2.04	3.69	1.89	
	HEMBB1001218	4.28	3.37	5.47	4.52	5.98	4.6	
	HEMBB1001221	1.72	1.65	2.75	1.54	4.29	1.34	
	HEMBB1001224	2.2	2.46	3.81	2.98	6.08	3.7	
	HEMBB1001230	1.51	2.09	4.36	2.55	4.95	2.22	
15	HEMBB1001234	5.24	6.05	29.26	31	44.04	30.75	
	HEMBB1001235	12.72	10.54	21.49	13.27	8.47	10.71	
	HEMBB1001237	11	10.54	21.03	32.1	26.16	36.86	* +
	HEMBB1001242	4.82	5.68	8.63	6.92	6.97	4.51	
20	HEMBB1001244	1.08	1.1	3.9	1.47	4.36	1.36	
	HEMBB1001249	1.26	1.63	2.99	1.84	5.52	1.98	
	HEMBB1001253	1.53	1.92	5.68	1.96	4.89	2.39	
	HEMBB1001254	1.27	1.19	3.73	1.22	5.09	2.45	
	HEMBB1001266	2	4.32	4.75	4.49	6.09	4.63	
25	HEMBB1001267	3.51	2.92	9.98	8.43	7.63	8.01	
	HEMBB1001271	2.25	2.93	3.89	2.59	5.85	3.91	
	HEMBB1001282	2.27	2.68	3.9	2.77	4.86	2.99	
	HEMBB1001287	54.06	45.71	83.21	72.79	57.33	77.51	
	HEMBB1001288	2.45	2.58	3.64	4.57	6.08	3.31	
30	HEMBB1001289	4.64	5.82	12.2	6.93	9.11	6.88	
	HEMBB1001290	2.82	1.27	4.55	2.89	4.14	1.96	
	HEMBB1001294	1.03	1.91	3.2	2.93	3.95	2.51	
	HEMBB1001299	7.06	7.64	12.49	16.26	14.41	17.87	* +
	HEMBB1001302	2.16	2.34	2.41	1.75	3.39	1.64	
35	HEMBB1001304	1.73	1.34	2.6	1.81	5.2	1.67	
	HEMBB1001314	1.16	1.07	2.47	1.3	3.63	1.25	
	HEMBB1001315	1.25	1.62	1.46	0.87	4	0.9	
	HEMBB1001317	2.1	3.38	6.51	4.12	8.01	4.41	
40	HEMBB1001326	0.88	1.54	2.36	1.51	3	1.69	
	HEMBB1001331	2.11	2.79	2.81	3.78	6.14	4.55	* +
	HEMBB1001335	1.39	0.9	1.44	1.4	2.81	1.92	
	HEMBB1001337	1.86	1.7	3.15	3.34	4.72	4.51	* +
	HEMBB1001339	4.17	3.87	5.91	5.83	7.91	5.25	
45	HEMBB1001344	1.27	1.36	2.25	1.62	3.44	1.29	
	HEMBB1001346	2.17	2.32	7.45	5.89	6.23	5.7	
	HEMBB1001348	0.68	1.37	4.05	1.38	3.68	2.82	
	HEMBB1001350	2.06	2.09	4.17	2.07	7.74	2.57	
	HEMBB1001356	1.4	1.9	2.33	1.74	5.54	2.29	
50	HEMBB1001364	0.53	1.28	1.25	1.49	2.47	1.43	
	HEMBB1001366	1.61	1.71	3.46	4.17	4.27	3.82	* +
	HEMBB1001367	1.11	2.19	3.79	5.05	6.25	5.75	* +
	HEMBB1001369	0.56	1.29	2.54	1.95	3.39	2.82	
	HEMBB1001380	3.13	3.56	6.65	5.43	7.36	7.75	
55	HEMBB1001381	8.45	6.07	9.53	10.2	14.39	11.86	

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	HEMBB1001384	3.48	4.92	5.66	9.52	13.27	11.91	**	+
	HEMBB1001387	1.19	1.57	3.1	2.36	4.34	1.33		
	HEMBB1001394	1.53	1.3	1.68	2.7	2.82	1.89	*	+
5	HEMBB1001407	0.68	0.83	0.99	0.62	1.33	0.97		
	HEMBB1001410	1.35	1.04	1.78	2.44	2.63	1.74		
	HEMBB1001413	1.68	1.84	3.32	3.48	3.27	4.04		
	HEMBB1001419	2.56	2.24	4.42	3.61	5.47	4.6		
10	HEMBB1001421	2.29	1.66	2.18	1.31	3.16	0.95		
	HEMBB1001424	0.51	1.2	1.67	-0.1	1.58	0.41		
	HEMBB1001426	2.04	1.51	3.7	2.66	5.67	4.21		
	HEMBB1001429	7.11	5.76	9.83	22.69	19.97	19.53	**	+
	HEMBB1001436	3.13	2.51	6.8	7.5	6.44	7.24		
15	HEMBB1001443	5.61	6.48	20.67	20.46	27.07	22.15		
	HEMBB1001449	2.02	2	4.92	4.26	6.35	4.27		
	HEMBB1001454	1.2	1.96	3.77	3.74	5.13	2.99		
	HEMBB1001458	4.72	6.48	12.41	7.88	9.04	6.89		
20	HEMBB1001461	0.55	1.38	2.01	2.11	2.65	1.07		
	HEMBB1001463	2.28	2.1	3.7	3.95	5.03	4.66	*	+
	HEMBB1001464	1.73	1.29	3.62	2.66	3.92	2.27		
	HEMBB1001466	1.15	1.84	2.75	1.88	3.77	2.73		
	HEMBB1001482	1.76	2.21	4.36	2.94	5.36	3.97		
	HEMBB1001500	1.01	1.08	1.77	1.96	4.39	1.97		
25	HEMBB1001505	3	3.32	5.87	9.35	14.06	11.17	*	+
	HEMBB1001521	2.06	2.43	5.4	5.15	5.78	7.14		
	HEMBB1001527	2.63	4.74	11.16	8.69	9.66	9.6		
	HEMBB1001530	4.15	3.51	6.57	9.43	12.39	7.05		
30	HEMBB1001531	1.11	1.34	4.62	2.99	5.16	4.17		
	HEMBB1001532	0.63	1.86	2.77	1.86	4.41	2.15		
	HEMBB1001535	1.99	2.01	4.22	3.34	4.32	5.75		
	HEMBB1001536	2.18	2.65	6.37	4.62	6.87	5.45		
	HEMBB1001537	1.31	2.24	3.7	3.21	6.12	2.75		
35	HEMBB1001542	4.39	4.72	6.28	5.26	7.83	5.7		
	HEMBB1001543	7.84	3.58	8.49	8.13	7.08	5.38		
	HEMBB1001547	2.02	2.25	2.65	4.2	4.27	2.79	*	+
	HEMBB1001548	2.53	2.62	11.82	17.73	29.92	23.34	*	+
	HEMBB1001551	0.89	1.7	4.47	2.93	5.96	2.65		
40	HEMBB1001555	2.13	2.79	4.78	3.73	5.8	4.64		
	HEMBB1001562	1.9	2.64	4.27	2.23	3.46	3		
	HEMBB1001564	132.08	140.08	310.28	333.18	233.12	279.03		
	HEMBB1001565	1.72	1.97	3.9	3.77	4.68	2.07		
	HEMBB1001569	0.79	0.8	3.04	2.49	3.68	1.44		
45	HEMBB1001573	1.9	1.04	3.58	4.18	5.53	4.12	*	+
	HEMBB1001585	1.5	1.96	10.91	3.75	7.14	4.87		
	HEMBB1001586	1.53	2.27	3.22	4.27	5.45	1.95		
	HEMBB1001588	1.33	2.9	5.74	4.72	6.32	5.06		
	HEMBB1001595	2.68	3.33	6.92	3.78	4.84	4.7		
50	HEMBB1001596	3.4	2.57	3.74	2.67	5.36	2.54		
	HEMBB1001599	1.45	1.57	3.21	3.07	3.47	2.06		
	HEMBB1001603	1.99	2.45	4.17	5.7	8.16	4.04		
	HEMBB1001606	1.35	2.28	2.42	2	2.39	1.53		
	HEMBB1001612	4.31	3.07	9.25	8.81	8.09	8.9		
55	HEMBB1001618	1.53	1.62	3.86	2.84	4.48	2.31		

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	HEMBB1001619	2.11	3.03	3.92	5.71	5.1	4.37	*	+
	HEMBB1001623	2.21	2.38	3.16	2.16	5.5	3.37		
	HEMBB1001625	3.73	3.04	4.33	2.93	4.81	3.79		
5	HEMBB1001630	1.31	2.36	3.54	1.84	4.3	1.23		
	HEMBB1001635	1.78	1.64	3.76	2.08	3.32	1.34		
	HEMBB1001637	1.76	1.14	3.98	2.09	4.4	3.58		
	HEMBB1001641	1.43	1.68	2.78	3.17	3.73	2		
10	HEMBB1001653	2.18	3.17	5.61	3.96	6.63	3.5		
	HEMBB1001665	1.08	2.17	2.04	2.5	4.43	0.88		
	HEMBB1001666	2.14	1.95	3.52	2.45	4.88	1.79		
	HEMBB1001667	2.37	2.25	3.26	2.94	5.13	3.17		
	HEMBB1001668	3.19	2.11	5.15	2.45	6.42	2.69		
15	HEMBB1001669	0.98	2.02	3.19	1.04	4.53	1.38		
	HEMBB1001670	4.02	4.82	6.88	10.7	9.71	8.65	*	+
	HEMBB1001673	1.48	2.97	3.61	3.51	4.52	4.43		
	HEMBB1001675	1.83	3.27	4.65	4.68	5.78	4.88		
	HEMBB1001679	2.52	2.34	5.06	2.19	3.87	1.88		
20	HEMBB1001684	2.13	1.55	3.89	5.17	6.77	5.05	*	+
	HEMBB1001685	3.41	1.61	4.43	2.91	6.24	2.49		
	HEMBB1001695	1.9	2.22	4.43	1.38	3.88	2.12		
	HEMBB1001703	1.25	2.3	5.74	3.58	3.79	4.1		
	HEMBB1001704	1.39	2.16	4.58	4.23	5.02	3.94		
25	HEMBB1001706	2.76	2.6	3.58	5.6	6.26	4.87	**	+
	HEMBB1001707	1.35	2.01	2.87	2.25	3.67	2.8		
	HEMBB1001717	1.68	2.21	3.23	2.61	3.34	2.83		
	HEMBB1001731	13.81	13.48	24.03	11.02	23.09	25		
30	HEMBB1001734	3.47	3.35	7.62	6.88	9.22	4.18		
	HEMBB1001735	1.35	1.4	3.4	1.58	3.52	2.03		
	HEMBB1001736	5.01	6.14	7.87	7.15	10.91	8.11		
	HEMBB1001747	0.92	1	3.23	1.87	3.67	2.82		
	HEMBB1001749	4.71	2.99	9.39	7.29	5.99	8.16		
35	HEMBB1001753	3.79	3.3	5.5	7.4	8.97	9.3	**	+
	HEMBB1001756	0.53	2.05	1.89	2.31	3.91	2.73		
	HEMBB1001757	1.08	1.8	2.64	3.04	4.86	4.54	*	+
	HEMBB1001760	1.32	0.98	3.74	1.49	3.56	2.13		
	HEMBB1001762	0.9	0.61	2.62	1.57	2.95	2.07		
40	HEMBB1001780	9.82	12.28	11.34	16.64	26.06	22.06	*	+
	HEMBB1001785	0.89	1.24	1.02	0.62	2.88	1.64		
	HEMBB1001788	3.22	1.26	5.17	5.76	6.13	5.3		
	HEMBB1001793	5.6	4.73	18.12	22.08	20.38	22.86	*	+
	HEMBB1001797	1.61	1.82	2.28	2.94	4.97	5.54	*	+
45	HEMBB1001802	13.28	9.91	67.77	85.35	82.8	81.27	*	+
	HEMBB1001812	2.32	2.58	6.49	7.68	8.28	9.74	*	+
	HEMBB1001815	128.22	114.78	102.97	87.37	89.21	62.14	*	-
	HEMBB1001816	1.95	2.19	3.97	3.73	6.31	5.73		
	HEMBB1001831	0.69	0.98	1.54	0.72	3.28	1.16		
50	HEMBB1001834	16.15	9.68	133.91	102.49	173.48	141.04		
	HEMBB1001836	4.07	1.99	11.4	5.89	6.97	6.7		
	HEMBB1001839	0.89	0.86	1.43	1.08	1.95	1.21		
	HEMBB1001841	80.32	59.68	120.73	35.74	39.04	23.13	*	-
	HEMBB1001844	5.26	4.72	9.73	10.15	10.68	8.11		
55	HEMBB1001847	6.93	4.24	8.6	9.06	14.77	10.3		

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	HEMBB1001848	25.33	21.68	40.92	49.73	73.94	62.17	*	+
	HEMBB1001850	3.07	2.93	5.25	3.75	7.19	3.95		
	HEMBB1001859	13.4	8.82	20.85	39.61	27.01	40.75	*	+
5	HEMBB1001863	1.7	3.65	7.66	6.89	8.88	7.5		
	HEMBB1001867	1.69	1.93	3.16	3.16	4.14	3		
	HEMBB1001868	2.15	1.53	2.56	1.31	3.57	1.28		
	HEMBB1001869	1.5	2.3	4.23	4.62	8.15	3.58		
10	HEMBB1001872	1.21	0.79	2.23	1.77	4.17	1.75		
	HEMBB1001874	1.92	1.2	2.07	2.58	2.47	3.03	*	+
	HEMBB1001875	0.83	1.96	1.7	2.05	3.53	1.37		
	HEMBB1001880	2.68	2.17	6.79	4.41	8.91	8.35		
	HEMBB1001899	0.6	1.62	2.15	2.26	4.68	1.91		
15	HEMBB1001903	5.56	5.68	9.61	6.06	6.65	6.7		
	HEMBB1001905	2.04	2.82	5.49	4.98	6.07	7.14		
	HEMBB1001906	0.67	1.65	2.64	2.22	5.14	2.62		
	HEMBB1001908	1.82	1.63	5.26	3.31	6.56	3.59		
	HEMBB1001910	1.92	1.16	2.64	3.2	4.41	4.61	*	+
20	HEMBB1001911	2.06	1.11	4.2	5.73	4.81	4.33		
	HEMBB1001915	2.53	3.01	5.61	7.13	7.84	9.4	*	+
	HEMBB1001921	2.19	2.21	7.12	6.56	8.47	8.25		
	HEMBB1001922	1.74	1.77	3.66	4.91	5.85	3.7		
	HEMBB1001925	1.48	2.24	4.57	3.07	4.73	3.39		
25	HEMBB1001930	0.46	0.94	1.67	0.91	3.18	1.01		
	HEMBB1001944	1.72	1.88	5.45	4.83	4.6	4.49		
	HEMBB1001945	2.15	1.05	3.58	2.25	3.97	2.12		
	HEMBB1001947	2.28	1.13	3.23	5.35	5.98	3.15		
30	HEMBB1001950	3.49	1.95	5.38	5.15	5.46	3.3		
	HEMBB1001952	1.41	2.05	4.72	2.31	4.73	3.1		
	HEMBB1001953	1.62	2.09	3.45	3.63	5.78	3.75		
	HEMBB1001957	1.16	2.02	4.28	2.68	4.19	2.19		
	HEMBB1001959	2.05	3.31	4.07	4.22	5.75	3.68		
35	HEMBB1001962	5.54	2.61	5.11	3.34	6.28	2.54		
	HEMBB1001967	2.59	2.46	5.62	6.11	8.49	6.15		
	HEMBB1001973	2.25	2.4	6.14	7.62	10	7.28	*	+
	HEMBB1001978	2.08	1.71	6.29	7.2	7.57	5.83		
	HEMBB1001983	9.23	8.69	24.64	38.93	34.91	36.79	*	+
40	HEMBB1001987	1.78	2.34	3.64	1.66	4.75	2.38		
	HEMBB1001988	2.02	1.92	3.42	2.92	5.17	1.85		
	HEMBB1001990	7.65	7.72	9.18	12.44	11.53	15.42	*	+
	HEMBB1001996	1.54	1.47	3.89	1.61	3.51	1.22		
	HEMBB1001997	1.46	2.25	6.1	4.2	5.98	4.23		
45	HEMBB1001999	10.91	11.08	16.84	24.47	26.58	22.28	**	+
	HEMBB1002002	1.08	1.58	3.52	1.91	2.76	2.39		
	HEMBB1002005	1.88	2.91	4.8	4.82	7.6	4.22		
	HEMBB1002009	2.32	2.48	3.03	2.24	6.23	2.7		
	HEMBB1002013	0.96	2.07	3.78	1.95	4.26	1.41		
50	HEMBB1002015	3.95	4.25	9.47	5.82	8.92	6.73		
	HEMBB1002024	45.16	34.47	111.32	113.31	106.76	120.55		
	HEMBB1002035	2.15	1.91	2.87	2.11	4.5	2.68		
	HEMBB1002039	1.18	2.29	5.1	3.28	5.9	2.98		
	HEMBB1002041	3.31	4.13	8.49	15.49	14.42	13.38	**	+
55	HEMBB1002042	3.97	4.66	9.49	8.09	10.63	9.94		

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	HEMBB1002043	1.34	2.21	4.61	5.97	5.24	3.36	
	HEMBB1002044	0.4	1.19	2.68	1.25	4.19	1.92	
	HEMBB1002045	2.83	2.5	10.03	6.34	7.63	4.56	
5	HEMBB1002049	1.31	1.4	3.77	1.71	4.36	1.73	
	HEMBB1002050	1.62	1.61	4.5	3.31	4.53	2.94	
	HEMBB1002051	1.17	1.13	2.9	2.59	5.05	4.37	
	HEMBB1002068	1.69	2.44	2.43	2.3	4.42	2.07	
10	HEMBB1002069	3.39	3.94	7.83	6.86	7.55	5	
	HEMBB1002075	0.72	1.94	3.33	2.99	3.52	2.37	
	HEMBB1002079	1.2	1.8	1.89	1.22	2.84	1.3	
	HEMBB1002080	1.74	1.85	4.78	1.55	6.02	2.41	
	HEMBB1002082	1.03	1.85	4.59	2.38	4.38	1.96	
15	HEMBB1002084	25.86	22.68	51.44	33.52	35.54	38.37	
	HEMBB1002088	13.92	15.78	22.14	29.46	37.25	35.66	** +
	HEMBB1002092	2.51	2.24	4.48	5.34	3.65	6.27	
	HEMBB1002094	3.21	2.62	8.2	5.72	7.27	6.04	
	HEMBB1002103	2.42	2.97	3.51	3.74	5.58	4.47	
20	HEMBB1002109	4.27	3.47	4.84	5.72	7.83	6.36	* +
	HEMBB1002115	42.37	37.4	91.88	95.86	101.94	101.65	
	HEMBB1002120	0.89	1.22	2.91	0.86	2.94	2.41	
	HEMBB1002121	0.75	1.56	1.63	1.5	4.66	2.53	
25	HEMBB1002134	11.99	11.22	112.59	98.93	166.1	133.77	
	HEMBB1002136	1.29	1.65	2.9	2.59	3.26	2.58	
	HEMBB1002138	10.48	9.64	20.72	18.78	23.06	19.4	
	HEMBB1002139	1.84	1.6	5.46	4.69	6	5.84	
	HEMBB1002141	1.53	0.83	3.44	1.48	4.64	2.54	
30	HEMBB1002142	1.85	2	4.95	3.22	5.98	6.03	
	HEMBB1002145	1.62	0.83	2.96	1.49	3.07	2.42	
	HEMBB1002152	1.27	1.19	3.15	2.32	6.36	3.41	
	HEMBB1002162	1.25	1.55	3.92	3.42	5.14	3.61	
	HEMBB1002173	4.18	1.09	5.58	2.77	4.48	3.84	
35	HEMBB1002189	2.78	1.95	6.14	7.01	8.25	5.93	
	HEMBB1002190	1.81	2.2	6.36	8.01	6.93	8.36	* +
	HEMBB1002193	1.84	1.06	2.06	4.53	4.37	5.48	** +
	HEMBB1002217	3.82	2.26	6.02	3.61	6.06	3.23	
	HEMBB1002218	3.91	3.3	7.58	4.94	6.15	5.68	
40	HEMBB1002228	2.28	2.9	6.17	6.68	7.94	6.97	
	HEMBB1002232	1.15	1.4	2.24	2.14	5.79	3.03	
	HEMBB1002245	0.86	0.84	2.34	1.53	2.47	1.05	
	HEMBB1002247	1.72	0.59	2.44	1.38	2.24	1.03	
	HEMBB1002249	2.65	1.64	3.1	3.39	4.08	4.01	* +
45	HEMBB1002254	1.35	1.35	3.83	2.64	3.27	2.86	
	HEMBB1002255	0.99	1.37	2.6	1.19	2.93	1.4	
	HEMBB1002266	1.33	0.83	2.07	0.73	1.99	0.54	
	HEMBB1002271	14.89	9.5	29.42	32.9	41.53	37.28	* +
50	HEMBB1002280	1.62	0.78	1.6	1.55	2.93	1.12	
	HEMBB1002296	11.83	12.31	18.29	31.87	21.06	23.09	* +
	HEMBB1002300	0.78	2.31	3.48	1.49	4.63	3.12	
	HEMBB1002302	1.17	2.17	3.26	2.49	4.76	3.04	
	HEMBB1002306	1.83	1.96	4.28	2.91	4.34	2.6	
55	HEMBB1002316	0.66	1.38	2.36	1.19	2.9	0.97	
	HEMBB1002326	0.93	1.68	4.52	4.35	4.41	3.9	

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	HEMBB1002327	0.99	0.99	2.66	1.46	2.95	2.06		
	HEMBB1002329	2.89	3	3.81	6.39	5.88	5.53	**	+
	HEMBB1002340	0.6	1.8	2.05	2.29	3.38	2.22		
5	HEMBB1002342	8.12	9.23	14.09	21.68	18.15	18.03	*	+
	HEMBB1002358	1.09	3.22	6.37	6.52	7.91	9.2		
	HEMBB1002359	1.09	2.55	4.29	4.66	5.4	3.54		
	HEMBB1002364	1.28	1.82	2.33	3.17	5.15	3.11		
10	HEMBB1002366	13.63	21.17	32.35	56.28	57.48	53.09	**	+
	HEMBB1002371	0.83	0.63	1.72	2.32	2.82	2.1	*	+
	HEMBB1002381	0.97	1.16	1.74	2.83	3.16	6.26		
	HEMBB1002383	1.07	3.17	4.18	3.1	4.5	4.37		
	HEMBB1002387	0.98	2.36	2.68	2.09	3.68	2.96		
15	HEMBB1002409	6.85	7.27	46.98	69.94	70.04	64.2	*	+
	HEMBB1002413	3.92	2.99	8.34	9.46	8.16	10.16		
	HEMBB1002415	0.84	1.28	2.79	2.36	3.49	2.11		
	HEMBB1002424	1.04	1.17	1.63	2.89	3.04	2.66	**	+
	HEMBB1002425	1.12	1.69	5.86	6.46	10.1	5.26		
20	HEMBB1002427	1.5	1.59	2.32	3.72	7.82	3.65		
	HEMBB1002442	2.29	1.57	4.33	4.99	8.58	8.89	*	+
	HEMBB1002447	2.61	2.7	5.56	6.1	6.6	5.63		
	HEMBB1002453	2.5	2.48	6.56	6.31	7.55	5.25		
	HEMBB1002457	1.54	2.08	4.77	3.69	4.61	4.8		
25	HEMBB1002458	0.48	1.53	2.5	2.2	2.35	1.66		
	HEMBB1002463	1.36	1.84	6.55	6.24	6.11	8.87		
	HEMBB1002465	1.12	1.18	2.4	2.86	2.25	1.59		
	HEMBB1002477	0.71	0.66	4.43	3	4.39	4.86		
30	HEMBB1002479	22.08	21.58	27.54	16.12	19.41	17.27	*	-
	HEMBB1002489	0.86	3.02	3.9	5.73	5.51	7.68	*	+
	HEMBB1002492	1.27	1.23	3.07	3.53	4.08	3.39	*	+
	HEMBB1002495	1.85	1.85	3.2	2.61	5.02	3.98		
	HEMBB1002502	0.94	2.52	2.81	1.77	4.83	3.27		
35	HEMBB1002509	0.73	1.8	2.65	2.03	2.43	1.27		
	HEMBB1002510	0.49	1.68	3.06	1.78	2.5	0.81		
	HEMBB1002520	1.46	2.47	5.44	6.62	7.57	8.61	*	+
	HEMBB1002522	0.82	1.88	4.42	2.31	6.8	2.07		
	HEMBB1002527	11.47	13.79	12.46	24.19	10.37	17.52		
40	HEMBB1002530	1.43	2.15	3.44	2.93	4.92	2.26		
	HEMBB1002531	0.46	1.32	2.04	1.23	2.99	0.35		
	HEMBB1002534	1.35	2.27	2.73	4.54	4.08	3.92	**	+
	HEMBB1002536	6.58	5.93	46.38	45.93	63.71	42.88		
	HEMBB1002544	3.91	3.45	6.89	6.79	7.87	7.99		
45	HEMBB1002545	0.92	2.76	2.83	3.21	4.15	4.29		
	HEMBB1002550	1.32	1.69	1.86	2.99	4.68	2.42		
	HEMBB1002556	2.9	3.54	9.69	8.73	8.12	10.62		
	HEMBB1002571	17.25	14.03	19.8	21.91	16.59	24.61		
	HEMBB1002579	3.32	2.05	4.87	4.38	6.6	6.39		
50	HEMBB1002582	1.79	2.11	5.59	5.77	6.47	5.63		
	HEMBB1002584	2.82	1.94	6.09	3.94	4.67	3.62		
	HEMBB1002587	6.39	5.82	10.63	11.3	9.04	9.94		
	HEMBB1002590	1.6	3.07	7.46	5.86	7.3	5.84		
	HEMBB1002596	1.5	2.01	3.17	5.59	4.94	4.21	*	+
55	HEMBB1002600	1.55	2.72	3.81	5.02	7.18	3.93		

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	HEMBB1002601	1.28	2.23	3.9	2.51	5.59	2.99		
	HEMBB1002603	2.37	1.64	5.48	3.53	6.59	5.6		
	HEMBB1002607	1.48	1.15	4.34	2.59	4.26	2.99		
5	HEMBB1002610	1.2	0.96	3.48	1.95	3.79	3.45		
	HEMBB1002613	0.96	2.41	4.31	3.98	5.39	3.72		
	HEMBB1002614	3.18	3.34	5.35	3.87	6.08	9.76		
	HEMBB1002615	1.47	3.29	4.63	2.45	3.83	2.67		
10	HEMBB1002617	0.67	3.09	2.88	2.1	3.34	3.4		
	HEMBB1002623	2.31	3.63	4.36	3.96	6.28	5.91		
	HEMBB1002624	2.7	1.56	7.52	7.96	8.72	8.3		
	HEMBB1002631	1.65	2	4.28	2.14	3.72	1.74		
	HEMBB1002635	1.84	1.74	3.55	3.31	3.64	3.56		
15	HEMBB1002644	7.22	9.04	15.98	18.52	23.94	22.55	*	+
	HEMBB1002654	5.22	4.21	7.77	7.92	7.33	11.74		
	HEMBB1002661	1.93	2.16	3.96	1.99	4.13	5.33		
	HEMBB1002663	1.59	1.8	3.85	5.45	5.58	5.17	*	+
	HEMBB1002664	1.28	2.4	4.43	5.05	9.22	6.76	*	+
20	HEMBB1002677	1.88	1.83	1.86	1.81	4.79	2.34		
	HEMBB1002683	2.68	2.21	9.21	5.67	5.9	8.45		
	HEMBB1002684	1.71	0.81	2.53	1.92	2.74	2.63		
	HEMBB1002686	1.23	1.39	2.88	1.45	3.37	1.64		
	HEMBB1002692	0.99	1.4	1.87	2.5	2.53	2.98	*	+
25	HEMBB1002693	1.75	1.75	4.12	5.03	5.74	3.46		
	HEMBB1002697	1.09	2.8	2.73	4.17	5.58	5.34	*	+
	HEMBB1002699	1.59	2.27	4.93	4.72	6.74	6.97		
	HEMBB1002702	1.63	1.5	2.54	1.76	3.25	3.33		
30	HEMBB1002705	4.2	2.84	6.79	8.83	8.26	7.92	*	+
	HEMBB1002712	8.55	1.32	2.38	2.92	4.06	1.4		
	IMR321000028	1.03	1.71	2.88	1.63	2.76	1.63		
	IMR321000031	1.71	2.59	3.51	5.86	4.35	5.31	*	+
	IMR321000034	21.95	15.41	30.37	33.73	19.59	34.65		
35	IMR321000039	5.81	7.11	14.41	14.72	15.71	13.99		
	IMR321000044	0.81	2.37	1.44	1.01	3.26	2.06		
	IMR321000063	79.52	80.12	127.61	224.23	199.69	128.8		
	IMR321000085	21.02	18.07	26.38	30.28	48.13	47.89	*	+
	IMR321000089	1.51	1.42	3.86	3	6.7	5.84		
40	IMR321000091	4.79	2.91	6.5	8.35	11.38	8.55	*	+
	LIVER1000004	8.04	9.67	34.15	55.9	56.53	48.86	*	+
	LIVER1000008	1.13	1.36	3.06	1.68	4	2.17		
	LIVER1000011	3.03	5.9	26.65	37.8	54.37	45.77	*	+
	LIVER1000022	2.75	3.66	7.75	9.39	9.82	9.17	*	+
45	LIVER1000025	1.78	2.77	5.47	9.83	10.83	7.7	*	+
	LIVER1000030	1.05	0.96	2.12	2.04	2.56	1.23		
	LIVER1000045	1.33	1.37	3.11	5.11	5.12	5.89	**	+
	LIVER1000046	1.01	1.53	3.86	4.14	7.82	5.34		
	LIVER1000072	1.61	1.26	5.23	12.42	9.54	12.21	**	+
50	LIVER1000077	0.33	1.79	1.97	1.87	2.84	3.14		
	LIVER1000080	1.53	3	5.81	5.96	4.24	5.41		
	LIVER1000086	6.38	7.69	47.4	69.84	79.87	70.57	*	+
	LIVER1000092	1.6	1.46	3.09	3.85	3.83	2.41		
55	LIVER1000095	0.91	2.31	2.56	2.16	2.46	1.55		
	LIVER1000097	1.26	0.74	2.49	2.18	2.84	2.25		

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	LIVER1000098	0.43	1.37	2.57	2.76	3.95	2.29	
	LIVER1000100	3.3	2.82	5.82	4.99	7.44	3.74	
	LIVER1000101	0.36	1.81	2.4	1.69	4.25	2.74	
5	LIVER1000106	0.83	1.95	1.79	0.97	2.8	1.29	
	LIVER1000108	1.36	2.93	4.31	4.35	4.12	3.43	
	LIVER1000115	1.12	1.57	4.32	6.38	6.13	6.9	* +
	LIVER1000120	1.45	0.95	2.23	1.39	1.46	0.73	
10	LIVER1000138	0.6	1.27	1.86	2.11	2.36	1.6	
	LIVER1000146	1.38	2.69	6.24	7.17	7.01	7.02	
	LIVER1000148	0.88	1.24	2.65	1.68	5.68	3.51	
	LIVER1000157	30.11	26.71	67.66	123.41	85.61	124.96	* +
	LIVER1000161	1.3	1.59	2.3	1.73	3.37	1.84	
15	LIVER1000167	3.07	3.63	14.08	20.36	22.31	21.82	* +
	LIVER1000174	1.53	1.68	1.84	2.1	3.43	1.29	
	LIVER1000185	2.42	2.55	5.16	4.37	4.72	4.23	
	LIVER1000187	0.96	1.55	4.84	6.64	4.17	3.5	
	LIVER1000190	3.77	3.48	5.95	4.71	6.24	4.47	
20	LIVER1000192	2.37	2.92	3.93	4.1	5.23	4.04	
	MAMMA1000009	1.39	2.55	5.12	3.62	4.72	3.46	
	MAMMA1000015	1.72	1.59	4.78	5.23	4.42	6.42	
	MAMMA1000019	0.69	2.48	3.4	4.27	4.81	3.1	
	MAMMA1000020	2.79	2.35	5.63	6	7.86	5.75	
25	MAMMA1000024	0.65	1.76	3.79	2.42	2.91	1.61	
	MAMMA1000025	1.92	2.56	6.92	4.96	6.72	5.6	
	MAMMA1000043	1.06	2.36	6.43	6.93	8.22	6.6	
	MAMMA1000045	1.38	2.01	4.84	2.68	3.96	2.89	
30	MAMMA1000046	1.74	2.44	3.18	2.88	4.5	2.37	
	MAMMA1000055	8.51	8.71	9.57	9.38	10.74	9.36	
	MAMMA1000057	4.4	3.29	7.56	8.38	9.78	8.16	
	MAMMA1000060	26.78	24.33	45.25	48.69	33.84	48.6	
	MAMMA1000069	2.13	1.65	4.1	3.43	3.14	2.41	
35	MAMMA1000084	2.88	3	5.81	5.64	8.15	7.51	
	MAMMA1000085	2.75	3.74	7.02	6.45	5.82	6.97	
	MAMMA1000092	1.45	2.97	3.8	4.64	5.15	4.55	* +
	MAMMA1000096	4.45	4.96	9.29	8.15	9.11	6.09	
	MAMMA1000097	2.4	2.96	3.86	5.93	6.01	6.97	** +
40	MAMMA1000102	1.94	1.59	4.27	4.25	6.16	4.44	
	MAMMA1000103	1.52	1.65	5	2.39	4.56	2.83	
	MAMMA1000106	1.25	2.15	5.1	2.3	4.48	3.27	
	MAMMA1000117	1.19	2.12	3.72	1.84	3.32	2.77	
45	MAMMA1000118	1.03	2.06	3.08	3.38	3.21	4.56	
	MAMMA1000129	1.06	2.1	2.97	1.73	2.7	1.31	
	MAMMA1000133	1.09	1.96	3.67	2.8	3.87	2.02	
	MAMMA1000134	1.23	2.08	4.28	2.27	4.61	1.93	
	MAMMA1000139	1.45	1.91	2.69	2.13	3.98	1.85	
50	MAMMA1000141	1.97	2.27	5.47	3.67	3.61	3.42	
	MAMMA1000143	1.66	1.1	2.55	3.83	3.52	1.74	
	MAMMA1000150	4.11	4.95	8.99	6.49	6.4	8.66	
	MAMMA1000155	1.87	2.71	4.35	5.46	5.69	6.41	* +
	MAMMA1000163	1.65	2.82	2.62	3.45	4.54	4.97	* +
55	MAMMA1000171	1.96	2.43	5.53	4.12	6.52	4.97	
	MAMMA1000173	3.5	5.27	10.33	17.47	17.44	18.26	** +

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	MAMMA1000175	1.58	1.8	2.89	4.06	5.14	3.7	*	+
	MAMMA1000183	1.14	2.12	5.29	3.92	4.7	4.91		
	MAMMA1000191	3.25	3.34	14.68	12.56	14.7	18.23		
5	MAMMA1000192	5.76	8.53	9.67	16.66	19.91	17.65	**	+
	MAMMA1000193	1.68	1.54	0.86	1.33	2.25	1.94		
	MAMMA1000198	1.88	1.99	5.53	4.44	6.49	5.57		
	MAMMA1000204	1.75	2.25	3.39	3.56	4.13	2.85		
10	MAMMA1000207	1	3.2	3.41	2.86	4.96	3.47		
	MAMMA1000214	1.76	2.08	3.68	2.84	4.42	4.74		
	MAMMA1000220	6.19	6.12	11.51	12.49	18.06	16.72	*	+
	MAMMA1000221	0.57	1.04	1.68	1.14	4.51	0.87		
	MAMMA1000226	0.48	1.06	2.07	1.49	3.19	1.88		
15	MAMMA1000227	0.93	1.23	1.6	2.73	3.67	3.46	**	+
	MAMMA1000230	1	1.23	1.77	2.38	3.04	2.94	**	+
	MAMMA1000241	2.9	2.2	4.19	7.24	5.8	7.61	**	+
	MAMMA1000245	76.63	70.15	118.95	141.45	166.09	104.88		
	MAMMA1000248	6.79	4.17	13.48	13.18	13.44	18.8		
20	MAMMA1000251	1.68	1.72	4.7	5.55	5.39	5.29		
	MAMMA1000254	1.24	1.22	3.59	2.14	5.61	5.02		
	MAMMA1000257	5.39	2.62	25.06	32.2	43.78	35.79	*	+
	MAMMA1000262	15.48	9.75	18.2	40.81	33.23	34.89	**	+
	MAMMA1000264	0.99	1.2	2.3	4.43	2.57	3.4	*	+
25	MAMMA1000266	1.25	0.79	2.73	4.21	5.33	4.03	*	+
	MAMMA1000270	2.43	1.94	4.57	6.16	7.16	7.58	*	+
	MAMMA1000271	6.01	3.26	8.54	8.94	6.17	8.1		
	MAMMA1000277	0.89	0.93	2.56	2.46	2.75	2.09		
30	MAMMA1000278	1.84	2.01	4.29	2.18	5.06	3.51		
	MAMMA1000279	1.82	1.74	4.33	3.51	5.72	4.35		
	MAMMA1000283	0.99	1.51	2.36	1.37	2.66	2.71		
	MAMMA1000284	2.65	2.51	8.31	6.28	8.49	8.01		
	MAMMA1000287	1.58	2.13	6.27	5.55	6.94	7.1		
35	MAMMA1000294	4.72	5.45	9.44	3.84	8.21	4.74		
	MAMMA1000298	0.87	1.36	2.51	1.55	3.1	0.95		
	MAMMA1000302	0.9	1.18	4.73	2.22	4.9	2.56		
	MAMMA1000303	0.92	1.62	2.63	4.16	4.06	3.22	*	+
	MAMMA1000305	1.07	1.28	2.73	2.47	2.74	2.1		
40	MAMMA1000307	2.29	3.03	9.61	15.85	14.04	14.38	*	+
	MAMMA1000309	0.57	1.61	3.69	4.6	3.65	4.61		
	MAMMA1000312	3.55	4.99	8.08	6.19	5.18	6.55		
	MAMMA1000313	1.06	2.31	2.34	1.79	3.98	3.43		
	MAMMA1000331	1.08	1.65	3	3.33	6.01	3.21		
45	MAMMA1000335	7.38	9.1	14.27	19.49	16.28	16.92	*	+
	MAMMA1000339	0.33	0.39	2.17	1.46	2.09	0.66		
	MAMMA1000340	1.43	1.33	4.12	4.37	2.72	2.15		
	MAMMA1000348	1.2	1.27	4.6	3.14	4.82	6.11		
	MAMMA1000356	1.93	2.21	4.93	3.08	5.42	6.29		
50	MAMMA1000358	2.93	3.97	5.02	7.42	7.47	4.9		
	MAMMA1000360	1.41	1.92	4.6	3.76	5.2	4.63		
	MAMMA1000361	2.2	3.45	8.9	8.94	10.67	8.93		
	MAMMA1000363	1.09	1.69	3.86	1.87	4.37	4.1		
55	MAMMA1000370	0.92	0.71	1.76	2.02	2.62	2.57	*	+
	MAMMA1000371	2.09	1.73	6.35	10.02	12.1	10.1	*	+

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	MAMMA1000372	4.45	4.1	12.88	12.01	12.92	11.97		
	MAMMA1000385	1.79	2.36	6.41	6.41	7.66	8.72		
	MAMMA1000388	1.93	3.02	6.03	4.7	4.53	5.06		
5	MAMMA1000395	1.3	2.46	3.12	1.69	3.49	0.8		
	MAMMA1000402	1.69	1.68	5.62	3.33	4.35	4.63		
	MAMMA1000403	1.7	2.36	5.05	5.45	5.81	3.96		
	MAMMA1000410	0.87	1.25	2.71	3.23	3.35	3.25	*	+
	MAMMA1000413	1.52	0.47	2.48	3.51	3.76	3.61	*	+
10	MAMMA1000414	1.08	1.53	3.03	2.94	4.91	1.81		
	MAMMA1000416	3.3	4.01	10.2	15.8	23.14	20.47	*	+
	MAMMA1000421	2.61	2.83	6.11	7.7	7.42	7.09	*	+
	MAMMA1000422	2.83	2.53	7.46	9.18	6.64	12.05		
15	MAMMA1000423	1.7	1.26	6	5.9	6.62	5.89		
	MAMMA1000424	0.88	1.7	3.17	1.91	2.38	1.07		
	MAMMA1000429	8.73	10.07	13.78	14.98	16.3	11.17		
	MAMMA1000431	1.6	1.27	4.27	5.22	6.32	4.26		
	MAMMA1000432	1.05	2.33	2.85	2.63	2.82	1.41		
20	MAMMA1000437	4.61	4.75	8.44	10.54	11.52	8.12		
	MAMMA1000444	2.53	4.15	8.55	7.55	10.17	10.13		
	MAMMA1000446	1.19	2.07	3.87	2.03	3.63	2.49		
	MAMMA1000449	1.77	1.59	3.54	3.37	4.31	3.22		
	MAMMA1000457	4.44	4.82	7.12	7.2	6.88	6.22		
25	MAMMA1000458	1.27	2.22	4.83	2.52	4.03	1.94		
	MAMMA1000468	0.55	1.12	2.2	0.51	2.25	1.16		
	MAMMA1000472	1.15	2.3	4.42	4.77	6.36	5.79	*	+
	MAMMA1000473	1.95	1.72	3.59	3.45	5.46	3.17		
	MAMMA1000477	3.86	3.29	5.67	8.71	9.92	7.97	**	+
30	MAMMA1000478	2.85	3.26	7.41	5.76	9.1	7.57		
	MAMMA1000483	4.16	3.16	8.3	8.09	6.5	8.63		
	MAMMA1000490	1.65	2.61	3.68	2.66	4.96	2.14		
	MAMMA1000496	1.18	1.7	3.44	1.3	3.79	2.01		
	MAMMA1000500	0.68	1.79	3.22	1.41	3.2	2.86		
35	MAMMA1000501	3.04	3.89	7.86	13.71	15.02	12.51	**	+
	MAMMA1000503	0.84	2.08	2.21	3.52	3.52	2.27		
	MAMMA1000506	10.14	8.79	32.66	34.77	26.7	18.31		
	MAMMA1000510	3.24	3.5	4.59	10.97	10.76	13.61	**	+
	MAMMA1000515	2.12	1.54	4.56	5.97	7.55	6.2	*	+
40	MAMMA1000516	2.18	2.4	6.29	3.89	3.85	5.07		
	MAMMA1000522	1.04	1.47	4.39	2.4	3.68	1.85		
	MAMMA1000524	2.04	2.09	3.53	3.82	6.18	3.96		
	MAMMA1000528	3.74	2.72	2.05	2.7	4.09	2.88		
45	MAMMA1000534	0.91	2.35	2.11	1.86	2.91	2.04		
	MAMMA1000541	2.85	3.16	11.29	11.22	8.81	12.04		
	MAMMA1000550	1.21	2.73	1.86	2.46	6.65	4.64		
	MAMMA1000556	1.78	1.32	4.25	2.66	3.37	1.4		
	MAMMA1000559	1.32	1.49	5.56	2.92	4.2	3.46		
50	MAMMA1000565	1.82	2.74	3.93	2.13	4.18	4.22		
	MAMMA1000567	0.99	2.16	3.77	2.3	4.07	3.64		
	MAMMA1000576	3.72	3.12	13.12	10.45	9.76	10.02		
	MAMMA1000582	2.07	2.7	5.64	4.13	4.81	6.31		
	MAMMA1000583	1.16	2.33	2.45	2.19	4.47	2.93		
55	MAMMA1000585	1.66	2.04	4.19	3.82	5.38	3.23		

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	MAMMA1000587	1.64	1.51	3.73	3.12	5.07	3.49		
	MAMMA1000591	0.96	1.34	3.11	1.45	3.74	1.72		
	MAMMA1000594	2.3	1.76	4.92	3.55	7.68	5.16		
5	MAMMA1000597	4.42	3.09	9.64	9.46	9.63	10.35		
	MAMMA1000605	2.84	3.94	11.44	18.34	15.85	17.89	*	+
	MAMMA1000612	1.91	2.15	5.22	3.85	4.33	4.95		
	MAMMA1000614	3.11	2.71	9.4	7.48	6.07	6.34		
10	MAMMA1000616	1.66	1.79	2.44	2.1	5.09	3.45		
	MAMMA1000621	1.39	1.67	3.36	3.15	6.31	7.02		
	MAMMA1000623	1.08	1.04	3.83	0.92	2.66	2.3		
	MAMMA1000625	7.39	6.32	23.76	19.68	25.39	29.8		
	MAMMA1000635	0.89	0.68	1.61	0.76	1.75	0.64		
15	MAMMA1000643	1.47	1.11	1.94	4.21	3.77	6.82	*	+
	MAMMA1000646	4.68	3.61	9.55	17.22	16.4	16.44	**	+
	MAMMA1000652	1.98	1.61	3.56	4.21	5.34	5.24	*	+
	MAMMA1000657	2.28	1.78	4.51	2.18	4.48	3.26		
	MAMMA1000664	1.78	1.49	5.35	2.9	6.43	6.85		
20	MAMMA1000667	1.24	1.68	2.17	1.96	5.64	2.41		
	MAMMA1000668	0.71	1.11	3.23	2.44	3.76	1.74		
	MAMMA1000669	0.76	0.97	2.01	0.9	3.94	2.06		
	MAMMA1000670	3.27	2.78	4.47	10.4	6.73	9.28	*	+
	MAMMA1000672	1.71	3.23	6.88	5.43	5.63	6.03		
25	MAMMA1000681	0.98	1.19	2.53	1.98	3.73	2.45		
	MAMMA1000684	6.87	11.61	18.54	30.76	32.53	30.62	**	+
	MAMMA1000696	1.64	3.39	4.99	7.89	14.39	8.69	*	+
	MAMMA1000702	3.12	3.07	5.9	7.47	10.05	7.55	*	+
	MAMMA1000706	0.63	1.07	1.79	1.08	1.52	0.66		
30	MAMMA1000707	0.74	1.26	1.76	0.83	1.87	0.63		
	MAMMA1000713	1.53	2.14	5.33	5.43	5.8	6.96		
	MAMMA1000714	1.19	1.84	4.31	2.64	4.96	4.94		
	MAMMA1000718	1.32	2.79	4.84	5.53	7.12	4.37		
	MAMMA1000720	1.33	2.19	5.14	4.95	8.51	5.44		
35	MAMMA1000723	1.22	1.65	4.17	3.26	4.81	3.68		
	MAMMA1000731	1.24	1.17	3.11	3.04	4.99	3.26		
	MAMMA1000732	1.37	1.59	3.02	4.86	6.5	6.05	**	+
	MAMMA1000733	0.58	0.82	1.54	2.31	2.41	1.22		
40	MAMMA1000734	12.22	11.56	22.62	21.95	22.19	13.18		
	MAMMA1000736	4.26	4.34	11.96	4.92	5.77	6.14		
	MAMMA1000738	0.8	2.06	3.82	2.52	4.15	1.95		
	MAMMA1000744	1.12	2	5.52	3.27	3.97	4.67		
	MAMMA1000746	1	2.03	2.24	2.38	4.27	2.48		
45	MAMMA1000748	8.23	8.93	13.13	15.53	16.06	15.05	*	+
	MAMMA1000751	10.46	7.63	32.43	45.16	40.03	54.65	*	+
	MAMMA1000752	1.5	2.37	8.68	11.52	14.2	12.68	*	+
	MAMMA1000757	1.89	2.48	5.54	7.9	8.53	10.86	*	+
	MAMMA1000760	3	2.99	6.77	4.65	8.01	7.12		
50	MAMMA1000761	1.86	2.58	5.73	4.87	6.29	4.99		
	MAMMA1000775	1.37	1.83	4.43	3.23	4.29	2.64		
	MAMMA1000776	2.37	2.36	6.3	6.57	7	6.12		
	MAMMA1000778	2.14	2.28	5.19	4.95	3.99	3.84		
	MAMMA1000781	1.33	1.33	3.06	2.82	2.86	1.23		
55	MAMMA1000782	1.94	2.36	3.88	2.93	3.11	3.01		

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	MAMMA1000784	1.28	1.58	3.94	2.22	7.2	3.64		
	MAMMA1000788	3.05	4.31	4.38	4.16	5.12	2.21		
	MAMMA1000798	1.01	2.86	2.77	2.03	3.56	2.1		
5	MAMMA1000802	4.36	3.71	8.23	17.49	15.39	19.2	**	+
	MAMMA1000810	3.91	4.98	14.15	17.58	19.04	16.15	*	+
	MAMMA1000813	1.63	2.11	3.73	2.82	3.15	2.06		
	MAMMA1000814	2.56	2.97	7.82	7.28	7.26	6.61		
10	MAMMA1000824	12.58	11.27	34.16	62.44	72.28	50.62	*	+
	MAMMA1000827	1.83	2.04	5.05	3.3	4.77	4.31		
	MAMMA1000831	1.45	2.81	2.84	2.55	5.43	1.85		
	MAMMA1000838	6.85	9.27	7.86	13.01	8.43	14.52		
	MAMMA1000839	4.89	4.41	9	9.02	8.66	14.04		
15	MAMMA1000841	1.33	2.02	3.11	2.23	4.44	2.29		
	MAMMA1000842	2.48	1.88	3.59	3.03	3.74	1.82		
	MAMMA1000843	1.26	2.19	3.88	2.26	4.43	2.35		
	MAMMA1000845	0.83	1.01	2.4	2.35	3.88	1.24		
20	MAMMA1000851	1.3	3.42	5.35	7.83	5.9	6.65		
	MAMMA1000854	2.77	3.7	6.33	5.08	5.68	5.13		
	MAMMA1000855	0.37	2.97	2.62	2.51	3.74	1.78		
	MAMMA1000856	0.87	1.39	3.11	2.05	6.37	3.19		
	MAMMA1000859	9.88	8.56	20.5	19.52	18.47	24.31		
25	MAMMA1000862	1.13	1.55	3.53	1.17	3.18	0.79		
	MAMMA1000863	2.62	2.08	4.72	2.59	5.24	4.91		
	MAMMA1000865	0.35	0.82	2.48	0.4	1.84	0.35		
	MAMMA1000867	1.08	2.83	2.87	1.95	3.68	4.76		
	MAMMA1000875	0.89	2.72	2.34	3.31	3.57	2.59		
30	MAMMA1000876	1.23	1.64	4.59	2.4	3.37	3.22		
	MAMMA1000877	3.15	2.89	9.22	8.39	10.32	10.07		
	MAMMA1000878	3.05	3.61	8.94	6.33	8.52	9.62		
	MAMMA1000880	1.46	1.15	4.77	2.45	3.96	3.01		
	MAMMA1000881	1.81	2.09	4.52	3.77	6.07	4.73		
35	MAMMA1000883	0.57	0.79	2.1	1.37	2.14	2.11		
	MAMMA1000897	0.76	2.39	0.36	1.19	2.99	6.19		
	MAMMA1000898	1.06	1.99	1.75	1.41	2.49	3.7		
	MAMMA1000905	1.8	2.75	4.68	8.32	6.86	10.64	*	+
	MAMMA1000906	1.17	2.49	2.63	2.45	4.27	4.08		
40	MAMMA1000908	1.59	1.63	4.3	1.77	3.05	1.43		
	MAMMA1000911	4.97	6.25	8.37	21.77	20.01	20.98	**	+
	MAMMA1000914	1.14	0.85	2.41	1.1	2.23	1.61		
	MAMMA1000920	1.99	2.17	4.41	10.82	10.67	9.11	**	+
45	MAMMA1000921	1.03	1.02	2.41	3.47	3.84	3.17	*	+
	MAMMA1000931	2.68	3.44	3.95	6.78	7.66	7.32	**	+
	MAMMA1000940	1.67	1.84	6.05	5.78	6.84	6.3		
	MAMMA1000941	3.74	2.55	8.61	9.01	10.11	9.46		
	MAMMA1000942	2.75	1.85	7.46	8.27	8.47	7.2		
50	MAMMA1000943	2.16	2.84	10.49	9.04	11.08	8.74		
	MAMMA1000952	2.6	1.93	8.65	9.03	7.47	6.75		
	MAMMA1000956	0.93	1.24	3.11	3.64	3.1	3.47		
	MAMMA1000957	2.5	1.41	2.62	4.81	5.73	6.85	**	+
	MAMMA1000962	3.25	3.57	10.48	13.62	11.18	16.85	*	+
55	MAMMA1000966	1.85	2.19	6.04	6.34	6.23	7.04		
	MAMMA1000968	1.6	1.46	5.49	4.79	5.62	4.97		

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	MAMMA1000972	2.4	1.41	3.83	3.34	3.91	4.32		
	MAMMA1000973	5.14	3.37	12.58	7.02	8.56	10.31		
	MAMMA1000975	1.44	1.99	3.34	2.37	4.9	5.05		
5	MAMMA1000976	2.46	2.71	8.57	9.22	11.17	8.92		
	MAMMA1000979	1.46	2.62	3.06	4.34	4.41	7.71		
	MAMMA1000986	5.75	5.32	10.24	8.83	11.32	13.95		
	MAMMA1000987	1.44	1.36	3.99	2.43	3.74	5.66		
10	MAMMA1000988	3.76	4.86	8.88	10.18	11.34	10.5	*	+
	MAMMA1000994	9.82	7.58	15.88	12.02	11.56	9.25		
	MAMMA1000998	1.51	1.07	3.13	4.21	5.42	4.04	*	+
	MAMMA1001003	1.98	1.83	5.97	4.2	6.86	4.39		
	MAMMA1001007	0.38	1.03	1.77	0.14	1.38	0.32		
15	MAMMA1001008	11.76	11.09	40.52	56.73	50.93	45.37	*	+
	MAMMA1001013	3.62	4.16	12.14	8.42	11.54	10.08		
	MAMMA1001014	1.4	1.79	5.49	4.36	5.16	4.26		
	MAMMA1001021	0.49	2.08	7.85	6.46	5.47	4.26		
	MAMMA1001024	0.85	1.59	3.14	2.55	3.92	1.96		
20	MAMMA1001025	1.03	1.47	2.94	1.27	2.95	1.41		
	MAMMA1001028	1.3	1.09	2.23	3.07	4.73	3.28	*	+
	MAMMA1001030	1.63	0.48	2.22	3.06	3.24	2.08		
	MAMMA1001035	2.48	2.92	10.31	9.29	11.92	11.54		
	MAMMA1001036	4.69	4.01	10.7	11.23	8.22	11.33		
25	MAMMA1001037	1.91	2.88	6.49	5.28	7.53	4.69		
	MAMMA1001038	1.18	1.59	4.28	4.12	3.85	4.45		
	MAMMA1001041	1.64	1.87	3.18	3.75	4.04	2.64		
	MAMMA1001043	1.09	1.24	3.67	3.44	3.35	3.18		
30	MAMMA1001050	1.52	1.55	5.94	8.4	8.28	6.51	*	+
	MAMMA1001054	2.04	2.58	6.99	9.29	11.07	8.36	*	+
	MAMMA1001059	2.66	4.71	9.73	8.85	9.72	8.46		
	MAMMA1001066	3.64	2.97	12.26	14.08	12.09	8.96		
	MAMMA1001067	1.26	2	4.77	3.53	5.33	3.29		
35	MAMMA1001072	1.44	2.06	7.76	6.38	7.13	7.2		
	MAMMA1001073	1.17	0.79	1.47	1.49	2.74	1.34		
	MAMMA1001074	0.78	1.47	3.97	6.24	5.4	4.9	*	+
	MAMMA1001075	4.87	4.41	10.48	11.24	9.82	8.21		
	MAMMA1001078	1.7	1.83	7.96	9.69	9.99	9.37	*	+
40	MAMMA1001080	3.77	3.93	6.97	8.71	10.33	5.57		
	MAMMA1001082	1.51	2.03	4.03	1.73	5.23	1.6		
	MAMMA1001091	1.17	1.36	2.02	1.81	3.03	1.47		
	MAMMA1001092	1.93	2.09	4.81	3.17	3.57	1.89		
	MAMMA1001094	1.73	4.28	4.65	4	5.62	4.7		
45	MAMMA1001105	2.45	2.62	7.7	6.99	7.57	6.06		
	MAMMA1001110	0.4	1.01	2.74	1.42	2.53	0.47		
	MAMMA1001126	1.96	3.09	10.92	8.39	9.27	6.08		
	MAMMA1001133	2.5	3.44	10.94	9.48	10.83	10.68		
	MAMMA1001139	87.88	86.18	214.31	193.19	47.2	160.92		
50	MAMMA1001141	1.33	2.89	3.65	3.69	5.25	5.46		
	MAMMA1001143	2.02	1.79	4.23	3.95	6.69	4.34		
	MAMMA1001145	3.1	2.22	3.39	6.37	7.13	2.84		
	MAMMA1001150	1.34	2.48	3.95	3.06	3.31	2.11		
	MAMMA1001154	2.16	2.8	5.57	5.44	7.13	5.22		
55	MAMMA1001159	4.19	4.01	11.06	11.31	5.89	9.45		

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	MAMMA1001161	4.3	5.27	19.53	18.34	10.8	14.8	
	MAMMA1001162	1.98	1.77	3.16	5.25	5.13	2.25	
	MAMMA1001181	2.44	2.28	4.87	5.06	4.74	3.62	
5	MAMMA1001186	2	2.66	4.66	5.38	5.48	3.9	
	MAMMA1001189	2.23	3.68	7.17	11	11.17	9.9	*
	MAMMA1001191	2.54	2.07	5.49	4.37	3.89	2.97	+
	MAMMA1001198	368.47	416.05	784.82	647.17	738.61	605.52	
10	MAMMA1001202	11.78	11.85	30.06	34.39	28.74	25.16	
	MAMMA1001203	2.57	3.01	7.15	8.72	6.26	5.56	
	MAMMA1001206	1.91	3.28	4.5	3.69	6.66	2.65	
	MAMMA1001208	2.66	2.93	3.31	3.82	4.95	3.19	
	MAMMA1001215	2.9	3.08	6.55	3.49	8.09	4.74	
15	MAMMA1001220	2.63	3.03	7.25	7.16	7.17	6.03	
	MAMMA1001222	1.25	1.18	4.18	2.18	5.85	0.53	
	MAMMA1001223	2.48	3.32	6.53	4.95	6.51	4.1	
	MAMMA1001232	2.82	4.27	8.08	12.22	8.82	9.57	
	MAMMA1001234	1.25	3.27	3.17	5.05	3.91	3.26	
20	MAMMA1001237	1.22	1.56	4.21	1.94	3.66	2.09	
	MAMMA1001243	2.18	2.28	4.06	4.05	4.89	1.99	
	MAMMA1001244	1.22	1.16	2.86	2.96	4.79	2.22	
	MAMMA1001249	2.3	1.89	5.93	5.19	5.8	3.75	
	MAMMA1001256	3	3.09	8.29	5.89	7.83	8.01	
25	MAMMA1001259	4.38	3.25	7.15	7.94	9.24	6.63	
	MAMMA1001260	1.76	2.71	5.42	6.51	5.33	7.33	
	MAMMA1001262	2.1	4.11	5.28	7.86	8.04	6.25	*
	MAMMA1001268	2	2.16	4.59	2.56	4.23	2.48	+
30	MAMMA1001271	4.84	5.78	17.37	18.29	14.24	15.67	
	MAMMA1001274	2.88	3.06	6.17	6.22	8.55	7.93	
	MAMMA1001280	2.09	1.48	4.36	1.84	3.78	1.73	
	MAMMA1001283	1.63	1.71	6.34	6.88	5.63	4.83	
	MAMMA1001284	2.27	2	8.67	5.08	9.09	9.51	
35	MAMMA1001286	13.83	9.72	17.39	12.15	11.83	14.63	
	MAMMA1001289	17.63	13.49	23.32	21.02	26.39	36.8	
	MAMMA1001292	3	3.01	5.94	7.26	6.31	6.85	*
	MAMMA1001296	3.55	3.76	12.61	14.11	12.37	12.8	+
	MAMMA1001298	1.26	1.7	6.26	4.25	6.78	4.07	
40	MAMMA1001305	0.86	1.59	4.43	2.49	4.07	2.63	
	MAMMA1001309	0.61	0.9	2.7	1.84	3	1.49	
	MAMMA1001310	1.72	2.17	3.64	4.81	7.38	4.42	
	MAMMA1001322	0.99	1.54	1.83	2.83	1.77	2.13	
	MAMMA1001324	1.3	1.12	3.16	2.03	2.83	1.94	
45	MAMMA1001330	3.35	2.65	9.53	7.93	9.75	5.36	
	MAMMA1001333	3.1	3.74	10.23	9.88	11.4	9.07	
	MAMMA1001334	5.53	4.17	4.83	10.97	8.23	10.16	**
	MAMMA1001337	2.49	3.54	6.6	6.99	9.16	8.05	*
	MAMMA1001341	1.21	1.14	3.48	1.54	5.66	1.41	+
50	MAMMA1001343	2.37	1.89	8.07	8.17	9.75	10.95	
	MAMMA1001344	9.59	9.07	11.75	13.63	11.67	15.98	
	MAMMA1001346	1.34	1.25	3.9	2.05	3.9	2.94	
	MAMMA1001383	3.07	3.61	8.52	8.3	9.02	9.38	
	MAMMA1001388	1.62	1.93	5.34	3.38	6.11	4.58	
55	MAMMA1001396	4.2	2.12	8.12	11.39	10.42	8.68	

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	MAMMA1001397	2.59	2.27	5.79	8.33	8.96	7.78	*	+
	MAMMA1001401	26.87	16.48	32.72	43.47	57.55	45.66	*	+
5	MAMMA1001408	1.06	1.06	2.57	0.65	4.22	1.19		
	MAMMA1001411	1.65	1.26	3.84	4.38	3.33	3.51		
	MAMMA1001414	3.12	3.85	5.74	12.58	10.67	15.28	**	+
	MAMMA1001415	2.45	3.16	11.93	14.57	20.15	13.69	*	+
	MAMMA1001418	0.66	2.2	5.36	3.57	6.04	4.46		
10	MAMMA1001419	0.8	2.43	4.93	6.03	7.01	3.92		
	MAMMA1001420	0.96	3.09	4.5	3.23	4.11	3.41		
	MAMMA1001426	20.24	32.21	42.42	44.31	39.63	38.75		
	MAMMA1001428	1.94	2.83	6.35	3.8	6.93	4.33		
	MAMMA1001432	1.19	2.33	8.19	5.62	6.19	6.68		
15	MAMMA1001435	1.43	0.78	3.32	3.48	3.67	2.64		
	MAMMA1001442	1.96	3.94	7.41	8.18	8.6	6.63		
	MAMMA1001446	2.17	2.57	6.71	6.9	7.34	7.97		
	MAMMA1001450	1.22	2.05	3.58	2.81	4.18	2.39		
20	MAMMA1001452	1.99	1.78	5.92	8.38	6.19	4.83		
	MAMMA1001465	3.93	3.25	13.61	16.65	14.6	13.82		
	MAMMA1001476	1.63	1.09	4.25	5.87	5.95	4.64	*	+
	MAMMA1001478	2.28	2.12	5.98	3.55	6.27	4.19		
	MAMMA1001479	3.11	4.71	8.32	5.58	6.74	6.21		
25	MAMMA1001487	1.1	1.14	3.84	4.73	3.26	2.08		
	MAMMA1001498	1.93	3.41	7.78	6.17	7.45	5.64		
	MAMMA1001501	0.88	1.97	4.49	2.8	4.77	2.36		
	MAMMA1001502	1.82	1.91	6.48	3.29	6.29	6.26		
	MAMMA1001510	0.48	0.78	2.92	0.54	3.04	1.19		
30	MAMMA1001522	1.03	1.29	3.94	5.05	4.9	3.39		
	MAMMA1001529	0.72	2.06	3.22	3.74	4.07	2.57		
	MAMMA1001532	1.74	1.86	4.27	3.79	5.71	3.12		
	MAMMA1001533	0.61	1.31	2.9	1.52	3.06	1.64		
	MAMMA1001534	0.44	2.59	2.4	1.48	3.64	1.14		
35	MAMMA1001535	1.38	1.91	3.99	2.12	3.98	2.38		
	MAMMA1001547	2.8	2.89	7.77	9.23	8.22	6.22		
	MAMMA1001551	1.1	1.48	4.46	2.23	2.88	2.99		
	MAMMA1001569	1.27	1.68	3.41	2.03	3.41	1.94		
	MAMMA1001575	1.48	2.41	3.42	4.01	4.43	2.81		
40	MAMMA1001576	4.79	8.23	9.65	14.75	9.39	17.03		
	MAMMA1001584	0.89	2.48	3.33	3.11	4	3.09		
	MAMMA1001586	1.43	2.41	3.34	3.78	3.31	1.84		
	MAMMA1001590	2.96	2.53	5.55	5.44	6.47	6.04		
	MAMMA1001599	4.64	7.15	16.79	15.8	15.18	15.06		
45	MAMMA1001600	1.45	2.22	4.73	2.98	4.68	2.11		
	MAMMA1001604	1.03	1.76	3.62	2.35	4.01	1.64		
	MAMMA1001606	1.64	2.04	5.15	3.58	5.45	4.27		
	MAMMA1001609	1.31	2.37	4.36	3.05	5.43	1.59		
	MAMMA1001614	2.91	3.57	6.15	5.94	6.11	4.14		
50	MAMMA1001615	3.98	2.61	10.12	8.87	8.29	8.41		
	MAMMA1001619	7.73	7.8	14.29	16.33	12.93	14.61		
	MAMMA1001620	2.53	2.41	7.98	5.77	7.13	4.54		
	MAMMA1001623	4.11	4.58	9.3	7.34	9.28	6.75		
	MAMMA1001626	0.83	1.98	2.52	3.24	3.93	1.93		
55	MAMMA1001627	1.11	1.98	3.57	2.63	3.68	1.63		

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	MAMMA1001630	2.02	3.08	7.83	7.49	7.53	4.29	
	MAMMA1001633	2.64	3.12	8.8	12.09	9.59	6.16	
	MAMMA1001634	2.83	2.7	6.11	8.69	8.27	6.9	* +
5	MAMMA1001635	5.65	2.39	9.52	7.92	8.3	8.37	
	MAMMA1001649	1.61	1.63	4.71	2.95	4.62	2.53	
	MAMMA1001654	8.14	9.45	39	43.4	55	46.79	
	MAMMA1001660	19.61	17.92	37.43	40.94	27.03	34	
	MAMMA1001663	1.9	4.73	9.42	9.59	9.56	6.58	
10	MAMMA1001670	1.12	2.66	3.97	3.65	4.09	2.62	
	MAMMA1001671	1.08	1.42	3.56	1.37	4.64	1.77	
	MAMMA1001679	6.85	6.37	13.89	11.48	17.04	13.91	
	MAMMA1001683	2.15	3.29	9.6	6.58	6.53	6.96	
	MAMMA1001686	1.25	1.34	3.77	1.39	2.97	3.06	
15	MAMMA1001688	113.39	113.61	245.56	392.2	458.41	413	** +
	MAMMA1001689	1.01	3.76	4.1	5.04	3.79	4.44	
	MAMMA1001692	1.97	2.59	5.37	3.66	5.3	3.88	
	MAMMA1001711	1.99	3.64	8.65	4.35	5.51	6.1	
20	MAMMA1001715	1.31	1.64	3.95	4.64	4.87	4.13	
	MAMMA1001730	2.01	2.15	2.5	2.8	4.42	2.83	
	MAMMA1001735	44.73	48.32	102.35	94.99	156.23	119.88	
	MAMMA1001740	0.64	1.6	4.59	2.06	3.91	1.95	
	MAMMA1001743	9.84	11.15	33.16	41.97	51.62	49.6	* +
25	MAMMA1001744	0.63	0.72	0.86	1.1	1.72	1.71	* +
	MAMMA1001745	1.41	2.15	6.15	3.27	4.46	3.93	
	MAMMA1001751	1.38	2.41	3.24	2.85	4.51	4.32	
	MAMMA1001752	4.7	4.78	9.75	6.12	9.61	8.4	
	MAMMA1001754	7.25	7.89	7.34	11.04	9.63	9.39	* +
30	MAMMA1001757	1.21	1.1	2.32	2.21	3.25	2.43	
	MAMMA1001760	3.87	4.52	20.01	22.91	24.2	27.59	* +
	MAMMA1001764	2.62	2.36	5.97	7.13	10.17	6.51	
	MAMMA1001767	1.22	1.55	2.13	1.61	2.96	1.55	
	MAMMA1001768	0.57	1.18	4.25	4.74	4.72	4.37	
35	MAMMA1001769	2.48	2.83	9.22	9.3	9.81	8.94	
	MAMMA1001771	2.66	1.58	3.74	2.86	5.85	6.77	
	MAMMA1001773	2.7	3.53	3.87	4	6.29	7.61	
	MAMMA1001778	0.88	1.92	3.14	3.13	4.21	3.61	
40	MAMMA1001783	2.01	2.1	11.25	11.63	18.46	13.04	
	MAMMA1001785	3	3.52	8.85	10.56	13.38	11	* +
	MAMMA1001788	0.49	0.86	1.21	0.72	1.72	1.11	
	MAMMA1001790	1.68	1.67	5.1	2.37	3.73	3.93	
	MAMMA1001800	0.83	0.99	1.47	1.5	2.24	3.25	
45	MAMMA1001804	1.02	1.41	3.18	2.37	4.16	2.4	
	MAMMA1001806	2.13	2.78	6.4	3.15	5.5	4.72	
	MAMMA1001812	1.46	1.33	5.52	4.21	5.86	5.05	
	MAMMA1001815	0.33	1.76	3.07	1.22	3.67	1.24	
	MAMMA1001817	3.19	3.38	9.5	6.78	10.89	13.3	
	MAMMA1001818	1.68	2.08	3.41	3.94	8.52	3.41	
50	MAMMA1001819	2.57	4.12	5.82	8.7	10.29	7.87	* +
	MAMMA1001820	2.68	4.51	8.27	7.51	10.98	6.07	
	MAMMA1001824	1.66	2.83	8.36	7.55	9.8	7.11	
	MAMMA1001832	6.72	7.99	11.85	20.17	21.28	17.21	** +
55	MAMMA1001836	1.74	1.66	5.08	4.79	8.19	4.88	

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	MAMMA1001837	2.61	2	5.84	7.1	9.19	5.37	
	MAMMA1001848	1.02	1.61	3.3	2.81	5.33	3.18	
	MAMMA1001850	3.79	4.51	9.31	9.98	9.93	14.19	
5	MAMMA1001851	1.49	2.33	4.98	4.97	4.12	4.02	
	MAMMA1001852	2.98	4	9.68	6.4	7.56	6.8	
	MAMMA1001854	2.56	3.11	9.16	10.59	10.64	9.98	
	MAMMA1001858	3.11	2.22	5.28	9.93	7.91	8.87	** +
	MAMMA1001864	1.69	1.91	4.09	8.91	6.18	4.37	
10	MAMMA1001868	0.71	0.92	2.64	1.68	2.58	0.91	
	MAMMA1001874	1.2	0.87	2.52	1.06	3.48	1.17	
	MAMMA1001878	3.1	3.46	10.86	7.7	13.37	6.77	
	MAMMA1001880	2.67	2.99	7.24	5.58	7.17	8.12	
	MAMMA1001885	1.14	1.93	6.19	4.7	5.54	4.58	
15	MAMMA1001890	3.54	3.95	12.93	13.59	13.29	12.2	
	MAMMA1001893	3.74	3.42	6.25	6.59	5.49	5.58	
	MAMMA1001901	1.13	1.5	5.4	4.53	5.72	2.67	
	MAMMA1001907	2.57	1.62	6.43	4.15	7.36	6.34	
	MAMMA1001908	3.2	3.36	8.35	11.83	12.96	12.46	* +
20	MAMMA1001919	0.23	0.97	3.3	2.24	3.9	2.07	
	MAMMA1001931	0.76	1.65	4.04	3.36	5.89	3.25	
	MAMMA1001937	2.27	3.15	5.5	6.44	5.06	3.78	
	MAMMA1001951	1.74	2.57	6.47	6.48	6.15	4.83	
25	MAMMA1001956	3.02	3.48	9.72	8.52	7.66	6.76	
	MAMMA1001957	3.39	3.51	9.15	7.88	9.47	7.66	
	MAMMA1001960	3.1	3.34	7.24	12.06	9.14	6.1	
	MAMMA1001963	0.57	0.78	2.14	1.3	2.36	1.06	
	MAMMA1001969	1.7	3.43	10.86	8.54	11.14	8.74	
30	MAMMA1001970	2.86	3.04	8.48	13.11	6.59	6.64	
	MAMMA1001978	0.57	1.85	1.76	2.42	3.87	1.53	
	MAMMA1001992	2.07	2.04	5.65	6.79	6.75	5.09	
	MAMMA1001994	7.97	3.65	11	18.83	13.23	17.17	* +
	MAMMA1002008	3.28	3.77	6.42	3.43	4.06	1.24	
35	MAMMA1002009	1.46	2.94	5.17	5.73	7.57	4.06	
	MAMMA1002011	1.77	1.71	4.26	6.5	6.45	3.37	
	MAMMA1002022	1.51	2.1	5.92	6.64	7.42	5.2	
	MAMMA1002024	9.79	9.67	19.03	17.61	16.96	22.43	
	MAMMA1002032	2.78	2.41	7.25	5.29	6.16	8.07	
40	MAMMA1002033	3.23	3.95	7.73	11.24	7.23	6.62	
	MAMMA1002041	2.87	2.25	3.18	4.74	5.39	1.71	
	MAMMA1002042	2.54	2.34	5.66	5.65	5.78	3.76	
	MAMMA1002045	2.33	3.51	7.28	8.39	5.05	4.44	
	MAMMA1002047	2.58	2.98	8.83	8.7	8.9	6.89	
45	MAMMA1002056	2.01	5.78	11.14	11.35	10.64	9.14	
	MAMMA1002058	1.67	2.61	8.19	4.84	4.66	4.27	
	MAMMA1002060	1.08	2.08	1.41	2.5	4.09	1.2	
	MAMMA1002065	1.81	2.75	6.04	7.19	5.19	3.26	
50	MAMMA1002068	2.43	1.84	5.29	4.98	5.6	4.47	
	MAMMA1002070	4.5	2.92	4.15	2.58	5.23	2.81	
	MAMMA1002078	1.32	1.43	2.94	1.12	4.4	1.07	
	MAMMA1002080	7.98	9.71	13.38	14.92	20.84	14.26	
	MAMMA1002082	2.54	4.96	13.04	9.67	8.15	7.78	
55	MAMMA1002084	1.78	3.47	3.38	4.68	4.48	3.6	

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	MAMMA1002087	1.12	2.15	5.37	3.6	4.67	2.36		
	MAMMA1002091	3.79	3.22	4.32	7.18	6.76	6.41	**	+
	MAMMA1002093	0.72	1.4	4.31	2.74	4.39	2.33		
5	MAMMA1002095	2.4	3.22	7.5	4.73	7.52	4.54		
	MAMMA1002108	1.84	1.02	2.63	1.87	3.24	1.31		
	MAMMA1002112	2.94	3.4	7.03	12.79	16.02	11.28	**	+
	MAMMA1002118	1.02	1.61	2.24	1.41	3.18	2.01		
10	MAMMA1002119	0.76	2.15	3.61	1.51	3.12	2.54		
	MAMMA1002125	1.79	2.61	6.95	4.52	4.19	4.11		
	MAMMA1002126	3.72	4.25	9.79	10.08	9.02	11.03		
	MAMMA1002128	0.9	2.36	3.07	2.7	3.49	2.88		
	MAMMA1002132	3.78	3.24	11.42	6.18	9.05	6.81		
15	MAMMA1002140	1.46	1.87	3.68	2.18	3.24	2.33		
	MAMMA1002142	3.13	3.43	7.06	5.18	7.62	5.46		
	MAMMA1002143	5.42	2.27	7.96	7.98	9.87	13.23		
	MAMMA1002145	1.47	1.34	3.3	2.9	4.02	2.64		
	MAMMA1002147	0.81	1.59	2.9	2.71	4.4	3		
20	MAMMA1002153	0.99	1.92	5.55	3.52	6.41	4.75		
	MAMMA1002155	2.11	1.93	6.76	4.4	6.46	4.46		
	MAMMA1002156	0.81	0.8	1.94	0.67	2.63	0.78		
	MAMMA1002158	1.38	1.83	5.12	4.09	7.73	5.2		
	MAMMA1002164	2.01	2.09	5.86	3.17	3.18	4.04		
25	MAMMA1002165	4.04	4.29	7.25	8.65	8.1	6.81		
	MAMMA1002170	1.01	1.48	154.53	2.65	3.24	4.11		
	MAMMA1002174	1.66	2.9	5.83	4.55	7.78	8.58		
	MAMMA1002175	3.27	3.3	7.02	6.95	6.64	7.22		
	MAMMA1002180	8.59	6.53	35.97	55.49	48.49	51.08	*	+
30	MAMMA1002198	3.11	2.3	9.33	7.6	11.22	7.13		
	MAMMA1002205	2.93	1.66	6.15	6.3	8.04	7.54		
	MAMMA1002206	4.6	3.59	8.14	12.4	13.97	11.74	**	+
	MAMMA1002209	1.7	1.93	4.03	4.43	4.23	4.57		
	MAMMA1002215	4.17	2.72	15.2	11.05	12.43	17.14		
35	MAMMA1002219	1.57	1.96	4.99	4.84	6.34	5.96		
	MAMMA1002224	3.18	2.9	8.13	5.49	7.25	5.86		
	MAMMA1002229	3.74	2.21	8.83	8.48	9.26	6.82		
	MAMMA1002230	2.02	2.21	6.63	5.31	8.91	6.58		
	MAMMA1002233	3.01	1.6	6.03	4.21	7.91	6.14		
40	MAMMA1002234	3.05	3.06	6.7	8.6	10.45	10.76	*	+
	MAMMA1002236	4.13	3.68	14.08	26.56	20.38	24.71	*	+
	MAMMA1002243	0.97	2.48	3.48	3.28	3.43	2.96		
	MAMMA1002250	1.06	2.09	5.2	3.95	6.82	6.01		
45	MAMMA1002253	2.77	2.39	3.45	4.84	6.18	3.37		
	MAMMA1002267	17.17	19.95	51.7	130.02	108.53	115.75	**	+
	MAMMA1002268	1.72	2.28	5.82	6.92	11.3	6.52		
	MAMMA1002269	0.89	0.73	2.25	2.32	2.58	1.67		
	MAMMA1002282	0.86	1.09	4.95	5.87	5.31	6.81		
	MAMMA1002292	2.71	2.25	7.77	10.57	10.52	11.53	*	+
50	MAMMA1002293	3.71	3.31	12.31	8.54	10.47	12.05		
	MAMMA1002294	0.9	1.71	4.61	3.68	6.03	4.2		
	MAMMA1002297	1.53	3.25	7.45	5.77	7.8	6.91		
	MAMMA1002298	1.48	1.4	3.93	3.85	3.11	2.46		
55	MAMMA1002299	1.5	1.69	3.16	3.91	2.97	2.2		

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	MAMMA1002308	1.39	1.35	6.55	4.5	3.11	2.54		
	MAMMA1002310	3.56	3.84	12.73	9.92	12.66	11.48		
	MAMMA1002311	2.52	2.13	6.82	9.61	9.66	6.9	*	+
5	MAMMA1002312	1.63	2.22	5.19	3.51	8.45	2.55		
	MAMMA1002317	2.08	2.55	4.89	4.08	3.85	4.09		
	MAMMA1002319	0.8	2.78	3.51	2.68	3.97	2.85		
	MAMMA1002322	2.48	3.23	7.84	12.21	10.02	8.55	*	+
10	MAMMA1002329	1.64	1.67	2.93	2.9	3.3	2.76		
	MAMMA1002332	2.17	2.38	4.58	5.98	4.14	3.05		
	MAMMA1002333	1.7	1.74	4.19	5.35	5.07	3.54		
	MAMMA1002335	1.75	2.72	8.53	6.93	11.32	4.23		
	MAMMA1002339	2.09	2.42	7.34	5.21	7.5	5.14		
15	MAMMA1002347	1.7	2.3	6.39	5.5	5.32	4.64		
	MAMMA1002351	2.08	2.68	5.74	3.03	4.48	4.84		
	MAMMA1002352	1.27	2.28	3.66	3.53	4.63	2.8		
	MAMMA1002353	4.46	2.5	5.84	5.95	4.19	4		
	MAMMA1002355	3.97	3.38	8.37	7.98	7.31	8.57		
20	MAMMA1002356	2.18	1.49	4.36	5.43	4.13	3.75		
	MAMMA1002359	3.95	3.35	16.09	23.81	24.53	19	*	+
	MAMMA1002360	0.93	1.73	3.77	2.48	3.2	1.67		
	MAMMA1002361	2.01	2.64	4.53	4.17	4.95	4.03		
	MAMMA1002362	2.33	2.33	3.36	5.31	5.51	3.99	*	+
25	MAMMA1002367	2.97	3.64	14.63	18.34	21.06	21.56	*	+
	MAMMA1002371	2.28	3.75	8.3	6.15	6.74	5.88		
	MAMMA1002380	1.81	2.26	4.9	4.71	5.76	3.55		
	MAMMA1002384	2.14	1.53	4.73	4.48	5.36	4.05		
	MAMMA1002385	1.19	2.05	5.63	3.34	4.8	2.47		
30	MAMMA1002390	1.41	2.04	3.75	5.48	5.4	3.43		
	MAMMA1002392	1.94	3.1	6.1	4.06	5.95	3.32		
	MAMMA1002396	4.87	3.49	12.87	10.79	12.9	8.08		
	MAMMA1002399	4.42	5.13	10.69	10.95	8.66	4.57		
	MAMMA1002400	3	2.22	4.69	3.11	4.36	3.53		
35	MAMMA1002409	51.57	55.16	63.3	77.54	80.62	77.88	**	+
	MAMMA1002411	1.08	1.88	4.13	3.43	5.49	1.92		
	MAMMA1002413	2.02	3.01	9.19	5.93	7.17	6.75		
	MAMMA1002417	1.83	2.24	4.87	3.45	4.25	2.63		
	MAMMA1002427	1.5	2.38	4.54	4.78	5.56	3.41		
40	MAMMA1002428	2.47	2.26	5.38	4.46	5.11	4.28		
	MAMMA1002433	1.74	2.18	6.84	6.72	6.96	6.22		
	MAMMA1002434	2.94	2.4	7.38	5.34	4.65	5.03		
	MAMMA1002446	1.39	2.34	5.62	3.98	5.84	5.96		
	MAMMA1002447	2.51	1.38	6.4	5.11	6.26	5.45		
45	MAMMA1002454	7.77	9.16	18.07	21.71	17.12	18.35		
	MAMMA1002461	2.06	4.11	7.7	4.92	5.41	6.47		
	MAMMA1002463	3.28	3.32	8.09	6.98	7.82	5.39		
	MAMMA1002464	16.58	16.77	20.05	19.41	20.41	18.09		
	MAMMA1002466	9.48	9.89	14.22	14.58	15.75	13.93		
50	MAMMA1002470	1.39	1.51	5.13	3.54	5.01	3.73		
	MAMMA1002475	0.72	1.85	5.03	3.86	5.17	4.65		
	MAMMA1002480	0.66	1.21	2.31	1.68	2.84	2.03		
	MAMMA1002485	29.98	27.24	46.09	64.83	74.9	80.68	**	+
55	MAMMA1002494	2	2	4.11	4.48	5.12	5.13	*	+

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	MAMMA1002498	0.97	2.57	3.16	2.07	3.18	1.55	
	MAMMA1002524	3.04	2.96	6.43	5.18	7.34	6.1	
5	MAMMA1002530	2.5	3.24	4.88	3.17	4.41	2.55	
	MAMMA1002538	2.34	2.38	5.62	5.46	5.13	4.91	
	MAMMA1002545	2.37	2.64	6.26	4.56	6.49	4.56	
	MAMMA1002554	1.96	1.42	5.43	5.3	6.01	7.81	
	MAMMA1002556	1.3	1.9	3.6	3.73	5.75	3.89	
10	MAMMA1002561	2.3	2.99	7.19	8.13	10.46	7.98	
	MAMMA1002565	1.22	2.15	3.52	2.57	4.51	2.55	
	MAMMA1002566	0.98	1.87	6.21	1.65	4.7	3.9	
	MAMMA1002571	0.53	1.8	3.06	1.43	3.1	4.3	
	MAMMA1002573	2.14	1.86	7.06	4.54	5.66	5.97	
15	MAMMA1002576	118.77	131.84	363.97	348.62	471.73	358.66	
	MAMMA1002584	3.52	2.27	11.91	12.86	17.82	13.46	
	MAMMA1002585	0.76	1.86	4.38	1.85	3.6	5.26	
	MAMMA1002586	1.98	2.55	3.85	4.12	5.02	3.3	
20	MAMMA1002589	1.08	1.26	2.44	2.36	5.06	3.19	
	MAMMA1002590	1.01	1.57	5.87	2.58	6.75	4.57	
	MAMMA1002593	2.48	2.48	4.89	4.18	4.07	3.04	
	MAMMA1002597	2.47	2.52	7.25	8.06	9.48	8.78	* +
	MAMMA1002598	12.12	13.52	30.83	37.28	48.14	38.91	* +
25	MAMMA1002603	1.2	1.39	3.69	3.25	6.24	4.35	
	MAMMA1002612	3.51	3.39	12.6	7.66	7.78	9.76	
	MAMMA1002617	4.3	3.41	10.15	6.3	7.29	10.05	
	MAMMA1002618	1.68	2.27	4.02	2.76	3.59	3.91	
	MAMMA1002619	2.96	2.8	5.24	3.22	5.88	3.49	
30	MAMMA1002622	2.51	2.12	8.02	7.1	7.18	7.15	
	MAMMA1002623	2.31	2.21	6.27	5.89	6.17	6.19	
	MAMMA1002625	1.32	1.3	3.23	2.3	6.42	2.6	
	MAMMA1002627	0.98	0.82	2.93	0.6	1.29	0.21	
	MAMMA1002629	1.8	2.23	6.09	5.03	6.74	7.02	
35	MAMMA1002631	1	1.86	3.61	3.07	4.55	2.97	
	MAMMA1002633	6.61	7.44	21.47	19.33	24.55	21.53	
	MAMMA1002636	1.02	2.46	6.97	6.79	8.77	9.25	
	MAMMA1002637	1.05	1.4	4.66	3.39	4.85	4.28	
	MAMMA1002646	1.69	0.8	3.32	2.33	2.86	1.53	
40	MAMMA1002648	10.51	14.07	21.18	42.29	31.45	39.76	** +
	MAMMA1002650	1.33	0.56	1.62	1.76	2.08	0.57	
	MAMMA1002652	1.76	2.82	7.31	7.5	7.41	9.79	
	MAMMA1002655	1.7	2.11	3.65	2.54	4.23	3.78	
	MAMMA1002662	0.84	2.24	4.33	3.57	5.68	4.13	
45	MAMMA1002665	3.61	3.57	10.05	13.42	17.97	19.59	* +
	MAMMA1002671	2.84	3.63	10.17	17.04	16.47	19.3	** +
	MAMMA1002673	1.32	2.14	4.93	4.07	5.03	2.82	
	MAMMA1002684	2.95	3.11	3.84	6.61	8.19	7.54	** +
	MAMMA1002685	0.68	1.49	2.57	2.05	3.74	2.97	
50	MAMMA1002692	1.28	1.96	5.45	2.46	4.14	3.62	
	MAMMA1002693	1.84	4.18	8	4.63	7.68	6.61	
	MAMMA1002698	0.99	1.91	4.05	2.92	4.42	3.3	
	MAMMA1002699	2	2.35	4.43	4.05	5.22	3.64	
55	MAMMA1002701	2.41	2.56	8.46	6.72	8.94	8.93	
	MAMMA1002708	1.51	1.55	5.38	4.08	6.16	6.18	

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	MAMMA1002711	1.58	2.08	7.04	4.37	7.35	5.81		
	MAMMA1002712	3.05	3.13	6.98	4.88	7.12	7.39		
	MAMMA1002716	0.56	1.75	3.39	2.38	6.29	2.9		
5	MAMMA1002721	2.11	2.01	5.57	3.72	6.34	4.59		
	MAMMA1002723	2.43	2.46	4.91	3.85	5.98	4.88		
	MAMMA1002727	3.85	5.55	5.78	5.29	4.45	6.22		
	MAMMA1002728	21.35	22.03	57.81	49.09	54.73	65.13		
	MAMMA1002742	4.12	4.39	10.35	7.92	8.63	7.61		
10	MAMMA1002743	4.12	3.89	6.17	13.81	14.09	13.46	**	+
	MAMMA1002744	2.07	3.15	9.18	9.33	12.98	13.16		
	MAMMA1002746	0.93	1.28	3.09	2.29	4.31	1.68		
	MAMMA1002748	2.71	2.65	4.52	7.15	5.86	4.72	*	+
15	MAMMA1002754	1.12	2.41	5.56	5.05	5.65	6.26		
	MAMMA1002758	0.71	1.66	2.55	1.57	4.41	1.69		
	MAMMA1002762	11.3	11.14	36.64	38.42	34.23	48.71		
	MAMMA1002764	1.83	3.2	5.95	5.11	6.06	4.26		
	MAMMA1002765	1.19	1.63	4.29	4.63	5.26	2.67		
20	MAMMA1002769	7.4	6.44	13.04	13.78	8.03	12.41		
	MAMMA1002771	1.41	2.41	3.31	3.54	5.39	4.39		
	MAMMA1002775	4.56	4.48	19.79	22.54	29.77	24.29	*	+
	MAMMA1002780	2.59	1.83	3.03	2.11	4.89	3.78		
	MAMMA1002782	1.43	2.49	3.85	2.51	4.79	4.11		
25	MAMMA1002795	1.89	2.03	3.46	6.45	7.68	5.35	**	+
	MAMMA1002796	4.35	3.97	7.51	7.2	8.09	8.17		
	MAMMA1002805	6.61	11.12	16.52	15.95	24.7	16.5		
	MAMMA1002806	1.47	2.02	3.51	2.28	4.62	2.17		
	MAMMA1002807	1.63	2.4	6.77	6.78	9.66	6.4		
30	MAMMA1002814	3.43	3.52	7.92	9.58	12.39	10.66	*	+
	MAMMA1002817	1.28	1.56	2.87	2.89	5.43	2.91		
	MAMMA1002820	1.66	1.93	2.61	2.52	4.77	2.21		
	MAMMA1002830	67.67	70.46	130.59	165.92	139.33	187.18	*	+
	MAMMA1002833	4.16	2.88	9.4	8.22	10.68	10.58		
35	MAMMA1002835	0.77	1.87	4.03	1.73	3.97	2.79		
	MAMMA1002838	1.85	2.66	5.31	2.91	4.44	3.93		
	MAMMA1002842	1	3.83	3.84	3.32	4.63	5.15		
	MAMMA1002843	1.72	2.92	2.33	4.09	4.81	3		
	MAMMA1002844	3.05	3.64	6.52	5.26	7.3	4.09		
40	MAMMA1002845	1.25	1.57	2.45	3.59	3.55	4.67	*	+
	MAMMA1002857	92.1	106.97	208.17	209.17	202.29	249.13		
	MAMMA1002858	317.94	188.78	378.89	560.7	620.76	724.33	**	+
	MAMMA1002863	2.17	2.83	6.91	3.51	5.12	3.96		
	MAMMA1002868	2.73	3.7	6.26	6.35	9.53	10.25	*	+
45	MAMMA1002869	5.43	6.83	26.64	22.68	30.03	29.85		
	MAMMA1002871	0.61	1.7	1.78	1.9	3.8	1.97		
	MAMMA1002875	1.9	2.59	3.99	4.48	6.35	4.06		
	MAMMA1002879	8.42	9.2	14.19	22.55	23.63	27.96	**	+
50	MAMMA1002880	1.23	2.02	2.12	1.48	5.42	2.03		
	MAMMA1002881	1.21	1.43	1.84	3.01	5.43	2.46		
	MAMMA1002885	0.96	1.59	2.71	2.6	3.26	1.59		
	MAMMA1002886	2.63	2.52	3.9	6.01	5.37	7.05	**	+
	MAMMA1002887	1.28	1.83	2.78	2.98	5.14	4.32	*	+
55	MAMMA1002890	0.79	1.7	4.05	4.39	4.8	4.01		

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	MAMMA1002892	1.35	2.45	4.98	6.64	6.24	5.84	*	+
	MAMMA1002893	4.52	3.58	5.4	7.6	8.03	8.43	**	+
	MAMMA1002895	1.43	1.31	3.28	1.81	3.89	1.64		
5	MAMMA1002898	0.53	1.67	4.15	2.69	4.72	1.42		
	MAMMA1002905	1.32	1.58	2.51	4.1	5.01	3.87	**	+
	MAMMA1002906	15.12	10.76	15.42	19.47	13.76	15.58		
	MAMMA1002908	0.99	1.24	4.28	3.53	4.24	4.07		
	MAMMA1002909	1.92	2.64	5.67	6.82	8.18	6.57	*	+
10	MAMMA1002918	2.75	2.69	5.42	5.27	7.26	6.58		
	MAMMA1002925	92.88	85.77	163.7	127.31	122.97	178.98		
	MAMMA1002926	6.08	6.31	16.25	16.64	19.48	19.9		
	MAMMA1002930	1.21	1.59	5.67	4.88	8.91	4.21		
	MAMMA1002937	4.91	3.87	30.71	40.45	75.17	61.59	*	+
15	MAMMA1002938	1.67	1.86	2.42	2.35	3.2	3.56		
	MAMMA1002941	0.49	1.48	2.78	2.53	3.59	2.24		
	MAMMA1002947	2.24	2.59	4.55	6	6.8	7.94	*	+
	MAMMA1002964	1.73	2.9	5.91	6.91	7.24	7.16	*	+
20	MAMMA1002967	1.94	1.59	2.28	2.9	4.19	2.79		
	MAMMA1002970	2.72	1.77	6	7.59	7.28	8.96	*	+
	MAMMA1002971	1.52	1.6	2.9	2.51	7.27	3.93		
	MAMMA1002972	1	1.32	2.95	1.74	4.56	2.12		
	MAMMA1002973	1.38	2.45	6.73	4.36	6.72	6.78		
25	MAMMA1002979	55.6	60.16	121.72	134.02	101.19	107.19		
	MAMMA1002982	0.53	1.98	2.28	2.04	3.28	1.9		
	MAMMA1002987	1.56	2.11	5.56	3.14	5.55	4.14		
	MAMMA1003003	0.77	2.18	4.78	4.46	6.47	5.08		
	MAMMA1003004	1.65	1.86	3.7	3.64	3.59	3.16		
30	MAMMA1003007	0.69	1.16	2.73	1.88	3.7	2.32		
	MAMMA1003011	1.56	1.8	3.67	3.77	5.41	3.94		
	MAMMA1003013	3.67	5.57	39.41	47.56	59.11	54.29	*	+
	MAMMA1003015	1.16	1.8	2.21	2.54	2.9	2.19		
	MAMMA1003019	0.6	1.61	2.1	3.12	4.61	2.63		
35	MAMMA1003020	2.96	4.19	5.34	11.31	10.33	10.09	**	+
	MAMMA1003026	1.29	1.56	2.95	2.66	4.25	2.25		
	MAMMA1003031	0.61	1.71	5.64	4.13	5.85	5.89		
	MAMMA1003033	1.34	1.65	4.13	2.84	5.11	3.64		
	MAMMA1003035	1.66	2.5	5.44	5.12	7.03	4.9		
40	MAMMA1003039	0.95	0.75	3.31	2.15	4.73	2.48		
	MAMMA1003040	1.38	2.54	5.32	4.57	7.47	7.43		
	MAMMA1003044	2.36	2.96	6.52	4.29	6.41	5.99		
	MAMMA1003047	1.82	3.67	7.61	5.74	7.05	7.13		
	MAMMA1003049	0.47	1.72	2.03	1.08	1.56	1.45		
45	MAMMA1003055	1.24	1.67	4.92	3.77	5.14	3.44		
	MAMMA1003056	0.9	0.91	1.85	1.22	2.26	1.02		
	MAMMA1003057	2.53	3.34	6.76	7.25	9.2	5.01		
	MAMMA1003066	1.65	2.06	4.73	4.1	7.08	5.07		
	MAMMA1003075	1.11	1.71	3.16	1.85	4.37	2.32		
50	MAMMA1003089	1.69	2.11	7.13	7.85	8.66	7.43		
	MAMMA1003092	1.25	1.79	3.21	2.62	4.08	1.76		
	MAMMA1003095	2.27	3.33	5.4	7.24	8.57	5.34		
	MAMMA1003099	1.88	2.51	4.95	4.09	6.45	4.35		
55	MAMMA1003102	1.33	2.04	2.88	3.2	3.27	2.39		

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	MAMMA1003104	0.64	1.07	3.17	2.15	3.25	1.56	
	MAMMA1003113	4.22	4.21	6.98	9.22	7.02	7.07	
	MAMMA1003126	12.93	14.72	20.89	19.28	12	15.63	
5	MAMMA1003127	2.95	3.14	5.91	3.88	6.12	5.19	
	MAMMA1003131	2.82	3.51	4.86	3.82	5.91	5.88	
	MAMMA1003135	3.66	4.65	7.61	2.33	4.04	2.64	
	MAMMA1003140	0.73	2.01	3.59	2.3	3.32	1.89	
	MAMMA1003146	2.08	2.24	3.89	3.17	5.09	3.3	
10	MAMMA1003150	1.18	1.8	3.01	3.37	4.29	3.45	* +
	MAMMA1003154	0.54	1.41	2.29	2.21	3.57	2.34	
	MAMMA1003155	8.08	9.18	20.88	21.41	17.68	20.56	
	MAMMA1003157	5.94	4.82	6.07	5.18	7.05	7.89	
15	MAMMA1003163	1.74	1.69	4.23	2.55	5.46	3.08	
	MAMMA1003164	2.94	4.56	6.23	4.08	9.9	8.18	
	MAMMA1003166	3.62	3.5	5.77	6.24	8.66	6.12	
	NB9N31000010	2.5	3.88	7.58	9.63	12.26	9.5	* +
	NB9N31000016	0.73	2.8	5.21	4.04	4.41	3.15	
20	NB9N31000043	8.1	8.88	19.71	12.51	12.3	12.64	
	NB9N31000045	167.24	153.32	255.96	401.78	320.53	296.06	* +
	NB9N31000054	7.29	4.42	11.75	11.15	11.87	13.43	
	NB9N31000076	2.31	1.94	3.51	4.5	6.35	4.44	* +
	NB9N31000086	2.62	2.65	6.23	3.61	9.71	7.69	
25	NT2RM1000001	2.56	2.45	6.24	5.7	7.05	6.32	
	NT2RM1000018	3.84	4.69	10.6	6.58	9.09	6.92	
	NT2RM1000032	1.12	2.64	3.88	2.28	4.92	3.21	
	NT2RM1000035	1.72	3.68	5.53	5.44	5.21	5.98	
	NT2RM1000037	1.38	2.98	2.75	2.41	4.15	2.11	
30	NT2RM1000039	3.45	5.13	5.9	6.51	7.26	8.4	* +
	NT2RM1000042	33.96	32.7	65.25	57.46	67.15	64.39	
	NT2RM1000055	0.85	1.74	3.34	1.16	3.55	1.16	
	NT2RM1000059	3.26	3.16	7.66	4.69	5.97	5.78	
	NT2RM1000062	1.13	1.21	1.9	3.47	4.33	2.46	* +
35	NT2RM1000065	23.8	16.41	34.06	36.15	35.1	51.38	
	NT2RM1000066	4.13	4.31	8.98	7.23	10.95	9.81	
	NT2RM1000071	49.63	37.81	86.71	73.04	63.32	84.05	
	NT2RM1000080	1.37	2.04	3.8	5.1	5.94	4.5	* +
	NT2RM1000086	4.04	4.65	4.08	5.01	6.23	5.58	* +
40	NT2RM1000092	6.17	6.93	15.76	14.48	25.91	15.13	
	NT2RM1000118	0.63	1.12	1.22	0.63	1.7	0.44	
	NT2RM1000119	1.32	2.27	1.96	1.84	3.38	2.99	
	NT2RM1000121	1.13	1.84	1.76	2.92	3.84	2.78	* +
	NT2RM1000122	3.5	3.78	7.34	5.5	8.86	9.57	
45	NT2RM1000127	0.69	1.34	1.47	2.14	3.36	3.32	* +
	NT2RM1000131	0.71	1.7	1.47	1.36	3.02	2.53	
	NT2RM1000132	3.2	4.88	4.83	6.86	6.46	6.31	* +
	NT2RM1000153	1.75	1.9	3.68	2.38	4.45	4.84	
	NT2RM1000184	72.82	77.46	151.91	106.39	163.07	125.55	
50	NT2RM1000186	1.55	1.46	4.32	2.67	4.72	3.94	
	NT2RM1000187	3.11	1.96	5.16	10.09	9.1	8.78	** +
	NT2RM1000199	1.12	1.37	2.11	2.41	3.51	2.72	* +
	NT2RM1000213	1.32	1.75	2.38	2.66	2.71	2.22	
55	NT2RM1000215	10.95	11.07	17.21	19.51	22.84	15.14	

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	NT2RM1000218	9.72	9.95	23.71	26.94	24.74	29.21	
	NT2RM1000224	8.8	8.63	15.2	15.51	21.29	17.61	
	NT2RM1000236	30.38	24.19	61.14	72.86	82.44	71.5	* +
5	NT2RM1000242	0.23	1.17	1.32	0.39	2.27	0.12	
	NT2RM1000244	1.41	1.48	3.43	6.9	3.69	6.7	* +
	NT2RM1000252	1.75	1.5	3.4	3.4	3.06	3.18	
	NT2RM1000256	7.88	5.89	9.46	26.12	29.45	36.8	** +
	NT2RM1000257	1.98	3.01	5.09	4.64	6.83	6.65	
10	NT2RM1000260	7.9	7.01	13.32	9.18	12.49	11.77	
	NT2RM1000269	3.87	2.87	5.12	6.63	9.78	3.87	
	NT2RM1000271	0.71	0.8	1.87	0.46	2.47	0.51	
	NT2RM1000272	117.67	92.26	202.95	249.32	333.98	356.74	* +
	NT2RM1000273	10.03	9.45	20.12	22.32	16.68	15.76	
15	NT2RM1000274	63.11	66.41	123.01	137.14	91.97	104.48	
	NT2RM1000280	3.95	4.18	8.18	6.71	8.72	7.93	
	NT2RM1000295	0.49	1	2.2	1.12	3.16	0.87	
	NT2RM1000300	1.51	1.87	2.78	3.63	5.75	3.09	
20	NT2RM1000304	58.38	98.72	161.87	187.58	185.55	204.78	* +
	NT2RM1000314	1.8	2.12	3.6	3.84	4.07	4.33	
	NT2RM1000318	12.6	14.04	20.81	35.01	29.96	29.8	** +
	NT2RM1000335	2.76	2.57	4.34	6.29	5.41	4.09	
	NT2RM1000341	0.46	1.27	1.95	1.41	2.33	0.99	
25	NT2RM1000350	3.04	3.47	5.52	7.32	5.63	6.44	
	NT2RM1000354	0.55	1.31	1.31	5.43	7.2	5.72	** +
	NT2RM1000355	30.24	31.5	56.85	74.62	50.25	61.33	
	NT2RM1000361	3.63	3.87	7.23	14.39	20.29	18.78	** +
	NT2RM1000365	0.58	1.08	1.71	1.27	1.82	0.52	
30	NT2RM1000372	14.99	19.56	30.06	42.71	46.67	45.44	** +
	NT2RM1000377	2.04	2.18	9.66	13.38	14.74	13.48	* +
	NT2RM1000388	0.35	1.57	3.01	2.2	3.8	2.42	
	NT2RM1000394	0.45	1.31	1.87	1.43	2.72	0.69	
	NT2RM1000399	0.53	1.57	3.25	1.98	3.2	1.81	
35	NT2RM1000407	1.13	1.52	2.17	1.02	2.7	1.51	
	NT2RM1000421	0.84	0.57	2.78	1.06	1.77	1.13	
	NT2RM1000422	20.65	23.31	54.69	87.5	82.91	79.47	* +
	NT2RM1000430	1.22	1.57	2.01	3.2	3.67	2.95	** +
	NT2RM1000462	1.55	2.33	7.32	5.59	7.28	8.16	
40	NT2RM1000499	1.36	2.09	4.74	5	6.16	6.37	* +
	NT2RM1000512	12.49	13.22	19.22	10.54	14.15	19.84	
	NT2RM1000519	33.96	37.54	55.78	31.14	29.25	47.55	
	NT2RM1000527	7.97	8.92	37.68	55.15	60.19	46.68	* +
	NT2RM1000539	3.45	3.59	12.93	15.52	17.01	18.1	* +
45	NT2RM1000542	0.85	1.05	2.99	1.17	2.35	1.02	
	NT2RM1000553	3.7	2.42	22.32	42.83	42.96	34.5	* +
	NT2RM1000555	11.3	11.6	23.97	34.11	29.67	22.76	
	NT2RM1000558	2.09	5.34	9.74	9.56	16.24	14.29	
50	NT2RM1000563	1.47	2.42	3.36	4.07	5.58	3.95	* +
	NT2RM1000566	0.88	1.57	3.5	3.62	6.01	2.79	
	NT2RM1000570	96.92	77.32	137.63	167.35	105.47	174.1	
	NT2RM1000571	13.21	11.87	22.51	43.87	40.18	28.45	* +
	NT2RM1000574	0.84	2.15	2.55	2.15	3.07	1.67	
55	NT2RM1000580	1.37	2.18	4.07	5.15	7.98	2.96	

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	NT2RM1000620	2.61	2.95	8.2	8.35	9.58	7.26	
	NT2RM1000623	1.25	1.2	2.38	1.75	2.81	0.62	
	NT2RM1000630	0.79	2.28	2.39	1.68	3.51	1.67	
5	NT2RM1000633	30.97	39.36	36.34	54.43	44.6	43.59	* +
	NT2RM1000634	1.91	4.16	8.12	2.56	7.05	5.57	
	NT2RM1000642	3.85	5.37	8.13	8.21	8.56	8.52	
	NT2RM1000647	41.3	39.09	62.11	57.72	68.29	62.69	
10	NT2RM1000648	2.49	2.65	4.61	6.14	5.63	4.51	
	NT2RM1000650	2.46	3.05	7.6	5.4	6.07	6	
	NT2RM1000661	4.48	5.7	15.82	15.48	13.45	13.18	
	NT2RM1000666	1	1.77	1.99	1.37	2.8	0.71	
	NT2RM1000669	3.51	2.76	4.67	3.63	5.42	3.28	
15	NT2RM1000672	2.23	3.95	7.81	3.98	8.47	7.22	
	NT2RM1000681	99.53	86.09	118.7	105.41	90.59	124.14	
	NT2RM1000691	2.02	2.61	5.74	3.61	7.69	3.76	
	NT2RM1000698	1.11	1.43	4	6.42	6.29	4.11	* +
	NT2RM1000699	1.85	2.86	3.17	3.67	4.35	4.15	* +
20	NT2RM1000702	3.71	4.64	9.47	9.31	9.72	11.4	
	NT2RM1000703	11.56	12.36	25.24	26.72	20.42	21.06	
	NT2RM1000704	24.48	23	32.91	46.54	24.13	40.82	
	NT2RM1000725	60.92	59.45	88.28	94.89	82.36	105.67	
	NT2RM1000726	1.85	2.02	5.75	1.97	4.8	4	
25	NT2RM1000731	1.11	2.24	4.98	2.45	3.47	3.43	
	NT2RM1000741	1.38	1.87	3.16	2.69	4.15	2.9	
	NT2RM1000742	2.61	4.6	7.41	9.55	10.94	9.84	* +
	NT2RM1000744	2.1	3.61	7.14	4.05	5.24	5.05	
	NT2RM1000746	2.25	2.47	2.95	2.22	4.01	3.89	
30	NT2RM1000747	23.34	23.92	46.23	44.66	50.12	55.15	
	NT2RM1000752	3.83	2.36	4.62	3.95	4.88	3.46	
	NT2RM1000767	4.14	7.27	35.27	25.27	38.02	28.81	
	NT2RM1000770	2.97	3.08	6.36	4.71	6.71	5.67	
	NT2RM1000772	0.76	0.7	1.07	1.34	1.69	0.44	
35	NT2RM1000779	13.03	12.11	42.22	53.91	45.61	66.73	* +
	NT2RM1000780	1.16	2.9	3.74	3.09	4.32	3.01	
	NT2RM1000781	1.07	0.98	1.71	2.58	4.4	1.93	
	NT2RM1000789	5.28	5.15	29.74	29.63	46.72	36.53	
	NT2RM1000800	2.87	2.63	6.37	5.66	9.57	6.96	
40	NT2RM1000802	2.44	2.99	7.5	4.34	5.47	4.82	
	NT2RM1000811	1.78	1.6	2.13	2.26	4.96	2.76	
	NT2RM1000826	6.06	6.36	13.34	14.42	20.73	20.98	* +
	NT2RM1000829	3.91	2.87	6.39	6.73	8.48	8.41	* +
45	NT2RM1000831	81.54	64.45	185.14	182.43	179.79	197.27	
	NT2RM1000833	14.58	13.33	42.25	76.74	73.25	67.48	** +
	NT2RM1000834	4.06	3.09	6.2	8.49	9.42	10.49	** +
	NT2RM1000841	12.34	10.01	21.15	34.98	36.63	30.81	** +
	NT2RM1000848	4.79	4.42	6.44	9.36	12.74	10.45	** +
	NT2RM1000850	2.66	3.42	13.41	8.55	11.79	9.74	
50	NT2RM1000852	1.34	1.94	3.23	3.01	5.76	2.61	
	NT2RM1000853	1.19	2.85	2.15	3.11	3.26	3.23	
	NT2RM1000855	29.27	24.82	45.19	52.48	45.32	58.45	
	NT2RM1000857	4.63	5	10.67	8.76	11.3	10.76	
55	NT2RM1000858	7.3	7.6	15.86	9.09	11.56	10.93	

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	NT2RM1000867	19.42	15.85	28.1	32.52	35.03	24.06		
	NT2RM1000874	3.15	2.65	7.03	5.17	9.62	5.31		
	NT2RM1000882	2.36	1.37	3.71	5.39	9.31	5.45	*	+
5	NT2RM1000883	5.21	3.34	7.42	5.18	11.3	7.9		
	NT2RM1000885	3.86	4.43	9.4	7.59	8.15	9.8		
	NT2RM1000893	3.15	3.41	8.14	7.73	6.17	8.39		
	NT2RM1000894	3.29	4.4	6.18	8.14	6.11	6.61		
10	NT2RM1000898	3.72	7.33	10.02	13.4	17.51	12.41	*	+
	NT2RM1000899	1.02	2.22	3.07	3.68	7.49	4.69		
	NT2RM1000905	11.92	17.41	30.36	37.19	45.16	37.3	*	+
	NT2RM1000910	7.5	8.78	20.16	36.37	36.98	37.5	**	+
	NT2RM1000914	6.46	7.69	19.74	14.28	17.33	17.77		
15	NT2RM1000919	6.1	3.92	9.91	14.61	17.49	15.37	**	+
	NT2RM1000921	0.72	1.9	3.69	2.79	4.27	3.32		
	NT2RM1000922	4.7	6.11	8.09	9.03	5.21	6.36		
	NT2RM1000924	0.89	3.03	3.04	3.08	2.89	3		
20	NT2RM1000927	1.35	1.78	2.85	3.07	4.72	3.46		
	NT2RM1000951	7.95	11.33	26.73	32.33	34.46	31.18	*	+
	NT2RM1000956	7.91	6.36	13.35	23.61	27.46	21.91	**	+
	NT2RM1000960	12.48	10.27	29.06	34.95	37.47	38.96	*	+
	NT2RM1000961	3.28	3.61	7.45	9.44	13.18	8.11		
	NT2RM1000962	4.14	3.5	8.18	7.59	10.15	9.86		
25	NT2RM1000973	16.71	15.79	29.32	31.15	11.56	27.73		
	NT2RM1000978	0.57	1.46	1.58	0.95	2.64	0.44		
	NT2RM1000982	2.34	2.29	3.52	3.57	4.94	4.54	*	+
	NT2RM1000991	1.61	1.78	4.25	3.88	5.56	5.23		
30	NT2RM1000994	6.36	6.16	12.57	16.52	16.64	14.53	*	+
	NT2RM1001002	5.11	6.69	15.34	21.78	22.69	22.28	*	+
	NT2RM1001003	5.42	5.15	11.98	16.24	9.06	8.46		
	NT2RM1001008	1.4	2.22	2.48	1.83	4.34	4.33		
	NT2RM1001011	6.29	5.43	7.86	14.4	10.46	14.72	*	+
35	NT2RM1001013	2.9	2.75	4.75	8.29	7.96	5.81	*	+
	NT2RM1001017	1	1.82	3.44	3.28	4.86	3.92		
	NT2RM1001018	65.15	74.45	146.86	134.65	125.46	113.93		
	NT2RM1001026	1.37	2.64	3.17	2.99	4.61	3.31		
	NT2RM1001028	0.98	1.73	2.91	1.74	1.89	0.76		
40	NT2RM1001043	4.47	3.64	8.42	11.43	12.7	8.01		
	NT2RM1001044	2.23	3.17	4.92	5.03	5.51	3.93		
	NT2RM1001059	1.47	3.72	4.12	4.05	6.11	3.02		
	NT2RM1001063	4.11	3.29	6.1	4.22	5.64	5.6		
45	NT2RM1001066	0.86	1.85	2.44	2.23	3.99	2.85		
	NT2RM1001072	1.8	2.8	4.33	1.94	3.74	1.52		
	NT2RM1001074	1.66	2.38	5.18	5.18	4.19	2.67		
	NT2RM1001076	1.39	2.2	4.94	3.43	4.42	1.72		
	NT2RM1001082	1.79	2.6	5.23	5.31	5.92	4.57		
	NT2RM1001085	1.25	1.65	2.81	1.16	3.27	1.17		
50	NT2RM1001092	3.82	4.2	5.57	9.34	7.94	9.82	**	+
	NT2RM1001102	1.7	2.3	4.4	2.49	5.94	4.64		
	NT2RM1001103	4.37	3.88	7.18	6.25	10.28	8.08		
	NT2RM1001105	1.77	2.02	4.63	2.49	5.11	3.51		
	NT2RM1001112	2.68	2.66	3.69	3.85	4.75	2.43		
55	NT2RM1001115	1.44	1.57	4.72	3	6.46	3.73		

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	NT2RM1001122	2.84	3.35	7.3	9.43	9.75	9.54	*	+
	NT2RM1001136	0.88	1.41	2.71	2.31	3.87	1.59		
	NT2RM1001139	3.9	3.7	5.38	5.33	11.18	6.77		
5	NT2RM2000003	2.45	3.33	2.4	4.5	6.29	4.88	*	+
	NT2RM2000006	2.34	2.95	7.25	5.12	7.11	6.24		
	NT2RM2000010	12.79	13.03	22.58	20.2	17.11	21.83		
	NT2RM2000013	8.1	9.44	50.36	68.75	95.32	74.36	*	+
10	NT2RM2000030	4.8	2.21	23.41	26.33	32.15	28.69		
	NT2RM2000032	2.76	2.92	8.53	10.01	12.19	10.67	*	+
	NT2RM2000039	3.94	4.67	4.75	6.42	5.78	4.99		
	NT2RM2000042	3.5	4.9	11.69	17.71	17.4	15.02	*	+
	NT2RM2000092	1	2.38	1.98	1.29	4.69	2.25		
15	NT2RM2000093	8.37	6.63	11.41	9.02	12.23	10.18		
	NT2RM2000101	9.2	9.94	40	61.09	76.38	69.62	*	+
	NT2RM2000104	6.82	8.02	46.75	51.34	68.83	43.48		
	NT2RM2000124	1.54	2.23	6.33	7.73	8.84	8.47	*	+
	NT2RM2000155	5.08	3.77	5.8	9.45	11.58	12.51	**	+
20	NT2RM2000191	3.33	5.68	28.62	26.54	34.38	31.6		
	NT2RM2000192	1.03	1.29	2.45	6.3	4.75	3.83	*	+
	NT2RM2000239	1.92	2.79	3.09	2.85	5.02	3.1		
	NT2RM2000240	32.78	29.59	74.35	61.15	60.54	61.71		
	NT2RM2000241	4.49	5.9	6.35	8.24	11.72	6.78		
25	NT2RM2000250	1.29	1.54	4.16	2.09	5.05	2.54		
	NT2RM2000259	3.06	3.42	3.59	6.38	8.44	6.74	**	+
	NT2RM2000260	2.53	2.05	3.12	4.23	4.07	5.79	*	+
	NT2RM2000265	0.91	1.55	0.99	1.43	2.4	1.09		
30	NT2RM2000287	4.7	4.23	10.82	10.69	11.54	14.73		
	NT2RM2000306	12.24	9.36	10.48	23.63	14	20.79	*	+
	NT2RM2000312	19.4	17.81	25.01	38.39	31.27	24.8		
	NT2RM2000322	1.93	1.82	4.48	3.79	7.05	3.32		
	NT2RM2000343	7.74	8.38	41.34	63.81	79.6	71.12	*	+
35	NT2RM2000359	3.67	2.86	4.95	4.93	9.55	4.72		
	NT2RM2000362	20.09	18.2	62.29	94.88	111.25	95.66	*	+
	NT2RM2000363	1.08	1.89	2.97	4.2	4.32	3.33	*	+
	NT2RM2000368	2.84	2.4	4.74	6.15	5.98	5.29	*	+
	NT2RM2000371	76.64	65.68	119.32	135.82	125	44.64		
40	NT2RM2000374	1.68	1.92	5.75	3.34	4.8	3.58		
	NT2RM2000387	8.98	9.83	11.92	20.02	25.18	17.11	*	+
	NT2RM2000393	1.7	1.63	3.75	3.31	7.65	3.28		
	NT2RM2000395	1.07	1.51	1.98	1.72	4.34	2.23		
	NT2RM2000402	12.38	11	15.78	25.15	18.31	22.51	*	+
45	NT2RM2000405	1.33	1.25	2.2	1.52	3.08	3.16		
	NT2RM2000407	0.76	1.78	2.49	1.89	2.72	2.89		
	NT2RM2000410	0.79	1.94	2.23	1.98	2.84	2.09		
	NT2RM2000420	3.09	2.52	4.43	4.24	4.5	3.26		
	NT2RM2000422	3.22	2.44	5.81	3.61	6.17	2.87		
50	NT2RM2000423	1.91	1.96	5.69	3.89	7.64	4.18		
	NT2RM2000452	3.46	3.18	4.31	7.35	8.65	9.57	**	+
	NT2RM2000469	3.28	3.28	4.44	1.87	2.33	2.46	*	-
	NT2RM2000490	6.03	6.03	9.18	5.55	6.16	6.9		
	NT2RM2000497	3.29	3.29	4.59	3.15	5.48	2.43		
55	NT2RM2000502	4.69	4.69	10.24	5.87	7.08	7.02		

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	NT2RM2000504	7.37	7.37	12.93	10.83	4.49	11.2	
	NT2RM2000514	2.75	2.75	6.23	3.11	3.32	3.8	
	NT2RM2000522	1.9	1.9	3.27	1.94	1.18	1.13	
5	NT2RM2000540	6.02	6.02	9.53	9.12	8.96	8.14	
	NT2RM2000556	2.09	2.09	2.8	1.24	2.33	0.93	
	NT2RM2000565	3.35	3.35	6.02	3.27	4.14	3.72	
	NT2RM2000566	6.59	6.59	15.8	9.09	9.21	9.57	
10	NT2RM2000567	2.16	2.16	5.64	2	5.67	3.82	
	NT2RM2000569	4.69	4.69	7.93	5.77	8.18	4.7	
	NT2RM2000577	11.08	11.08	15.39	11.79	14.95	14.48	
	NT2RM2000581	4.64	4.64	6.49	5.98	7.97	6.85	
	NT2RM2000582	5.23	5.23	10.34	8.34	9.14	7.19	
15	NT2RM2000588	21.84	21.84	65.91	40.15	44.01	45.21	
	NT2RM2000589	3.98	3.98	11.35	7.96	7.6	8.64	
	NT2RM2000594	1.87	1.87	4.38	1.62	2.71	1.92	
	NT2RM2000599	6.34	6.34	16.12	17.82	14.5	15.44	
	NT2RM2000609	4.61	4.61	6.77	3.76	5.81	5.48	
20	NT2RM2000612	3.52	3.52	6.4	5.93	7.47	4.55	
	NT2RM2000622	16.6	16.6	56.24	53.07	75.02	55.48	
	NT2RM2000623	2.66	2.66	7.1	7.92	6.03	5.58	
	NT2RM2000624	4.18	4.18	10.6	7.33	14.39	7.56	
	NT2RM2000632	2.8	2.8	6.73	4.1	6.4	4.73	
25	NT2RM2000635	3.42	3.42	8.09	5.41	6.29	5.31	
	NT2RM2000636	2.61	2.61	6.28	3.99	4.39	3.72	
	NT2RM2000639	3.73	3.73	8.26	5.42	7.79	5.99	
	NT2RM2000649	6.03	6.03	9.69	9.4	9.17	8.05	
30	NT2RM2000658	6.49	6.49	13.18	15.17	14.66	15.83	* +
	NT2RM2000660	11.45	11.45	18.34	17.03	7.1	20.16	
	NT2RM2000669	3.6	3.6	6.51	5.28	4.28	6.69	
	NT2RM2000689	31.07	31.07	59.7	37.03	16.51	70.9	
	NT2RM2000691	2.09	2.09	5.73	4.83	7.13	4.27	
35	NT2RM2000714	3.41	3.41	10.97	11.46	14.54	11.3	
	NT2RM2000718	4.08	4.08	7.15	2.88	5.42	4.33	
	NT2RM2000732	5.38	5.38	14.81	9.49	14.18	8.25	
	NT2RM2000735	3.72	3.72	6.16	4.27	6.55	6.49	
	NT2RM2000740	2.26	2.26	6.2	4.27	3.01	3.71	
40	NT2RM2000743	2.26	2.26	7.89	5.65	3.24	3.89	
	NT2RM2000772	6.43	6.43	8.48	5.24	6.72	9.47	
	NT2RM2000773	8.17	8.17	19.56	19.18	17.96	18.29	
	NT2RM2000776	13.96	13.96	17.16	24.24	9.95	26.76	
	NT2RM2000784	6.64	6.64	8.8	8.74	9.02	10.5	
45	NT2RM2000795	4.35	4.35	13.56	7.44	8.66	10.45	
	NT2RM2000796	2.27	2.27	4.64	1.71	2.31	1.38	
	NT2RM2000798	25.81	25.81	160.08	158.19	136.83	188.99	
	NT2RM2000801	45.09	45.09	161.29	160.44	152.13	189.56	
	NT2RM2000821	7.53	7.53	12.33	7.37	7.77	11.87	
50	NT2RM2000829	5.76	5.76	13.01	8.05	10.13	11.75	
	NT2RM2000837	3.29	3.29	7.28	4.27	6.08	4.18	
	NT2RM2000924	9.96	9.96	36.74	43.24	57.8	35.84	
	NT2RM2000930	10.64	10.64	18.29	24.45	27.78	28.34	** +
	NT2RM2000937	4.35	4.35	8.62	5.08	6.66	6.56	
55	NT2RM2000939	1.12	1.12	2.37	2.67	1.84	1.82	

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	NT2RM2000942	124.8	124.8	253.61	161.4	118.61	210.11	
	NT2RM2000951	1.01	1.01	2.6	2.13	3.12	1.6	
	NT2RM2000952	2.53	2.53	5.31	5.98	6.41	6.86	* +
5	NT2RM2000966	19.69	19.69	111.88	95.61	137.32	135.9	
	NT2RM2000973	23.45	23.45	16.81	39.12	39.51	33.8	** +
	NT2RM2000983	10.07	10.07	18.59	30.68	39.13	27.52	* +
	NT2RM2000984	6.48	6.48	7.71	4.88	5.64	5.26	* -
10	NT2RM2000994	8.27	8.27	16.47	13.2	8.36	21.81	
	NT2RM2001004	6.01	6.01	48.58	47.51	54.15	46.8	
	NT2RM2001022	101.09	101.09	350.92	239.63	304.37	490.04	
	NT2RM2001035	10.75	10.75	24.98	24.17	24.54	34.51	
	NT2RM2001038	5.77	5.77	9.86	10.48	11.75	7.9	
15	NT2RM2001043	4.45	4.45	10.02	5.1	7.41	6.74	
	NT2RM2001050	2.71	2.71	6.89	4.72	5.83	4.03	
	NT2RM2001055	3.78	3.78	5.89	4.24	6.31	4.7	
	NT2RM2001065	6.17	6.17	15.91	8.51	12.12	14.21	
	NT2RM2001075	39.81	39.81	188.21	154.65	156.72	168.68	
20	NT2RM2001083	2.23	2.23	5.57	4.01	5.8	3.01	
	NT2RM2001100	10.38	10.38	93.67	95.8	113.9	97.52	
	NT2RM2001105	6.34	6.34	8.27	11.35	5.34	11.8	
	NT2RM2001109	6.81	6.81	9.4	11.88	12.47	14.53	* +
	NT2RM2001110	7.67	7.67	21.63	21.2	30.71	23.29	
25	NT2RM2001126	6.1	6.1	6.53	5.32	6.44	7.27	
	NT2RM2001131	5.52	5.52	40.22	21.93	29.37	20.14	
	NT2RM2001141	1.64	1.64	6.84	7.09	6.4	5.45	
	NT2RM2001152	1.63	1.63	3.27	4.42	5.77	3.02	
	NT2RM2001177	3.42	3.42	7.23	10.28	7.25	8.24	
30	NT2RM2001194	2.74	2.74	7.51	6.68	5.77	8.17	
	NT2RM2001195	3.7	3.7	8.8	6.37	7.13	6.89	
	NT2RM2001196	5.24	5.24	6.35	5.19	6.46	4.64	
	NT2RM2001201	14.45	14.45	25.36	20.02	21.68	22.38	
35	NT2RM2001221	4.22	4.22	8.61	11.69	13.61	16.63	* +
	NT2RM2001238	2.87	2.87	5.65	3.91	3.88	1.96	
	NT2RM2001243	5.39	5.39	8.98	9.81	6.13	6.53	
	NT2RM2001244	3.91	3.91	10.63	6.58	9.24	6.41	
	NT2RM2001247	14.94	14.94	121.59	110.47	140.27	118.79	
40	NT2RM2001256	3.84	3.84	5.23	3.15	3.26	2.96	
	NT2RM2001269	4.4	4.4	5.98	4.8	5.63	4.74	
	NT2RM2001278	5.28	5.28	7.37	8.45	8.56	5.35	
	NT2RM2001291	3.05	3.05	5.18	3.24	4.62	2.9	
	NT2RM2001294	12.47	12.47	24.39	20.08	15.43	17.81	
45	NT2RM2001295	2.56	2.56	8.82	4.54	4.43	4.99	
	NT2RM2001302	2.38	2.38	4.55	2.3	4.5	2.81	
	NT2RM2001306	3.51	3.51	7.62	4.1	4.46	5.14	
	NT2RM2001312	2.34	2.34	3.72	1.92	2.84	1.68	
	NT2RM2001319	2.76	2.76	3.93	3.61	5.29	4.11	
50	NT2RM2001324	3.73	3.73	8.29	5.48	4.9	5.71	
	NT2RM2001345	8.53	8.53	10.01	6.83	11.12	14.14	
	NT2RM2001360	4.02	4.02	6.36	5.67	5.9	5.46	
	NT2RM2001370	5.75	5.75	14.53	8.56	9.86	11.69	
	NT2RM2001391	1.79	1.79	6.07	1.85	5.04	1.65	
55	NT2RM2001393	4.49	4.49	6.39	5.12	7.91	7.14	

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	NT2RM2001420	2.94	2.94	4.61	2.61	3.62	3.14		
	NT2RM2001423	5.44	5.44	9.53	8.64	11.95	11.36		
	NT2RM2001424	5.88	5.88	15.09	11.77	10.31	11.63		
5	NT2RM2001482	2.24	2.24	6.48	3.5	6.06	3.63		
	NT2RM2001499	1.4	1.4	5.81	2.84	4.3	2.17		
	NT2RM2001504	3.63	3.63	6.99	3.2	4.54	1.68		
	NT2RM2001524	2.51	2.51	5.81	2.34	2.22	3.51		
10	NT2RM2001530	2.56	2.56	4.42	2.68	4.35	3.52		
	NT2RM2001533	5.06	5.06	9.09	8.2	9.18	7.84		
	NT2RM2001540	5.77	5.77	8.36	14.57	17.99	27.1	*	+
	NT2RM2001544	2.4	2.4	6.12	3.7	3.72	2.31		
	NT2RM2001547	6.6	6.6	15.29	8.44	7.61	8.24		
15	NT2RM2001558	1.53	1.53	3.44	1.76	4.87	1.71		
	NT2RM2001575	2.45	2.45	4.57	3.36	4.38	2.29		
	NT2RM2001582	2.99	2.99	4.98	2.2	5.16	3.06		
	NT2RM2001588	3.69	3.69	8.8	6.39	9.14	6.6		
	NT2RM2001592	2.66	2.66	6.2	3.1	5.24	4.64		
20	NT2RM2001603	4.74	4.74	8.7	10.42	12.03	11.77	*	+
	NT2RM2001605	1.74	1.74	4.52	3.08	1.51	2.39		
	NT2RM2001611	2.28	2.28	8.63	3.74	3.34	3.51		
	NT2RM2001613	14.91	14.91	32.53	21.51	13.13	27.42		
25	NT2RM2001626	2.45	2.45	3.08	2.1	4.28	2.06		
	NT2RM2001632	4.93	4.93	7.07	4.67	4.88	5.42		
	NT2RM2001633	4.45	4.45	10.39	3.74	5.15	5.43		
	NT2RM2001635	4.33	4.33	9.54	4.3	5.81	4.7		
	NT2RM2001636	4.88	4.88	7.35	12.75	18.11	13.34	**	+
30	NT2RM2001637	1.25	1.25	6.48	4.18	3.68	2.51		
	NT2RM2001639	3.98	3.98	9.32	4.67	4.33	3.29		
	NT2RM2001641	1.63	1.63	4.69	4.84	6.02	2.71		
	NT2RM2001643	2.78	2.78	7.46	4.79	4.4	2.83		
	NT2RM2001648	12.97	12.97	18.91	20.13	17.07	25.5		
35	NT2RM2001652	6.32	6.32	5.65	4.29	8.13	4.46		
	NT2RM2001659	5.78	5.78	9.17	5.73	5.28	6.95		
	NT2RM2001660	3.44	3.44	3.86	2.08	2.29	2.63	**	-
	NT2RM2001664	1.24	1.24	6.12	4.51	4.89	4.8		
	NT2RM2001668	3.72	3.72	8.16	7.66	5.72	7.02		
40	NT2RM2001670	1.62	1.62	4.11	2.88	3.96	3.56		
	NT2RM2001671	2.67	2.67	5.57	3.9	6.46	4.85		
	NT2RM2001675	1.94	1.94	4.28	1.97	3.73	0.64		
	NT2RM2001681	2.47	2.47	5.91	3.13	4.64	3.39		
	NT2RM2001685	4.58	4.58	5.68	1.29	2.72	1.14	**	-
45	NT2RM2001688	5.46	5.46	4.14	3.11	3.82	2.46	*	-
	NT2RM2001695	15.09	15.09	35.18	17.41	19.26	34.51		
	NT2RM2001696	2.74	2.74	6.64	7.15	6.7	6.8		
	NT2RM2001698	1.44	1.44	3	4.06	3.49	1.65		
50	NT2RM2001699	1.63	1.63	5.03	4.19	3.75	5.48		
	NT2RM2001700	1.65	1.65	4.13	2.56	3.37	3.91		
	NT2RM2001704	2.68	2.68	5.46	3.89	3.85	3.99		
	NT2RM2001706	4.29	4.29	6.77	3.33	3.13	3.32		
	NT2RM2001714	6.48	6.48	6.64	5.62	7.33	5.18		
	NT2RM2001716	0.97	0.97	3.7	3.03	5.49	2.92		
55	NT2RM2001718	1.91	1.91	3.47	5	3.5	3		

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	NT2RM2001723	2.09	2.09	5.48	5.1	5.21	5.71	
	NT2RM2001727	3.08	3.08	6.25	7.51	7.28	5.7	
	NT2RM2001730	3.52	3.52	7.15	5.04	5.43	3.85	
5	NT2RM2001738	4.56	4.56	6.2	6.71	10.25	9.08	* +
	NT2RM2001743	2.95	2.95	5.81	4.39	5.02	4.46	
	NT2RM2001753	5.98	5.98	7.55	5.72	6.09	4.54	
	NT2RM2001755	0.89	0.89	2.82	2.4	2.83	2.67	
10	NT2RM2001760	14.77	14.77	33.17	27.49	25.48	36.23	
	NT2RM2001765	1.35	1.35	1.71	2.45	3.12	2.03	* +
	NT2RM2001767	12.04	12.04	120.66	148.84	168.4	146.29	* +
	NT2RM2001768	2.1	2.1	3.59	3.41	4.21	3.05	
	NT2RM2001771	4.82	4.82	5.65	7.15	5.97	5.05	
15	NT2RM2001778	2.89	2.89	4.09	2.34	3.24	1.48	
	NT2RM2001782	5.32	5.32	7.32	4.96	7.71	7.57	
	NT2RM2001784	0.84	0.84	2.19	2.81	2.5	1.41	
	NT2RM2001785	1.35	1.35	4.11	5.5	5.02	2.76	
	NT2RM2001792	6.03	6.03	8.53	5.49	5.54	5.76	
20	NT2RM2001795	3.97	3.97	6.15	7.62	5.96	8.9	
	NT2RM2001797	2.82	2.82	3.78	5	5.94	2.71	
	NT2RM2001800	3.46	3.46	4.26	5.01	4.03	5.24	
	NT2RM2001803	3.5	3.5	6.61	4.46	7.34	2.44	
	NT2RM2001805	3.65	3.65	3.21	2.53	4.2	1.71	
25	NT2RM2001806	7.34	7.34	17.96	15.62	15.23	21.11	
	NT2RM2001813	1.54	1.54	2.05	2.54	1.88	2.32	
	NT2RM2001814	2.46	2.46	4.71	3.52	2.89	4.42	
	NT2RM2001818	1.21	1.21	2.66	0.97	1.48	0.27	
	NT2RM2001823	1.4	1.4	3.24	1.87	2.46	1.37	
30	NT2RM2001825	14.79	14.79	36.08	34.68	34.2	35.81	
	NT2RM2001832	5.93	5.93	6.1	5.19	5.48	2.93	
	NT2RM2001839	67.48	67.48	123.46	152.63	157.11	121.35	
	NT2RM2001840	3.04	3.04	7.13	4.61	5.11	5.37	
	NT2RM2001851	3.92	3.92	7.61	3.78	4.74	6.49	
35	NT2RM2001855	8.21	8.21	11.51	10.22	12.06	15.41	
	NT2RM2001867	2.82	2.82	5.01	2.83	5.62	3.74	
	NT2RM2001869	60.8	60.8	90.58	101.19	79.67	105.32	
	NT2RM2001879	3.01	3.01	6.99	2.55	3.19	2.66	
	NT2RM2001883	1.52	1.52	3.26	0.98	2.28	0.73	
40	NT2RM2001886	1.57	1.57	4.56	2.48	3.51	2.42	
	NT2RM2001887	3.78	3.78	7.66	4.48	4.97	5.73	
	NT2RM2001896	274.2	274.2	378.57	325.68	216.52	497.31	
	NT2RM2001902	1.92	1.92	4.28	1.31	2.92	2.14	
45	NT2RM2001903	16.25	16.25	42.55	35.47	31.71	37.22	
	NT2RM2001930	2.11	2.11	6.3	2.3	5.86	5.44	
	NT2RM2001935	4.16	4.16	5.04	3.16	4.42	5.87	
	NT2RM2001936	2.81	2.81	4.9	2.99	3.44	4	
	NT2RM2001939	3.56	3.56	3.34	1.82	3.01	3.16	
50	NT2RM2001941	1.84	1.84	4.29	2.84	2.82	2.72	
	NT2RM2001950	4.66	4.66	10	6.01	6	8.69	
	NT2RM2001952	2.67	2.67	4.78	2.49	4.55	5.37	
	NT2RM2001976	11.48	11.48	18.2	14.58	11.46	35.27	
	NT2RM2001982	1.85	1.85	3.91	2.04	2.47	1.88	
55	NT2RM2001983	4.45	4.45	8.36	4.18	6.49	7.54	

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	NT2RM2001984	7.74	7.74	8.88	20.06	27.05	22.95	**	+
	NT2RM2001989	2.72	2.72	3.68	2.99	4.26	3.7		
	NT2RM2001996	7.51	7.51	8.09	4.8	8.01	5.29		
5	NT2RM2001997	3.65	3.65	7.29	3.18	5.09	6.78		
	NT2RM2001998	2.24	2.24	5.07	3.33	6.53	3.96		
	NT2RM2001999	4.86	4.86	7.69	6.88	6.02	4.01		
	NT2RM2002003	11.33	11.33	18.17	10.15	11	14.9		
	NT2RM2002004	1.99	1.99	5.79	2.51	2.09	1.9		
10	NT2RM2002009	5.35	5.35	9.03	9.85	11.04	11.09	*	+
	NT2RM2002014	2.62	2.62	3	3.65	4.47	4.03	**	+
	NT2RM2002019	25.1	25.1	38.52	19.47	14.2	16.35		
	NT2RM2002029	12.92	12.92	19.01	10.82	4.88	14.74		
15	NT2RM2002030	4.15	4.15	5.8	13.54	9.71	21.98	*	+
	NT2RM2002034	22.05	22.05	31.76	24.83	20.89	21.04		
	NT2RM2002049	7.4	7.4	12.12	9.76	10.42	13.22		
	NT2RM2002055	2.8	2.8	8.01	1.91	4.03	2.52		
	NT2RM2002072	9.26	9.26	12.88	12.28	19.12	12.82		
20	NT2RM2002088	4.82	4.82	13.85	11.35	11.7	15.28		
	NT2RM2002091	4.98	4.98	8.44	5.92	3.82	4.61		
	NT2RM2002100	3.26	3.26	6.05	4.82	4.24	3.19		
	NT2RM2002109	1.31	1.31	3.57	2.57	4.88	4.92		
	NT2RM2002126	21.41	21.41	32.24	35.28	22.31	31.52		
25	NT2RM2002128	3.7	3.7	5.17	2.74	3.86	2.41		
	NT2RM2002129	6.43	6.43	11.48	8.53	13.03	10.66		
	NT2RM2002142	5.72	5.72	9.74	5.26	8.91	6.4		
	NT2RM2002144	3.27	3.27	3.76	1.85	1.73	1.62	**	-
	NT2RM2002145	2.63	2.63	8.69	6.1	5.18	5.98		
30	NT2RM2002153	2.61	2.61	6.37	6.31	7.62	5.75		
	NT2RM2002163	0.97	0.97	3.41	1.87	3.4	0.64		
	NT2RM2002170	3.28	3.28	7.03	6.62	7.5	7.65		
	NT2RM2002178	3.99	3.99	3.67	3.5	5.48	2.9		
	NT2RM2002179	7.82	7.82	8.69	6.17	8.15	6.02		
35	NT2RM2002270	4.51	4.51	4.56	2.28	1.76	1.67	**	-
	NT2RM2002326	2.47	2.47	3.86	2.13	3.69	2.34		
	NT2RM2002337	1.88	1.88	3.97	5.4	4.22	4.79	*	+
	NT2RM2002339	2.83	2.83	6.29	5.26	5.22	3.85		
	NT2RM2002345	5.16	5.16	6.03	4.04	4.2	4.21	*	-
40	NT2RM2002368	2.43	2.43	5.86	6.05	7.01	4.96		
	NT2RM2002381	2.23	2.23	5.16	3.47	3.65	2.8		
	NT2RM2002424	4.64	4.64	7.1	6.69	8.5	6.3		
	NT2RM2002450	4.17	4.17	3.87	2.29	2.39	1.87	**	-
45	NT2RM2002482	3.93	3.93	4.65	2.66	3.2	3.79		
	NT2RM2002492	9.39	9.39	24.31	29.13	24.65	29.29		
	NT2RM2002575	3.26	3.26	5.23	5.99	6.03	5.07		
	NT2RM2002580	4.23	4.23	4.68	4.82	7.79	7.42		
	NT2RM2002592	7.7	7.7	12.59	13.07	15.28	14.69	*	+
50	NT2RM2002608	27.33	27.33	45.49	57.07	65.96	48.3	*	+
	NT2RM2002615	6.01	6.01	9.38	13.15	20.32	14.42	*	+
	NT2RM2002622	14.35	14.35	16.22	18.38	24.99	13.44		
	NT2RM2002630	4.86	4.86	6.63	8.05	7.37	6.7		
	NT2RM2002634	1.72	1.72	4.66	4.71	4.6	3.94		
55	NT2RM2002645	27.02	27.02	68.46	30.66	14.59	31.46		

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	NT2RM2002646	12.09	12.09	25.03	29.45	22.88	34.8	
	NT2RM2002647	7.68	7.68	17.56	19.5	17.74	23.44	
	NT2RM2002652	5.11	5.11	4.71	4.3	6.43	3.73	
5	NT2RM2002692	4.59	4.59	4.48	2.5	2.86	2.02	** -
	NT2RM2002721	30.26	30.26	46.01	62.71	84.18	61.02	* +
	NT2RM2002748	18.37	18.37	43.62	87.35	119.27	102.35	** +
	NT2RM2002764	2.28	2.28	5.3	5.05	5.95	4.07	
10	NT2RM2002772	3.15	3.15	9.32	9.66	7.81	5.44	
	NT2RM2002811	5.79	5.79	12.3	14.01	9.18	10.45	
	NT2RM2002818	2.03	2.03	7.94	5.86	5.42	7.13	
	NT2RM2002879	4.21	4.21	7.17	8.39	7.87	9.11	* +
	NT2RM2002979	11.79	11.79	19.66	24.49	23.23	21.79	* +
15	NT2RM2002981	4.42	4.42	3.78	3.58	4.95	2.63	
	NT2RM2002995	5.13	5.13	3.29	3.42	3.74	3.5	
	NT2RM2003031	1.37	1.37	2.63	3	2.58	1.9	
	NT2RM2003042	4.1	4.1	10.77	10.59	6.02	6.07	
	NT2RM2003044	1.88	1.88	4.11	2.13	5.11	1.2	
20	NT2RM2003090	4.4	4.4	7.64	9.36	7.91	10.68	* +
	NT2RM2003095	11.98	11.98	25.25	15.63	16.43	19.04	
	NT2RM2003116	11.16	11.16	16.09	17.96	21.43	22.08	* +
	NT2RM2003222	3.98	3.98	3.63	2.67	3.64	2.35	
	NT2RM2003224	11.29	11.29	15.33	24.29	29.77	20.76	* +
25	NT2RM2003250	14.18	14.18	86.06	85.79	96.6	94.15	
	NT2RM2003258	4.59	4.59	6.32	6.54	5.11	5.69	
	NT2RM2003262	5.07	5.07	7.33	5.06	7.76	5.72	
	NT2RM4000023	2.15	2.15	7.02	3.57	4.91	4.29	
30	NT2RM4000024	2.28	2.28	6.78	3.17	4.98	4.33	
	NT2RM4000027	4.74	4.74	7.77	4.85	6.94	11.32	
	NT2RM4000030	2.95	2.95	5.73	3.16	4.9	2.64	
	NT2RM4000033	2.51	2.51	4.77	2.36	3.89	4.61	
	NT2RM4000034	1.93	1.93	5.35	3.74	4.84	6.09	
35	NT2RM4000046	1.37	1.37	3.79	1.57	3.5	2.32	
	NT2RM4000052	1.82	1.82	3.55	1.72	2.96	1.98	
	NT2RM4000054	10.43	10.43	13.85	12.07	12.83	24.7	
	NT2RM4000061	1.65	1.65	4.17	1.66	4.54	0.83	
	NT2RM4000074	15.83	15.83	43.57	27.9	34.24	30.79	
40	NT2RM4000085	5.35	5.35	10.1	8.41	10.19	10.17	
	NT2RM4000086	3.06	3.06	4.5	3.84	5.25	3.71	
	NT2RM4000100	6.62	6.62	15.05	12.74	15.6	14.84	
	NT2RM4000101	3.77	3.77	9.11	7.17	7.71	8.78	
	NT2RM4000102	32.35	32.35	42.47	27.24	19.34	70.54	
45	NT2RM4000104	2.78	2.78	7.13	3.41	5.12	4.3	
	NT2RM4000115	2.87	2.87	6.1	3.91	5.86	4.08	
	NT2RM4000129	2.17	2.17	4.75	2.62	3.48	2.18	
	NT2RM4000139	3.17	3.17	3.31	3.58	4.82	6.49	
	NT2RM4000149	2.74	2.74	1.49	2.41	2.55	7.32	
50	NT2RM4000155	2.73	2.73	5.5	2.13	4.51	3.71	
	NT2RM4000156	5.94	5.94	16.74	20.45	21	21.96	* +
	NT2RM4000167	1.36	1.36	2.58	2.61	4.34	1.75	
	NT2RM4000169	9.95	9.95	36.53	29.12	24.89	23.57	
	NT2RM4000191	4.29	4.29	7.56	5.49	5.57	5.66	
55	NT2RM4000197	2.73	2.73	4.78	1.83	3.86	2.2	

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	NT2RM4000198	3.38	3.38	7.42	5.26	5.45	4.21	
	NT2RM4000199	2	2	3.51	2.8	4	3.76	
	NT2RM4000200	0.67	0.67	3.19	2.25	1.84	1.2	
5	NT2RM4000202	1	1	3.24	2.11	2.42	1.84	
	NT2RM4000210	1.46	1.46	3.72	2.41	3.08	2.21	
	NT2RM4000215	2.54	2.54	5.43	3.3	4.09	3.06	
	NT2RM4000220	6.42	6.42	10.52	8.68	11.08	15.14	
10	NT2RM4000229	3.26	3.26	6.62	1.46	2.34	1.76	
	NT2RM4000231	6.37	6.37	7.06	6.13	7.85	6.24	
	NT2RM4000233	4.83	4.83	17.3	11.9	14.34	13.4	
	NT2RM4000244	2.35	2.35	5.22	3.86	4.14	5.17	
	NT2RM4000251	3.85	3.85	10.97	4.82	6.52	4.59	
15	NT2RM4000255	2.28	2.28	4.7	3.79	4.89	1.42	
	NT2RM4000265	2.23	2.23	5.69	4.29	8.21	1.99	
	NT2RM4000283	18.14	18.14	26.21	37.17	39.88	44.79	** +
	NT2RM4000284	13.85	13.85	33.72	31.96	42.88	40.67	
	NT2RM4000290	6.31	6.31	7.76	3.77	4.92	4	*
20	NT2RM4000295	2.36	2.36	2.16	2.32	2.13	0.88	
	NT2RM4000306	3.79	3.79	7.76	7.1	6.14	5.02	
	NT2RM4000307	5.04	5.04	9.13	9.95	9.99	11.72	* +
	NT2RM4000309	2.48	2.48	5.34	3.92	6.52	5.52	
	NT2RM4000313	3.92	3.92	9.61	5.75	7.77	8.52	
25	NT2RM4000318	3.38	3.38	6.87	4.35	6.36	3.28	
	NT2RM4000324	4.93	4.93	5.93	2.79	4.98	2.12	
	NT2RM4000326	5.32	5.32	4.61	2.59	2.45	2.01	** -
	NT2RM4000327	4.97	4.97	10.95	7.94	10.32	7.71	
	NT2RM4000344	5.46	5.46	16.67	11.16	10.17	19.18	
30	NT2RM4000349	3.68	3.68	9.99	11.87	10.88	13.8	* +
	NT2RM4000354	1.65	1.65	3.13	4.2	4.31	3.1	
	NT2RM4000356	1.5	1.5	3.11	2.5	4.07	1.64	
	NT2RM4000366	15.75	15.75	44.48	38.81	44.07	58.06	
	NT2RM4000368	3.04	3.04	5.9	4.36	5.48	3.48	
35	NT2RM4000373	6.49	6.49	12.29	12.72	15.96	16.47	* +
	NT2RM4000386	4.92	4.92	4.71	3.81	4.57	4.6	
	NT2RM4000395	2.7	2.7	4.69	6.36	6.51	5.68	* +
	NT2RM4000414	1	1	2.76	2.38	2.9	2.19	
40	NT2RM4000417	1.66	1.66	2.83	3.9	3.95	3.25	* +
	NT2RM4000421	2.99	2.99	5.17	4.96	5.47	4.13	
	NT2RM4000425	10.56	10.56	26.8	26.49	31.48	45.28	
	NT2RM4000433	2.78	2.78	5.39	1.67	2.21	1.79	
	NT2RM4000436	3.8	3.8	9.47	11.84	16.75	16.38	* +
45	NT2RM4000444	4.51	4.51	12.97	7.29	8.54	7.38	
	NT2RM4000457	3.35	3.35	8.69	13.35	12.38	13.25	* +
	NT2RM4000471	1.73	1.73	4.01	4.17	4.87	2.49	
	NT2RM4000472	2.2	2.2	7.62	6.64	7.61	5.39	
	NT2RM4000486	2.98	2.98	5.92	6.85	7.54	6	
50	NT2RM4000490	3.85	3.85	6.41	7.16	5.1	5.86	
	NT2RM4000496	3.68	3.68	3.86	2.16	2.36	2.04	** -
	NT2RM4000505	26.85	26.85	60.33	68.9	80.59	70.67	* +
	NT2RM4000511	22.8	22.8	45.35	64.6	89.95	75.97	* +
	NT2RM4000514	2.61	2.61	6.75	10.47	7.53	9.25	* +
55	NT2RM4000515	3.75	3.75	8.81	7.27	7.94	4.66	

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	NT2RM4000517	34.51	34.51	74.2	76.45	53.07	79.47	
	NT2RM4000520	2.24	2.24	3.08	3.21	3.3	5.49	
	NT2RM4000531	2.76	2.76	5.71	4.41	5.5	4.22	
5	NT2RM4000532	3.03	3.03	5.56	2.72	3.54	2.39	
	NT2RM4000533	3.55	3.55	5.43	4.73	6.98	3.23	
	NT2RM4000534	5.17	5.17	2.92	2.73	4.62	1.94	
	NT2RM4000563	5.21	5.21	16.69	17.05	16.8	19.36	
	NT2RM4000566	1.79	1.79	4.6	7.14	5.27	7.91	* +
10	NT2RM4000568	10.48	10.48	19.4	28.18	22.91	33.06	* +
	NT2RM4000585	1.97	1.97	2.52	0.82	1.99	1.26	
	NT2RM4000587	3.88	3.88	6.15	6.66	5.75	5.15	
	NT2RM4000590	3.73	3.73	4.12	1.64	2.48	2.3	** -
	NT2RM4000593	4.46	4.46	7.83	10.21	12.36	7.45	
15	NT2RM4000595	3.94	3.94	3.91	2.27	4.36	2.45	
	NT2RM4000603	4.18	4.18	6.98	6.95	7.23	7.26	
	NT2RM4000611	9.81	9.81	18.02	17.1	17.38	25.49	
	NT2RM4000616	2.05	2.05	6.19	2.73	4.14	4.53	
20	NT2RM4000621	26.04	26.04	70.86	57.5	62.2	59.07	
	NT2RM4000648	2.78	2.78	7.83	2.66	2.67	3.88	
	NT2RM4000649	5.53	5.53	11.03	7.34	8.4	13.12	
	NT2RM4000658	3.22	3.22	8.18	4.22	6.14	8.14	
	NT2RM4000661	57.68	57.68	140.68	141.09	135.49	177.49	
25	NT2RM4000673	3.02	3.02	5.72	3.69	3.8	4.59	
	NT2RM4000674	2.23	2.23	4.27	2.89	2.63	2.99	
	NT2RM4000689	3.81	3.81	6.47	5.34	6.36	7.74	
	NT2RM4000698	14.85	14.85	20.92	25.12	23.66	26.39	* +
	NT2RM4000700	2.39	2.39	5.53	2.41	6.95	5.61	
30	NT2RM4000701	10.07	10.07	54.36	61.81	67.75	63.17	
	NT2RM4000712	3.5	3.5	7.9	5.97	8.03	9.55	
	NT2RM4000717	2.14	2.14	6.66	3.67	2.94	4.3	
	NT2RM4000733	4.37	4.37	7.8	4.16	6.93	11.03	
	NT2RM4000734	2.17	2.17	5.92	2.35	5.23	4.7	
35	NT2RM4000741	2.14	2.14	6.11	3.59	4.75	4.66	
	NT2RM4000744	1.76	1.76	7.05	2.76	4.4	10.18	
	NT2RM4000749	15.53	15.53	23.13	26.26	27.8	34.67	* +
	NT2RM4000751	2.88	2.88	6.54	6.23	6.11	5.94	
	NT2RM4000752	4.11	4.11	4.88	4.78	5.12	38.58	
40	NT2RM4000760	3.5	3.5	9.69	4.54	6.31	5.26	
	NT2RM4000761	237.9	237.9	478.3	219.65	302.54	336.34	
	NT2RM4000764	66.05	66.05	178	212.33	205.98	232.75	* +
	NT2RM4000768	6.11	6.11	11.21	15.56	10.14	21.17	
	NT2RM4000778	1.6	1.6	4.7	4.27	5.18	6.18	
45	NT2RM4000779	4.52	4.52	8.28	6.87	7.19	7.33	
	NT2RM4000787	2.55	2.55	7.49	3.64	4.9	4.53	
	NT2RM4000790	2.99	2.99	5.03	5.47	5.82	12.06	
	NT2RM4000795	1.99	1.99	3.67	2.36	1.2	2.51	
	NT2RM4000796	3.26	3.26	5.86	4.29	3.48	4.28	
50	NT2RM4000798	1.77	1.77	5.53	3.72	3.08	3.47	
	NT2RM4000800	4.15	4.15	8.16	8.7	9.44	9.06	
	NT2RM4000813	3.31	3.31	8.79	7.14	7.95	10.09	
	NT2RM4000820	4.89	4.89	9.14	5.39	6.27	5.44	
55	NT2RM4000827	7.1	7.1	18.55	16.3	15.8	17.88	

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	NT2RM4000830	3.27	3.27	7.35	5.28	7.8	8.38
	NT2RM4000833	2.51	2.51	6.84	4.48	3.35	4.87
	NT2RM4000841	4	4	15	10.57	8.84	10.1
5	NT2RM4000846	1.66	1.66	8.83	4.74	6.83	5.09
	NT2RM4000848	2.61	2.61	5.75	4.15	6.32	3.12
	NT2RM4000852	3.89	3.89	9.81	8.16	8.67	8.29
	NT2RM4000855	5.12	5.12	7.64	5.99	6.08	7.19
	NT2RM4000859	11.18	11.18	16.28	16.48	19.12	17.62
10	NT2RM4000868	3.06	3.06	6.47	5.23	6.91	7.05
	NT2RM4000870	4	4	9.82	7.06	3.87	6.59
	NT2RM4000879	1.67	1.67	6	4.15	3.31	3.11
	NT2RM4000882	18.99	18.99	28.36	20.33	16.5	12.55
	NT2RM4000887	2.16	2.16	6.01	3.53	4.91	1.6
15	NT2RM4000895	2.33	2.33	5.33	3.16	5.9	3.08
	NT2RM4000897	5.78	5.78	6.99	8.89	9.73	7.02
	NT2RM4000901	5.22	5.22	6.41	4.37	6.2	6.12
	NT2RM4000950	4.04	4.04	5.09	3.57	4.06	2.91
20	NT2RM4000965	2.89	2.89	4.54	5.98	4.04	6.18
	NT2RM4000971	2.49	2.49	4.78	4.84	4.29	7.62
	NT2RM4000979	5.16	5.16	12.71	10.23	10.46	7.87
	NT2RM4000987	1.9	1.9	4.59	3.64	4.22	3.21
	NT2RM4000989	2.51	2.51	5.17	4.2	5.16	4.99
25	NT2RM4000991	3.1	3.1	4.83	2.87	3.53	8.73
	NT2RM4000992	3.39	3.39	5.41	3.6	4.54	3.19
	NT2RM4000996	6.22	6.22	7.86	7.14	8	7.28
	NT2RM4000997	3.53	3.53	13.96	9.81	10.96	10.89
	NT2RM4001001	26.06	26.06	55.43	37.67	34.22	54.29
30	NT2RM4001002	5.13	5.13	11.03	11.54	11.33	19.44
	NT2RM4001016	1.63	1.63	2.73	4.07	5.31	3.76 * +
	NT2RM4001025	65.77	65.77	133.97	148.39	181.87	171.5 * +
	NT2RM4001027	2.49	2.49	3.66	1.67	1.77	4.31
	NT2RM4001032	2.55	2.55	6.74	4.94	5.46	3.84
35	NT2RM4001047	3.87	3.87	3.7	2.61	2.73	2.7 ** -
	NT2RM4001049	3.97	3.97	10.12	18.29	20.63	26.25 ** +
	NT2RM4001051	2.72	2.72	12.54	11.17	10.12	13.68
	NT2RM4001052	14.95	14.95	72.14	75.49	75.01	79.12
	NT2RM4001053	14.96	14.96	39.3	41.36	28.95	25.87
40	NT2RM4001054	3.13	3.13	5.17	5.34	5.69	5.01
	NT2RM4001059	3.65	3.65	6.37	4.91	3.52	4.48
	NT2RM4001071	4.03	4.03	7.35	6.8	7.34	6.55
	NT2RM4001084	8.04	8.04	6.52	9.49	10.53	9.53 * +
	NT2RM4001092	12.61	12.61	109.97	76.93	98.78	73.14
45	NT2RM4001100	6.72	6.72	20.93	22.35	15.18	18.98
	NT2RM4001116	1.17	1.17	2.5	2.77	2.96	2.16
	NT2RM4001119	1.74	1.74	4.82	4.72	4.22	4.15
	NT2RM4001140	2.65	2.65	7.49	8.27	7.78	9.03
	NT2RM4001148	6.59	6.59	13.68	12.1	12.92	15.83
50	NT2RM4001151	3.7	3.7	4.31	1.94	3.65	1.68
	NT2RM4001155	5.51	5.51	6.36	3.55	5.37	4.63
	NT2RM4001157	1.68	1.68	4.95	4.86	2.81	3.82
	NT2RM4001160	1.57	1.57	3.39	2.99	1.9	2.41
55	NT2RM4001163	42.35	42.35	86.27	106.63	52.13	98.56

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	NT2RM4001187	2.64	2.64	7.25	3.96	4.87	5.2
	NT2RM4001191	3.2	3.2	9.95	8.59	6.36	8.72
	NT2RM4001200	3.83	3.83	6.35	5.52	4.41	4.11
5	NT2RM4001203	9.93	9.93	20.29	22.65	25.36	21.82
	NT2RM4001204	3.23	3.23	3.59	3.17	2.83	2.6
	NT2RM4001217	4.62	4.62	12.16	11.26	13.39	13.72
	NT2RM4001245	7.31	7.31	17.14	13.76	14.49	17.16
10	NT2RM4001247	3.23	3.23	9.1	5.73	6.57	5.03
	NT2RM4001256	2.51	2.51	6.39	3.57	5.48	4.14
	NT2RM4001258	8.2	8.2	24.68	25.02	24.16	22.89
	NT2RM4001267	3.43	3.43	4.83	3.93	4.3	8.08
	NT2RM4001273	4.23	4.23	8.38	7.39	6.96	8.77
15	NT2RM4001281	4	4	10.54	10.15	9.05	10
	NT2RM4001286	345.27	345.27	526.77	215.2	220.51	552.53
	NT2RM4001290	23.51	23.51	61.5	56.51	48.6	59.58
	NT2RM4001309	2.64	2.64	6.81	3.17	5.42	4.05
	NT2RM4001313	2.63	2.63	8.62	3.81	6.36	7.03
20	NT2RM4001316	3.14	3.14	6.12	3.39	3.85	5.25
	NT2RM4001320	2.4	2.4	6.43	2.83	3.16	5.6
	NT2RM4001321	3.98	3.98	8.62	6.17	7.03	6.24
	NT2RM4001325	2.54	2.54	5.2	4.76	2.93	5.25
	NT2RM4001333	8.65	8.65	18.06	8.57	10.76	9.51
25	NT2RM4001340	4.81	4.81	12.27	6.99	7.72	11.24
	NT2RM4001344	4.09	4.09	4.69	3.04	3.44	4.93
	NT2RM4001347	6.49	6.49	9.8	10.53	9.72	17.71
	NT2RM4001357	7.59	7.59	12.09	8.58	11.68	9.37
	NT2RM4001360	2.79	2.79	5.11	3.82	2.85	3.07
30	NT2RM4001371	4.71	4.71	8.57	6.58	13.16	12.93
	NT2RM4001377	8.01	8.01	13.74	8.66	9.23	10.58
	NT2RM4001382	17.31	17.31	56.74	35.57	28.32	38.22
	NT2RM4001384	2.17	2.17	4.11	2.35	3.34	3.75
	NT2RM4001400	3.78	3.78	5.76	4.87	4.66	5.07
35	NT2RM4001409	2.55	2.55	6.82	4.82	4.63	5.27
	NT2RM4001410	5.48	5.48	21.69	17.34	21.09	18.91
	NT2RM4001411	2.66	2.66	6.5	5.86	6.64	6.77
	NT2RM4001412	1.75	1.75	3.33	2.39	2.52	2.79
	NT2RM4001414	2.18	2.18	4.83	2.45	2.4	3.77
40	NT2RM4001436	8.35	8.35	16.65	10.45	10.13	15.55
	NT2RM4001437	2.77	2.77	8.85	8.31	11.26	7.67
	NT2RM4001444	11.57	11.57	25.93	21.1	18.36	18.42
	NT2RM4001454	3.62	3.62	7.89	6.16	5.03	4.79
	NT2RM4001455	5.85	5.85	22.19	18.03	25.08	26.16
45	NT2RM4001483	4.37	4.37	8.77	4.97	5.43	6.46
	NT2RM4001489	3.12	3.12	7.04	3.64	4.19	5.46
	NT2RM4001495	1.35	1.35	5.13	2.85	3.29	3.37
	NT2RM4001499	1.74	1.74	4.98	3.65	2.77	3.3
	NT2RM4001515	0.95	0.95	3.38	2.65	5.38	3.41
50	NT2RM4001519	1.86	1.86	4.6	2.24	4.38	2.85
	NT2RM4001522	3.8	3.8	7.66	5.36	7.42	9.13
	NT2RM4001523	5.46	5.46	9.11	4.82	7.58	5.79
	NT2RM4001550	11.9	11.9	17.38	16.49	16.76	15.01
55	NT2RM4001553	7.88	7.88	13.4	23.26	23.53	23.87 ** +

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	NT2RM4001554	0.86	0.86	1.74	1.85	1.11	2.2	
	NT2RM4001557	2.5	2.5	6.33	5.05	3.36	4.89	
	NT2RM4001565	1.87	1.87	4.05	2.46	3.34	3.23	
5	NT2RM4001566	3.23	3.23	8.57	8.91	10.49	11.42	
	NT2RM4001569	1.47	1.47	5.4	3.35	4.15	1.56	
	NT2RM4001579	6.57	6.57	16.69	19.23	23.83	18.22	
	NT2RM4001582	4.06	4.06	5.97	2.16	3.17	2.67	*
	NT2RM4001589	21.51	21.51	37.16	42.45	55.76	47.57	* +
10	NT2RM4001592	1.37	1.37	2.96	3.02	2.14	3.71	
	NT2RM4001594	1.98	1.98	4.09	5.4	5.24	5.67	* +
	NT2RM4001597	2.65	2.65	5.64	5.17	4.97	4.33	
	NT2RM4001605	2.7	2.7	6.18	5.71	5.92	5.93	
	NT2RM4001609	23.65	23.65	45	61.08	78.89	77.31	* +
15	NT2RM4001610	48.1	48.1	69.16	132.54	132.39	115.22	** +
	NT2RM4001611	3.31	3.31	4.56	2.33	2.32	2.02	*
	NT2RM4001618	7.05	7.05	7.95	6.68	8.98	12.95	
	NT2RM4001622	13.53	13.53	19.88	14.67	24.67	28.46	
20	NT2RM4001624	1.6	1.6	3.02	3.92	2.66	4.43	
	NT2RM4001625	4.89	4.89	39.6	41.63	47.1	46.46	
	NT2RM4001629	3.82	3.82	8.82	12.09	12.08	13.38	* +
	NT2RM4001632	15.28	15.28	24.55	31.07	26.16	25.6	
	NT2RM4001642	3.29	3.29	4.17	2.89	3.62	2.1	
25	NT2RM4001647	4.44	4.44	6.83	4.04	5.48	4.67	
	NT2RM4001650	4.96	4.96	4.94	2.66	2.87	3.79	** -
	NT2RM4001662	2.18	2.18	5.47	8.31	6.54	9.39	* +
	NT2RM4001666	2.28	2.28	6.5	6.24	6.17	8.14	
	NT2RM4001670	3.52	3.52	10.77	11.16	10.82	14.91	
30	NT2RM4001682	12.66	12.66	31.6	33.03	26.04	37.07	
	NT2RM4001710	6.7	6.7	38.5	40.58	58.41	40.31	
	NT2RM4001712	4.06	4.06	7.61	10.19	10.7	9.98	* +
	NT2RM4001714	10.88	10.88	19.37	18.67	19.3	17.65	
	NT2RM4001715	10.77	10.77	11.6	13.55	16.86	12.99	
35	NT2RM4001727	3.41	3.41	5.92	4.83	5.89	7.6	
	NT2RM4001731	2.6	2.6	10.72	13.46	11.23	11.73	
	NT2RM4001735	12.84	12.84	21.53	22.01	20.88	34.93	
	NT2RM4001739	2.46	2.46	7.3	8.13	5.17	7.14	
40	NT2RM4001741	14.41	14.41	29.88	26.98	27.21	32.35	
	NT2RM4001746	3.65	3.65	6.76	6.89	6.5	5.33	
	NT2RM4001754	3.16	3.16	4.17	3.39	3.62	3.84	
	NT2RM4001757	5.02	5.02	5.78	4.7	6.31	7.97	
	NT2RM4001758	1	1	0.76	1.98	0.65	1.46	
45	NT2RM4001768	4.83	4.83	10.19	8.48	6.91	7.83	
	NT2RM4001775	3.23	3.23	2.76	1.9	1.85	1.71	** -
	NT2RM4001776	2.56	2.56	4.77	2.47	2.68	2.69	
	NT2RM4001783	2.88	2.88	3.22	3.12	3.48	3.68	
	NT2RM4001793	4.67	4.67	11.44	12.02	9.6	10.75	
50	NT2RM4001810	3.31	3.31	4.46	3.33	3.63	3.11	
	NT2RM4001813	3.9	3.9	4.15	4.71	4.19	5.36	
	NT2RM4001818	4.06	4.06	11.34	10.43	8.67	10.53	
	NT2RM4001819	2.35	2.35	5.6	2.37	3.02	4.58	
	NT2RM4001823	1.76	1.76	4.48	2.47	4.04	4.27	
55	NT2RM4001828	5.01	5.01	11.49	5.67	7.54	7.51	

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	NT2RM4001835	9.75	9.75	18.65	21.12	16.5	26.55		
	NT2RM4001836	3.27	3.27	8.32	3.65	3.54	5.58		
	NT2RM4001841	7.94	7.94	15.82	20.15	20.96	23.33	*	+
5	NT2RM4001842	2.1	2.1	4.44	3.5	3.35	4.85		
	NT2RM4001843	5.65	5.65	14.54	13.34	12.25	14.94		
	NT2RM4001856	4.42	4.42	7.16	7.65	4.71	16.83		
	NT2RM4001858	5.91	5.91	15.86	16.09	17.03	16.93		
	NT2RM4001861	2.91	2.91	9.57	6.31	8.66	9.28		
10	NT2RM4001863	8.06	8.06	9.5	15.16	15.68	11.77	*	+
	NT2RM4001865	5.04	5.04	11.25	7.44	10.24	9.03		
	NT2RM4001869	5.1	5.1	5.96	5.22	8.45	21.88		
	NT2RM4001873	9.62	9.62	18.43	13.33	15.49	19.21		
15	NT2RM4001876	2.24	2.24	6.94	3.65	4.39	7.25		
	NT2RM4001880	3.6	3.6	8.57	5.13	5.41	7.67		
	NT2RM4001885	5.71	5.71	11.11	7.11	6.56	11.98		
	NT2RM4001889	10.25	10.25	18.24	16.31	15.85	21.33		
	NT2RM4001894	2.61	2.61	6.07	3.58	3.65	3.49		
20	NT2RM4001897	7.87	7.87	20.24	18.41	20.4	23.46		
	NT2RM4001899	3.36	3.36	7.43	4.92	8.19	8.54		
	NT2RM4001905	3	3	4.84	3.3	4.53	7.1		
	NT2RM4001922	2.55	2.55	6.05	3.97	4.84	5.11		
	NT2RM4001930	2.64	2.64	8.9	2.88	6.53	6.38		
25	NT2RM4001938	2.65	2.65	4.91	5.09	5.65	6.43		
	NT2RM4001940	2.73	2.73	6.17	5.91	4.46	5.48		
	NT2RM4001942	37.36	37.36	32.02	53.86	59.28	82.77	*	+
	NT2RM4001953	4.65	4.65	9.68	5.04	6.79	4.91		
	NT2RM4001965	4.96	4.96	8.82	10.18	8.54	8.39		
30	NT2RM4001966	3	3	5.14	6.3	7.45	8.19	*	+
	NT2RM4001969	2.22	2.22	7.29	5.01	2.95	4.5		
	NT2RM4001974	1.19	1.19	4.61	1.89	2.96	4.83		
	NT2RM4001979	2.09	2.09	6.37	3.39	4.65	7.36		
	NT2RM4001980	4.3	4.3	7.59	7.58	8.02	9.33		
35	NT2RM4001984	2.31	2.31	5.36	2.68	3.49	4.57		
	NT2RM4001987	3.36	3.36	9.66	2.92	4.6	5.01		
	NT2RM4002013	6.62	6.62	15.13	13.47	17.16	19.8		
	NT2RM4002018	2.31	2.31	5.15	4.09	5.53	7.1		
	NT2RM4002033	3.19	3.19	8.16	4.91	3.27	5.93		
40	NT2RM4002034	1.89	1.89	6.19	4.82	4.38	4.03		
	NT2RM4002044	7.71	7.71	17.9	18.75	12.3	18.5		
	NT2RM4002047	3.88	3.88	5.19	2.68	5.38	9.2		
	NT2RM4002054	4.54	4.54	6.97	2.56	4.3	3.89		
	NT2RM4002055	13.72	13.72	74.75	60.51	91.27	61.53		
45	NT2RM4002059	23.73	23.73	31.85	48.05	63.09	52.61	**	+
	NT2RM4002061	3.72	3.72	5.32	3.59	3.69	4.81		
	NT2RM4002062	1.9	1.9	5.41	3.66	2.84	4.26		
	NT2RM4002063	2.21	2.21	8.1	7.64	7.35	3.79		
50	NT2RM4002066	2.07	2.07	5.29	4.42	6.32	4.07		
	NT2RM4002067	2.51	2.51	4.27	3.07	5.19	4.41		
	NT2RM4002073	3.73	3.73	7.24	5.51	7.69	5.16		
	NT2RM4002074	5.19	5.19	7.35	5.67	7.47	4.49		
	NT2RM4002075	5.13	5.13	5.9	3.16	3.18	2.91	**	-
55	NT2RM4002076	3.13	3.13	3.05	1.94	2.52	1.71	*	-

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	NT2RM4002078	10.3	10.3	28.06	23.95	20.81	26.64		
	NT2RM4002081	10.47	10.47	30.87	19.18	17.8	18.22		
	NT2RM4002082	1.25	1.25	3.02	3.85	2.58	1.23		
5	NT2RM4002093	2.82	2.82	3.9	4.79	4.66	4.79	*	+
	NT2RM4002109	4.42	4.42	11.51	13.95	15.12	15.21	*	+
	NT2RM4002115	2.86	2.86	4.51	4.81	4.8	2.52		
	NT2RM4002118	4.48	4.48	6.14	4.3	4.86	4.27		
10	NT2RM4002128	3.78	3.78	4.57	2.84	3.31	3.13	*	-
	NT2RM4002137	3.96	3.96	8.14	10.27	7.51	8.92		
	NT2RM4002139	3.78	3.78	8.98	7.03	7.84	7.87		
	NT2RM4002140	4.04	4.04	9.45	8.87	7.81	10.17		
	NT2RM4002145	5.99	5.99	17.51	25.81	31.07	24.47	*	+
15	NT2RM4002146	4.51	4.51	8.23	8.56	9	8.92		
	NT2RM4002161	2.33	2.33	4.97	1.38	3.15	5.3		
	NT2RM4002174	4.86	4.86	8.02	3.12	4.53	6.15		
	NT2RM4002178	7.3	7.3	24.43	28.61	33.13	29.27	*	+
	NT2RM4002180	3.47	3.47	11.93	9.27	10.02	11.28		
20	NT2RM4002185	5.94	5.94	35.51	31.59	32.34	31.69		
	NT2RM4002189	1.6	1.6	3.24	3.68	5.59	4.91	*	+
	NT2RM4002194	9.3	9.3	25.94	37.2	29.64	38.23	*	+
	NT2RM4002198	6.09	6.09	7.61	9.37	8.4	10.04	*	+
	NT2RM4002205	4.01	4.01	9.05	6.76	7.86	8.76		
25	NT2RM4002213	5.36	5.36	8.79	8.05	11.99	14.41		
	NT2RM4002216	7.35	7.35	12.58	16.58	23.93	18.16	*	+
	NT2RM4002226	3.84	3.84	9.71	20.85	16.65	16.5	**	+
	NT2RM4002237	4.19	4.19	10.13	10.37	7.64	13.22		
	NT2RM4002240	1.96	1.96	3.64	3.73	3.71	7.59		
30	NT2RM4002251	2.11	2.11	6.2	7.87	5.48	5.17		
	NT2RM4002256	4.38	4.38	10.68	10.7	9.46	9.64		
	NT2RM4002262	2.85	2.85	6.25	3.34	4.43	9.66		
	NT2RM4002266	3.93	3.93	4.76	2.76	3.55	4.47		
	NT2RM4002276	11.23	11.23	15.55	16.5	28.25	20.64		
35	NT2RM4002278	1.89	1.89	4.59	4.33	3.99	5.11		
	NT2RM4002281	17.71	17.71	59.08	62.68	51.19	59.89		
	NT2RM4002287	2.08	2.08	3.84	2.46	4.21	3.32		
	NT2RM4002294	3.19	3.19	6.99	6.28	6.09	8.69		
	NT2RM4002298	18.59	18.59	60.14	86.09	89.9	88.75	*	+
40	NT2RM4002301	3.2	3.2	6.85	4.63	5.94	4.02		
	NT2RM4002306	4.71	4.71	8.24	4.99	5.31	4.2		
	NT2RM4002323	3.9	3.9	4.06	4.11	4.39	3.11		
	NT2RM4002334	11.54	11.54	20.76	17.92	20.72	16.95		
45	NT2RM4002339	1.78	1.78	3.52	1.33	1.3	1.38		
	NT2RM4002344	2.36	2.36	5.74	2.87	3.57	7.92		
	NT2RM4002345	3.56	3.56	10.59	5.06	4.63	7.5		
	NT2RM4002352	2.04	2.04	7.67	3.99	5.14	3.74		
	NT2RM4002362	20.38	20.38	24.92	11.23	14.32	15.17	*	-
50	NT2RM4002373	2.1	2.1	3.96	3.21	2.55	3.63		
	NT2RM4002374	2.28	2.28	4.39	2.29	3.58	4.3		
	NT2RM4002376	4.02	4.02	6.03	3.31	2.97	5.52		
	NT2RM4002383	2.8	2.8	8.49	4.76	5.79	4.28		
	NT2RM4002390	3.03	3.03	6.01	4.06	5.27	7.37		
55	NT2RM4002398	5.16	5.16	43.18	33.97	50.73	30.41		

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	NT2RM4002409	2.11	2.11	5.93	3.37	4.29	1.9
	NT2RM4002414	4.73	4.73	6.21	7.37	9.12	14.53
	NT2RM4002438	2.07	2.07	5.28	3.03	4.38	7.18
5	NT2RM4002440	2.99	2.99	6.92	5.78	5.32	9.49
	NT2RM4002446	2.23	2.23	6.08	2.95	4.45	5.7
	NT2RM4002450	3.36	3.36	10.01	6.15	7.75	7.24
	NT2RM4002452	2.13	2.13	6.3	3.67	5.15	7.23
10	NT2RM4002457	2.68	2.68	4.44	2.66	3.26	4.52
	NT2RM4002458	3.06	3.06	5.77	3.32	5.34	4.04
	NT2RM4002460	2.43	2.43	3.68	1.57	2.45	1.43
	NT2RM4002464	5.4	5.4	12.62	14.39	13.72	14.3
	NT2RM4002479	4.66	4.66	6.69	4.91	7.98	11.54
15	NT2RM4002482	4.26	4.26	16.18	10.19	11.5	12.2
	NT2RM4002489	6.74	6.74	16.91	8.79	5.81	11.68
	NT2RM4002493	1.35	1.35	3.22	1.96	3.51	2.73
	NT2RM4002499	34.96	34.96	72.9	59.42	52.07	54.3
20	NT2RM4002504	5.15	5.15	10.68	10.57	13.51	9.8
	NT2RM4002506	4.77	4.77	9.4	4.93	7.59	8.53
	NT2RM4002510	2.03	2.03	3.27	1.66	2.97	2.48
	NT2RM4002527	1.57	1.57	3.14	1.83	2.31	4.47
	NT2RM4002532	2.45	2.45	7.75	5.88	3.37	5.19
25	NT2RM4002534	1.79	1.79	4.8	2.1	3.45	2.94
	NT2RM4002535	2.5	2.5	6.51	5.89	8.1	6.37
	NT2RM4002554	3.29	3.29	5.31	3.31	5.47	3.12
	NT2RM4002558	6.91	6.91	32.57	32.58	41.54	25.61
	NT2RM4002565	5.38	5.38	13.6	8.22	9.85	10.53
30	NT2RM4002567	3.34	3.34	5.43	4.21	4.49	7.22
	NT2RM4002571	4.48	4.48	15.61	11.95	16.47	15.24
	NT2RM4002572	5.57	5.57	17.2	13.7	9.59	13.48
	NT2RM4002577	7.76	7.76	15.25	6.59	5.87	5.65
	NT2RM4002583	1.08	1.08	3.58	2.28	4.83	2.44
35	NT2RM4002584	1.64	1.64	5.67	3.24	5.74	5.56
	NT2RM4002593	3.29	3.29	5.17	2.75	3.91	4.61
	NT2RM4002594	11.26	11.26	46.5	38.21	55.32	43.58
	NT2RM4002604	4.83	4.83	4.64	1.77	2.03	2.89 **
	NT2RM4002614	3.48	3.48	3.48	2.52	3.66	2.81
40	NT2RM4002616	1.07	1.07	2.73	2.88	2.71	2.38
	NT2RM4002623	1.39	1.39	4.89	3.92	3.72	5.06
	NT2RM4002634	1.41	1.41	4.38	3.42	4.91	2.96
	NT2RM4002636	2.22	2.22	3.93	3.92	4.18	4.12
	NT2RP1000002	8.82	8.82	52.94	75.1	92.89	81.45 * +
45	NT2RP1000006	4.68	4.68	6.28	4.25	4.48	2.56
	NT2RP1000015	4.86	4.86	5.27	2.74	1.99	2.28 **
	NT2RP1000018	5.45	5.45	5	5.55	4.83	4.96
	NT2RP1000034	18.22	18.22	49.95	38.04	30.76	50.07
	NT2RP1000035	1.93	1.93	3.2	5.26	3.23	3.96
50	NT2RP1000040	1.77	1.77	3.33	2.93	3.28	4.28
	NT2RP1000042	1.3	1.3	3.44	1.99	3.22	2.38
	NT2RP1000048	3.6	3.6	10.24	7.25	9.9	9
	NT2RP1000050	2.21	2.21	4.71	2.89	4	3.57
	NT2RP1000056	4.03	4.03	3.74	1.09	0.61	1.96 **
55	NT2RP1000058	3.49	3.49	2.03	1.84	2.07	2.48

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	NT2RP1000063	1.77	1.77	3.65	4.09	4	3.83		
	NT2RP1000068	1.89	1.89	3.99	3.12	3.33	2.43		
	NT2RP1000072	22.9	22.9	74.07	82.91	66.26	95.85		
5	NT2RP1000073	2.18	2.18	2.45	2.68	3.69	3.86	*	+
	NT2RP1000078	2.72	2.72	3.17	2.93	2.3	3.13		
	NT2RP1000079	4.13	4.13	5.32	3.6	4.48	2.5		
	NT2RP1000080	4.99	4.99	8.13	9.46	12.46	9.46	*	+
	NT2RP1000086	4.15	4.15	3.63	1.31	2.1	3.75		
10	NT2RP1000087	1.3	1.3	4.36	3.51	3.21	3.45		
	NT2RP1000089	4.5	4.5	9.98	12.69	11.3	14.93	*	+
	NT2RP1000090	45.76	45.76	96.6	94.37	53.44	93.42		
	NT2RP1000100	2.17	2.17	4.05	5.23	4.13	3.66		
	NT2RP1000101	3.44	3.44	5.22	4.41	2.88	4.81		
15	NT2RP1000111	3.24	3.24	5.56	4.51	3.9	3.69		
	NT2RP1000112	3.29	3.29	4.08	1.85	3.33	3		
	NT2RP1000124	5.57	5.57	4.96	3.11	5.73	5.5		
	NT2RP1000125	7.28	7.28	19.39	13.69	10.68	16.86		
20	NT2RP1000129	1.81	1.81	4.35	5.14	3.91	4.27		
	NT2RP1000130	2.31	2.31	4.11	5.31	5.62	16.86		
	NT2RP1000154	7.5	7.5	15.63	17.16	12.72	16.37		
	NT2RP1000163	2.42	2.42	3.51	2.72	2.99	3.59		
	NT2RP1000170	3.42	3.42	4.2	4.96	5.17	5.85	*	+
25	NT2RP1000174	3.5	3.5	3.42	1.3	2.38	2.12	**	-
	NT2RP1000181	6.14	6.14	7.22	10.97	14.98	9.38	*	+
	NT2RP1000191	1.08	1.08	5.61	4.94	3.59	5.71		
	NT2RP1000202	1.06	1.06	1.66	2.02	1.2	2.24		
	NT2RP1000239	1.53	1.53	4.1	2.15	0.94	2.07		
30	NT2RP1000243	2.37	2.37	2.04	1.31	1.14	1.64	**	-
	NT2RP1000255	1.94	1.94	3.02	2.11	2.26	1.78		
	NT2RP1000259	5.27	5.27	9.55	5.53	6.33	4.29		
	NT2RP1000261	2.76	2.76	4.4	2.07	1.64	2.64		
	NT2RP1000269	5.16	5.16	5.01	7.7	10.51	7.39	*	+
35	NT2RP1000271	7.79	7.79	15.88	13.16	15.11	18.48		
	NT2RP1000272	7.71	7.71	13.07	10.72	11.74	11.3		
	NT2RP1000279	2.19	2.19	5.24	2.23	3.91	2.62		
	NT2RP1000290	6.61	6.61	9.02	12.65	13.52	9.92	*	+
	NT2RP1000293	6.86	6.86	10.91	9.75	8.45	10.92		
40	NT2RP1000300	12.42	12.42	11.93	9.96	11.37	10.2	*	-
	NT2RP1000324	5.16	5.16	6	4.69	5.92	6.97		
	NT2RP1000325	54.42	54.42	101.4	70.46	57.52	78.6		
	NT2RP1000326	4.01	4.01	7.67	3.82	4.56	7.85		
	NT2RP1000331	12.16	12.16	24.08	12.19	10.5	20.1		
45	NT2RP1000333	4.18	4.18	7.52	6.66	6.53	6.98		
	NT2RP1000336	1.45	1.45	4.45	1.35	3.76	1.78		
	NT2RP1000347	3.05	3.05	8.75	7.26	8.31	6.38		
	NT2RP1000348	2.11	2.11	4.14	2.76	3	2.75		
	NT2RP1000349	2.12	2.12	3.92	3	4.39	4.11		
50	NT2RP1000353	40.87	40.87	83.5	51.49	47.8	66.02		
	NT2RP1000356	39.53	39.53	93.37	50.3	56.48	74.42		
	NT2RP1000357	3.89	3.89	9.63	8.43	8.7	8.72		
	NT2RP1000358	2.85	2.85	6.11	4.23	3.04	5.09		
55	NT2RP1000360	11.04	11.04	19.39	12.08	18.42	19.44		

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	NT2RP1000363	13.09	13.09	15.39	13.13	13.38	10.01	
	NT2RP1000376	1.81	1.81	3.8	2.09	1.9	2.24	
	NT2RP1000386	118	118	191.31	146.98	187.97	155.47	
5	NT2RP1000407	0.72	0.72	3.16	0.58	0.89	1.2	
	NT2RP1000409	2.05	2.05	5.39	2.84	6.59	3.83	
	NT2RP1000413	4.78	4.78	8.03	5.86	8.89	10.19	
	NT2RP1000416	1.5	1.5	2.01	0.93	3.17	0.7	
	NT2RP1000418	2.27	2.27	6.69	5.08	6.67	4.85	
10	NT2RP1000420	1.77	1.77	5.19	7.32	7.64	3.7	
	NT2RP1000434	1.48	1.48	4.39	1.27	3.12	1	
	NT2RP1000439	5.02	5.02	9.31	20.62	28.73	24.75	** +
	NT2RP1000443	1.8	1.8	3.46	2.24	1.61	1.63	
	NT2RP1000447	2.21	2.21	5.57	2.49	2.87	3.1	
15	NT2RP1000448	1.39	1.39	3.58	3.09	4.4	1.41	
	NT2RP1000451	4.2	4.2	6.37	5.72	7.27	7.04	
	NT2RP1000458	15.1	15.1	10.53	19.73	8.72	23.03	
	NT2RP1000460	7.55	7.55	13.82	8.76	11.49	8.62	
20	NT2RP1000465	4.58	4.58	20.97	20.41	19.98	22.46	
	NT2RP1000468	3.25	3.25	4.64	3.82	4.1	4.45	
	NT2RP1000470	2.38	2.38	5.67	3.99	2.35	3.8	
	NT2RP1000477	1.11	1.11	3.81	1.1	0.84	0.83	
	NT2RP1000478	4.53	4.53	12.55	19.87	18.75	20.39	* +
25	NT2RP1000481	1.23	1.23	3.89	2.48	4.09	1.2	
	NT2RP1000493	2.44	2.44	3.8	1.74	3.83	0.87	
	NT2RP1000513	13.07	13.07	16.37	17.06	17.57	18.97	* +
	NT2RP1000522	6.13	6.13	12.69	13.13	13.08	10.32	
	NT2RP1000533	3.72	3.72	6.17	2.92	4.49	2.17	
30	NT2RP1000544	1.53	1.53	2.45	1.38	1.24	1.44	
	NT2RP1000547	0.88	0.88	2.45	2	1.63	1.23	
	NT2RP1000551	1.7	1.7	2.62	2.13	3.2	1.1	
	NT2RP1000567	1.66	1.66	4.29	2.54	4.29	1.77	
	NT2RP1000574	1.99	1.99	4.28	1.5	3.43	1.38	
35	NT2RP1000577	3.14	3.14	6.01	3.16	5.31	2.05	
	NT2RP1000579	4.64	4.64	6.24	3.27	3.97	2.04	
	NT2RP1000581	5.22	5.22	3.58	2.07	1.61	0.93	** -
	NT2RP1000593	1.74	1.74	4.39	2.48	3.28	2.3	
	NT2RP1000604	3.85	3.85	7.75	17.25	13.78	16.39	** +
40	NT2RP1000609	1.15	1.15	2.21	2.84	2.61	1.55	
	NT2RP1000613	1.12	1.12	2.56	1.82	4.29	0.82	
	NT2RP1000622	5.94	5.94	15.9	14.91	19.42	15.46	
	NT2RP1000627	9.18	9.18	18.96	23.88	21.9	14.86	
	NT2RP1000629	4.18	4.18	5.9	5.92	5.32	3.17	
45	NT2RP1000630	6.54	6.54	7.84	7.21	7.67	7.92	
	NT2RP1000639	0.64	0.64	0.31	1.53	2.04	0.28	
	NT2RP1000640	130.14	130.14	307.77	227.5	176.05	232.29	
	NT2RP1000646	4.14	4.14	9.59	10.19	11.87	12.15	* +
	NT2RP1000659	2.65	2.65	7	8.91	7.99	6.04	
50	NT2RP1000674	13.48	13.48	28.08	43.62	45.82	56.95	** +
	NT2RP1000677	3.9	3.9	10.76	11.84	10.19	9.87	
	NT2RP1000679	2.38	2.38	3.76	2.3	2.35	1.05	
	NT2RP1000688	4.72	4.72	3.34	2.76	2.73	1.83	* -
55	NT2RP1000689	1.44	1.44	1.86	2.03	1.22	1.13	

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	NT2RP1000695	1.11	1.11	2.5	2.09	2.44	1.52		
	NT2RP1000701	0.89	0.89	1.08	2.62	2.74	1.71	*	+
	NT2RP1000702	1.12	1.12	2.28	3.74	4.07	3.15	*	+
5	NT2RP1000713	2.29	2.29	2.79	2.8	3.56	2.38		
	NT2RP1000721	4.14	4.14	4.49	4.48	3.92	3.78		
	NT2RP1000730	3.5	3.5	4.83	2.61	4.5	2.41		
	NT2RP1000733	6.08	6.08	6.56	4.91	8.12	5.65		
10	NT2RP1000738	3.18	3.18	8.04	5.16	5.71	7.11		
	NT2RP1000739	1.11	1.11	2.65	4.02	3.09	2.86		
	NT2RP1000740	1.41	1.41	3.13	3.63	3.57	3.77	*	+
	NT2RP1000746	1.15	1.15	3.58	2.28	3.74	1.37		
	NT2RP1000750	4	4	8.31	10.25	10.72	9.39	*	+
15	NT2RP1000751	33.15	33.15	59.65	67.84	64.22	66.55		
	NT2RP1000767	3.8	3.8	3.64	1.7	2.62	0.62	*	-
	NT2RP1000769	9.31	9.31	13.98	7.42	8.59	7.19		
	NT2RP1000780	0.86	0.86	1.01	1.87	1.13	0.89		
	NT2RP1000782	4.25	4.25	12.21	10.24	7.96	9.13		
20	NT2RP1000796	3.17	3.17	2.69	4.23	2.99	2.86		
	NT2RP1000797	12.31	12.31	22.78	19.44	18.64	21.78		
	NT2RP1000800	1.13	1.13	3.74	2.46	2.66	1.46		
	NT2RP1000825	2.38	2.38	2.91	1.04	1.88	0.87	*	-
	NT2RP1000833	2.5	2.5	2.85	0.92	2.39	1.26		
25	NT2RP1000834	35.44	35.44	66.57	73.98	90.28	71.45		
	NT2RP1000836	1.83	1.83	3.43	1.01	2.39	1.04		
	NT2RP1000837	3.36	3.36	6.66	3.22	4.71	3.67		
	NT2RP1000846	1.29	1.29	5.48	1.67	2.84	1.4		
	NT2RP1000847	1.99	1.99	5.49	2.15	5.12	1.64		
30	NT2RP1000851	4.67	4.67	9.32	6.18	7.94	6.72		
	NT2RP1000856	14.31	14.31	17.46	20.38	23.22	19.37	*	+
	NT2RP1000860	2.09	2.09	4.54	4.02	2.74	4.04		
	NT2RP1000902	5.31	5.31	11.6	6.94	9.91	7.34		
	NT2RP1000903	2.45	2.45	6.26	4.04	3.42	4.24		
35	NT2RP1000905	1.76	1.76	4.87	5.36	5.66	10		
	NT2RP1000915	5.51	5.51	10.01	6.72	8.59	9.91		
	NT2RP1000916	2.31	2.31	5.51	1.78	3.82	2.09		
	NT2RP1000921	9.38	9.38	8.73	8.23	9.13	7.92		
	NT2RP1000943	5.14	5.14	10.76	8.51	8.55	7.2		
40	NT2RP1000944	1.59	1.59	2.21	1.78	1.74	1.15		
	NT2RP1000947	8.5	8.5	14.91	16.51	15.04	14.22		
	NT2RP1000954	2.11	2.11	4.96	2.74	5.55	3.04		
	NT2RP1000958	6.48	6.48	14.73	4.54	10.17	10.21		
	NT2RP1000959	124.81	124.81	209.45	128.43	72.65	206.1		
45	NT2RP1000966	9.96	9.96	12.96	14.28	15.36	21.39		
	NT2RP1000974	2.46	2.46	5.38	3.98	6.08	3.71		
	NT2RP1000980	3.07	3.07	5.5	4.04	4.53	4.02		
	NT2RP1000981	4.3	4.3	8.09	5.68	7.26	5.27		
	NT2RP1000988	6.45	6.45	10.46	9.62	6.44	7.87		
50	NT2RP1001002	2.8	2.8	7.36	3.94	4.57	4.3		
	NT2RP1001004	4.72	4.72	8.25	3.65	4.9	5.37		
	NT2RP1001007	1.42	1.42	3.42	1.69	3.84	2.03		
	NT2RP1001011	1.94	1.94	5.93	3.82	5.46	4.83		
55	NT2RP1001013	4.45	4.45	9.41	5.92	8.62	5.04		

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	NT2RP1001014	2.21	2.21	5.89	3.76	6.64	3.49	
	NT2RP1001020	1.87	1.87	4.11	2.08	3.75	2.36	
	NT2RP1001023	62.79	62.79	145.09	101.48	105.86	143.96	
5	NT2RP1001027	18.11	18.11	82.66	51.63	59.05	68.9	
	NT2RP1001031	1.83	1.83	3.31	2.05	3.53	2.25	
	NT2RP1001033	2.43	2.43	6.09	5.68	5.98	4.27	
	NT2RP1001042	2.94	2.94	6.47	2.99	3.85	2.04	
	NT2RP1001045	15.95	15.95	23.24	40.66	47.04	44.53	** +
10	NT2RP1001073	6.64	6.64	10.57	8.32	10.46	7.33	
	NT2RP1001079	2.91	2.91	6.37	2.16	2.58	1.48	
	NT2RP1001080	2.16	2.16	4.89	6.88	4.2	4.56	
	NT2RP1001113	1.07	1.07	3.64	3.55	3.94	3.26	
	NT2RP1001159	21.42	21.42	43.84	22.89	23.31	34.25	
15	NT2RP1001173	1.7	1.7	3.07	1.38	4.28	1.52	
	NT2RP1001176	7.4	7.4	10.13	13	9.31	13.95	
	NT2RP1001177	5.31	5.31	5.75	3.01	5.5	2.02	
	NT2RP1001185	6.42	6.42	9.37	3.79	4.63	2.73	* -
20	NT2RP1001199	3.9	3.9	7.67	6.93	5.22	3.28	
	NT2RP1001205	7.78	7.78	19.46	16.66	12.64	23.28	
	NT2RP1001215	1.82	1.82	5.02	3.79	4.12	3.15	
	NT2RP1001225	4.54	4.54	7.96	7.56	8.77	6.31	
	NT2RP1001245	7.27	7.27	10.86	19.68	21.03	22.13	** +
25	NT2RP1001247	2.04	2.04	4.01	1.77	2.89	1.67	
	NT2RP1001248	2.81	2.81	6.79	3.94	4.63	2.4	
	NT2RP1001253	5.02	5.02	6.39	4.48	4.38	3.32	
	NT2RP1001286	6.18	6.18	7.69	3.79	3.88	4.12	** -
	NT2RP1001294	2.4	2.4	4.47	3.6	2.73	4.18	
30	NT2RP1001302	2.46	2.46	4.51	4.89	2.9	5.39	
	NT2RP1001310	15.54	15.54	34.01	21.13	20.75	27.15	
	NT2RP1001311	1.9	1.9	3.22	2.66	3.16	2.38	
	NT2RP1001313	2.6	2.6	7.72	5.45	7.85	5.78	
	NT2RP1001324	2.47	2.47	5.3	3.34	4.17	2.35	
35	NT2RP1001349	3.3	3.3	6.29	3.63	3.92	2.14	
	NT2RP1001361	19.41	19.41	18.28	23.28	28.33	24.16	* +
	NT2RP1001379	3.82	3.82	9.52	4.97	7.97	7.06	
	NT2RP1001385	2.06	2.06	4.51	4.09	3.89	4.4	
	NT2RP1001395	4.96	4.96	7.86	6.01	6.32	8.13	
40	NT2RP1001410	8.75	8.75	20.39	15.74	15.66	9.94	
	NT2RP1001424	2.39	2.39	3.34	3	3	1.73	
	NT2RP1001432	4.33	4.33	3.86	2.19	1.76	2.05	** -
	NT2RP1001449	6.23	6.23	7.5	6.29	8.21	4.63	
	NT2RP1001457	4.09	4.09	4.21	2.11	2.26	2.63	** -
45	NT2RP1001459	21.54	21.54	132.97	90.96	107.97	81.08	
	NT2RP1001466	5.73	5.73	14.97	11.31	9.39	10.99	
	NT2RP1001475	2.45	2.45	6.31	5.98	6.67	3.9	
	NT2RP1001482	3.93	3.93	9.18	15.88	13.03	8.2	
	NT2RP1001494	1.61	1.61	4.6	4.34	4.18	2.25	
50	NT2RP1001500	3.39	3.39	8.13	8.09	8.65	7.42	
	NT2RP1001517	5.11	5.11	7.37	4.41	5.38	2.36	
	NT2RP1001540	4.74	4.74	5.03	4.6	4.86	3.11	
	NT2RP1001543	1.02	1.02	1.83	1.49	1.12	0.98	
55	NT2RP1001546	22.51	22.51	51.51	34.99	22.76	33.42	

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	NT2RP1001550	9.33	9.33	21.4	14.35	12.21	13.42	
	NT2RP1001553	2.07	2.07	6.07	5.69	6.04	4.45	
	NT2RP1001555	36.28	36.28	58.55	41.1	53.63	54.35	
5	NT2RP1001563	2.28	2.28	3.44	2.07	2.24	1.31	
	NT2RP1001569	9.43	9.43	16	17.31	18.21	13.04	
	NT2RP1001584	15.6	15.6	19.66	28.1	32.53	25.83	** +
	NT2RP1001599	1.18	1.18	1.95	1.27	1.19	1.24	
	NT2RP1001616	5	5	11.95	9.49	6.7	8.95	
10	NT2RP1001654	11.78	11.78	18.07	16.27	16.54	18.38	
	NT2RP1001665	2.77	2.77	4.72	2.73	2.05	2.05	
	NT2RP1001679	76.31	76.31	195.7	199.2	240.87	222.46	
	NT2RP1001681	10.11	10.11	15.1	20.39	21.03	23.99	** +
	NT2RP1001694	3.58	3.58	3.82	2.45	2.38	1.97	** -
15	NT2RP2000001	5.23	5.23	5.53	4.17	4.54	3.74	** -
	NT2RP2000006	3.49	3.49	7.32	4.12	3.88	3.4	
	NT2RP2000007	3.18	3.18	6.56	4.68	5.66	4.92	
	NT2RP2000008	2.77	2.77	6.72	3.66	5.3	4.9	
20	NT2RP2000010	2.89	2.89	5.59	2.99	5.06	2.5	
	NT2RP2000011	7.08	7.08	17.96	14.55	14.74	15.15	
	NT2RP2000027	2.28	2.28	7.42	4.52	4.89	3.61	
	NT2RP2000028	22.93	22.93	62.54	46.48	51.47	53.47	
	NT2RP2000032	2.5	2.5	5.85	3.11	3.71	6.42	
25	NT2RP2000040	11.57	11.57	23.92	14.38	14.5	23.1	
	NT2RP2000042	5.28	5.28	10.32	6.89	7.21	12.64	
	NT2RP2000045	5.7	5.7	9.42	5.27	6.45	6.3	
	NT2RP2000051	3.16	3.16	6.29	9.23	9.96	9.53	** +
	NT2RP2000054	2.55	2.55	6.42	3.81	5.42	2.53	
30	NT2RP2000056	3.68	3.68	6.23	5.67	6.89	5.8	
	NT2RP2000057	60.79	60.79	174.83	212.63	239.81	221.98	* +
	NT2RP2000067	3.1	3.1	3.86	2.98	4.36	5.72	
	NT2RP2000070	2.91	2.91	6.27	5.7	5.95	8.21	
	NT2RP2000076	1.66	1.66	4.45	2.98	3.58	3.23	
35	NT2RP2000077	1.67	1.67	4.73	2.43	4.94	3.14	
	NT2RP2000079	3.76	3.76	9.24	5.15	4.81	5.47	
	NT2RP2000088	2.9	2.9	5.22	2.18	3.07	2.21	
	NT2RP2000091	5.84	5.84	6.54	6.62	8.28	6.72	
	NT2RP2000092	4.37	4.37	6.7	6.06	7.67	5.65	
40	NT2RP2000097	2.74	2.74	3.39	3.4	4.13	4.13	* +
	NT2RP2000098	3.44	3.44	6.83	6.69	9.01	6.27	
	NT2RP2000108	1.93	1.93	7.24	4.8	6.31	6.68	
	NT2RP2000114	1.95	1.95	3.65	2.58	4.41	2.9	
	NT2RP2000116	3.17	3.17	7.36	5.35	3.85	9.42	
45	NT2RP2000119	3.14	3.14	7.16	4.58	7.96	5.6	
	NT2RP2000120	3.91	3.91	7.62	5.57	8.5	5.8	
	NT2RP2000126	2.86	2.86	4.86	3.88	5.1	3.44	
	NT2RP2000133	1.83	1.83	3.66	3.13	4.05	2.01	
50	NT2RP2000147	6.28	6.28	12.88	11.64	6.51	8.58	
	NT2RP2000153	4.61	4.61	9.55	10.57	6.49	12.05	
	NT2RP2000156	3.27	3.27	8.24	5.59	6.55	4.07	
	NT2RP2000157	3.7	3.7	6.33	6.57	5.02	4.15	
	NT2RP2000161	4.45	4.45	8.82	7.52	7.5	6.02	
55	NT2RP2000168	4.22	4.22	12.63	3.94	6.03	3.88	

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	NT2RP2000173	12.56	12.56	81.37	72.12	92.12	78.68	
	NT2RP2000175	1.9	1.9	3.78	2.03	3.33	4.43	
	NT2RP2000178	2.06	2.06	6.06	3.23	3.01	3.81	
5	NT2RP2000183	1.64	1.64	7.82	5.82	6.21	6.03	
	NT2RP2000195	3.1	3.1	6.65	6	6.71	3.22	
	NT2RP2000204	73.6	73.6	93.43	102.95	40.16	62.34	
	NT2RP2000205	4	4	6.56	3.91	5.74	4.5	
10	NT2RP2000208	3.06	3.06	9.42	4.23	6.77	3.36	
	NT2RP2000224	13.3	13.3	31.75	18.34	21.15	20.93	
	NT2RP2000230	9.96	9.96	18.99	12.16	16.4	11.95	
	NT2RP2000231	4.3	4.3	7.41	4.24	3.43	4.54	
	NT2RP2000232	1.08	1.08	2.75	1.53	2.45	0.74	
15	NT2RP2000233	8.04	8.04	60.44	47.2	64.72	52.31	
	NT2RP2000239	3	3	4.7	8.93	8.93	7.01	** +
	NT2RP2000240	2.01	2.01	5.25	2.49	3.41	1.45	
	NT2RP2000248	4.29	4.29	6.09	2.82	2.39	0.96	* -
	NT2RP2000256	5.7	5.7	8.25	5.62	6.22	5.44	
20	NT2RP2000257	3.47	3.47	6.92	4.86	6.52	4.34	
	NT2RP2000258	1.53	1.53	3.83	3.88	2.93	3.02	
	NT2RP2000261	2.95	2.95	3.94	4.47	3.59	2.91	
	NT2RP2000270	3.12	3.12	6.26	6.66	4.06	4.3	
	NT2RP2000274	1.78	1.78	3.87	3.48	5.16	2.56	
25	NT2RP2000277	2.18	2.18	6.13	3.19	4.02	2.98	
	NT2RP2000279	2.26	2.26	4.92	2.43	2.52	2.17	
	NT2RP2000283	5.75	5.75	27.65	21.53	27.32	24.78	
	NT2RP2000288	6.29	6.29	7.46	8.9	10.89	8.64	* +
	NT2RP2000289	1.12	1.12	2.79	3.09	2.77	1.93	
30	NT2RP2000297	2.57	2.57	5.7	4.8	4.53	6.09	
	NT2RP2000298	3.61	3.61	9.64	8.51	7.66	8.24	
	NT2RP2000310	1.43	1.43	2.3	2.46	3.41	1.7	
	NT2RP2000327	2.12	2.12	3.96	3.13	3.49	1.57	
	NT2RP2000328	6.95	6.95	11.56	13.43	16.7	14.68	* +
35	NT2RP2000329	10.73	10.73	10.17	17.55	23.92	18.52	** +
	NT2RP2000333	6.35	6.35	6.4	6.83	7.17	4.64	
	NT2RP2000337	2.05	2.05	5.16	4.43	5.32	5.31	
	NT2RP2000346	2.55	2.55	5.18	7.2	5.63	4.95	
	NT2RP2000357	1.57	1.57	6.87	5.48	5.14	5.35	
40	NT2RP2000358	2.09	2.09	4.52	5.03	4.9	4.01	
	NT2RP2000366	3.23	3.23	4.08	4.16	4.25	2.32	
	NT2RP2000369	7.22	7.22	9.94	44.13	45.2	44.34	** +
	NT2RP2000376	26.92	26.92	108.62	84.48	134.63	85.95	
	NT2RP2000394	6.49	6.49	5.92	5.08	8.52	4.21	
45	NT2RP2000396	2.71	2.71	6.55	7.52	6.8	5.02	
	NT2RP2000412	4.48	4.48	23.45	21.42	24.93	20.49	
	NT2RP2000414	8.03	8.03	18.69	23.83	18.98	23.37	
	NT2RP2000420	1.12	1.12	4.11	3.54	3.25	1.97	
	NT2RP2000422	6.41	6.41	13.18	17.56	17.88	18.67	* +
50	NT2RP2000426	21.59	21.59	80.94	87.94	110.97	74.98	
	NT2RP2000428	24.92	24.92	43.91	34.21	35.59	30.95	
	NT2RP2000438	5.06	5.06	5.17	5.62	6.94	5.11	
	NT2RP2000447	4.14	4.14	9.68	7.3	7.08	7.16	
55	NT2RP2000448	3.03	3.03	4.63	4.57	3.57	3.17	

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	NT2RP2000459	2.47	2.47	4.93	2.82	3.15	2.09	
	NT2RP2000479	3.3	3.3	7.51	5.33	5.71	5.06	
	NT2RP2000498	3.07	3.07	6.25	4.48	5.09	3.9	
5	NT2RP2000503	2.47	2.47	4.46	2.54	2.82	1.52	
	NT2RP2000510	4.01	4.01	6.19	5.08	6.45	3.7	
	NT2RP2000514	2.65	2.65	2.51	1.94	2.25	1.63	*
	NT2RP2000516	4.72	4.72	9.77	4.92	5.29	5.18	
10	NT2RP2000523	2.21	2.21	3.17	1.92	2.44	2.63	
	NT2RP2000533	17.82	17.82	29.05	22.57	27.56	30.78	
	NT2RP2000540	1.98	1.98	4.66	3.01	5.41	5.18	
	NT2RP2000547	3.1	3.1	5.26	4.38	5.27	3.71	
	NT2RP2000557	4.26	4.26	6.96	4.34	6.5	3.32	
15	NT2RP2000558	3.43	3.43	7.17	6.43	7.11	8.26	
	NT2RP2000564	3.04	3.04	7.2	3.49	8.03	4.77	
	NT2RP2000565	4.54	4.54	11.07	7.64	9.24	9.98	
	NT2RP2000583	14.8	14.8	44.9	49.6	34.93	49.08	
	NT2RP2000591	0.81	0.81	3.81	1.53	2.61	1.21	
20	NT2RP2000599	1.85	1.85	4.1	1.97	3.43	2.36	
	NT2RP2000601	1.78	1.78	4.67	1.28	2.48	1.3	
	NT2RP2000603	2.58	2.58	4.44	2.54	2.84	2.98	
	NT2RP2000610	3.77	3.77	7.23	6.32	7.62	5.53	
	NT2RP2000614	75.85	75.85	129.42	130.63	184.38	188.58	* +
25	NT2RP2000616	1.81	1.81	4.89	3.9	5.1	3.83	
	NT2RP2000617	2.17	2.17	6.73	5.78	6.82	6.26	
	NT2RP2000623	3.1	3.1	5.36	3.46	5.1	3.49	
	NT2RP2000634	1.56	1.56	3.92	2.29	3.34	2.02	
	NT2RP2000636	3.78	3.78	8.64	6.27	7.6	6.62	
30	NT2RP2000638	4.37	4.37	8.91	4.57	7.41	5.69	
	NT2RP2000644	2.22	2.22	5.47	3.41	4.16	3.45	
	NT2RP2000649	8.96	8.96	15.76	13.65	17.22	13.07	
	NT2RP2000652	3.35	3.35	4.58	3.57	4.36	2.72	
	NT2RP2000656	3.73	3.73	6.93	4.83	3.91	4.08	
35	NT2RP2000658	1.08	1.08	2.64	1.51	3.18	1.43	
	NT2RP2000663	4.23	4.23	6.9	5.98	7.21	5.9	
	NT2RP2000664	4.24	4.24	10.24	12.72	12.54	16.44	* +
	NT2RP2000668	7.49	7.49	26.84	16.92	20.41	17.17	
	NT2RP2000678	1.77	1.77	3.19	1.77	2.09	1.13	
40	NT2RP2000694	4.89	4.89	8.39	11.06	13	13.36	** +
	NT2RP2000704	1.8	1.8	5.63	2.99	3.13	3.67	
	NT2RP2000710	4.51	4.51	9.96	6.72	8.08	7.23	
	NT2RP2000712	1.43	1.43	5.35	3.39	3.57	2.95	
45	NT2RP2000715	3.42	3.42	7.43	6.04	7.56	4.49	
	NT2RP2000720	4.92	4.92	11.76	7.24	8	7.11	
	NT2RP2000731	3.92	3.92	9.15	3.7	4.5	2.61	
	NT2RP2000739	3.23	3.23	5.67	2.62	3.32	5.65	
	NT2RP2000748	1.59	1.59	4.2	1.42	1.81	1.62	
50	NT2RP2000749	11.84	11.84	21.88	14.4	8.47	13.91	
	NT2RP2000758	1.6	1.6	3.17	2.65	6	1.17	
	NT2RP2000764	1.51	1.51	5.74	2.95	5.22	1.95	
	NT2RP2000766	9.08	9.08	52.24	46.37	59.37	52.89	
	NT2RP2000777	12.28	12.28	18.43	26.91	28.56	24.47	** +
55	NT2RP2000786	21.32	21.32	73.91	55.85	67.59	58.16	

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	NT2RP2000793	5.32	5.32	6.9	4.32	3.57	4.38	*	-
	NT2RP2000796	5.32	5.32	7.41	7.38	9.17	6.66		
	NT2RP2000809	3.25	3.25	8.3	6.46	4.69	5.45		
5	NT2RP2000812	6.65	6.65	17.51	16.43	14.35	16.89		
	NT2RP2000814	4.16	4.16	4.97	3.75	4.6	3.29		
	NT2RP2000816	1.84	1.84	5.64	4.64	5.19	3.58		
	NT2RP2000818	3.28	3.28	5.19	3.18	3.66	1.95		
10	NT2RP2000819	2.76	2.76	5.79	3.03	3.05	1.94		
	NT2RP2000841	4.35	4.35	4.51	2.17	2.48	1.65	**	-
	NT2RP2000842	7.8	7.8	9.57	13.62	14.25	12.66	**	+
	NT2RP2000845	2.52	2.52	8.31	7.51	6.76	6.93		
	NT2RP2000863	2.45	2.45	3.48	3.82	3.37	2.47		
15	NT2RP2000880	5.96	5.96	11.61	9.5	11.13	10.25		
	NT2RP2000892	4.3	4.3	6.43	6.54	6.97	5.01		
	NT2RP2000894	5.59	5.59	11.88	5.41	5.59	2.16		
	NT2RP2000903	5.71	5.71	9.12	10.73	11.92	7.44		
	NT2RP2000906	4.56	4.56	5.39	2.63	3.78	2.19	*	-
20	NT2RP2000910	4.34	4.34	4.26	2.9	2.7	1.68	**	-
	NT2RP2000931	10.97	10.97	18.36	20.51	19.28	24.6		
	NT2RP2000932	2.86	2.86	5.43	4.8	4.72	4.21		
	NT2RP2000938	18.41	18.41	42.99	35.71	30.01	43.52		
	NT2RP2000943	7.02	7.02	14.98	18.7	14.88	14.48		
25	NT2RP2000957	3.19	3.19	4.11	4.26	3.66	2.71		
	NT2RP2000958	7	7	6.84	10.43	12.36	7.8		
	NT2RP2000959	9.88	9.88	14.99	13.92	17.38	10.69		
	NT2RP2000965	5.05	5.05	7.82	15.73	18.97	16.02	**	+
	NT2RP2000970	2.31	2.31	6.72	5.14	5	4.62		
30	NT2RP2000973	0.9	0.9	1.47	2.56	2.64	1.57	*	+
	NT2RP2000985	2.69	2.69	6	9.28	6.29	13.98		
	NT2RP2000987	1.89	1.89	3.31	4.54	3.17	1.66		
	NT2RP2000997	13.83	13.83	23.99	38.12	29.73	40.96	*	+
	NT2RP2001024	2.86	2.86	5.34	3.61	3.12	2.36		
35	NT2RP2001028	4.66	4.66	4.2	2.65	4.09	0.99		
	NT2RP2001036	5.14	5.14	8.86	6.16	6.44	4.91		
	NT2RP2001039	1.08	1.08	3.18	3.47	1.14	2.24		
	NT2RP2001044	1.13	1.13	2.5	2.53	1.89	2.8		
	NT2RP2001056	4.97	4.97	28.32	20.16	26.9	18.16		
40	NT2RP2001065	2.38	2.38	6.24	7.45	7.4	5.69		
	NT2RP2001067	2.98	2.98	5.38	4.12	5.29	2.41		
	NT2RP2001070	3.3	3.3	7.63	4.72	6.17	3.58		
	NT2RP2001081	2.91	2.91	8.19	4.8	6.68	3.9		
45	NT2RP2001087	3.93	3.93	2.36	2.06	2.92	1.61		
	NT2RP2001094	0.69	0.69	1.37	1.25	1.15	1.04		
	NT2RP2001119	2.02	2.02	6.11	5.86	4.44	4.35		
	NT2RP2001127	1.53	1.53	4.04	2.69	1.85	2.1		
	NT2RP2001133	2.45	2.45	4.73	4.06	3.61	3.6		
50	NT2RP2001137	2.68	2.68	4.07	2.3	2.82	2.9		
	NT2RP2001142	3.88	3.88	7.47	3.37	2.83	2.42		
	NT2RP2001149	2.7	2.7	2.98	2.11	3.39	1.32		
	NT2RP2001168	6	6	7.81	6.8	7.01	5.75		
	NT2RP2001173	4.15	4.15	7.88	3.98	3.09	5.44		
55	NT2RP2001174	9.23	9.23	14.98	14.12	15.45	18.01		

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	NT2RP2001184	2.78	2.78	5.46	4.21	7.18	4.64
	NT2RP2001196	1.62	1.62	5.93	3.14	3.28	2.94
	NT2RP2001200	3.85	3.85	9.36	5.02	4.25	7.88
5	NT2RP2001218	2.29	2.29	5.69	2.55	3.89	3.6
	NT2RP2001223	2.65	2.65	5.03	1.95	3.69	3.31
	NT2RP2001226	4.34	4.34	10.19	6.95	5.72	7.35
	NT2RP2001227	4.45	4.45	6.12	3.2	3.62	6.01
10	NT2RP2001232	6.44	6.44	13.95	7.13	9.79	13.66
	NT2RP2001233	4.02	4.02	10.57	7.04	7.77	8.01
	NT2RP2001245	4.21	4.21	8.03	9.47	11.82	11.16 * +
	NT2RP2001246	6.3	6.3	9.84	9	11.28	11.57
	NT2RP2001268	6.19	6.19	18.1	17.61	16.26	18.55
15	NT2RP2001270	4.78	4.78	9.11	5.68	8.7	10.04
	NT2RP2001276	4.92	4.92	13.29	12.73	10.92	12.73
	NT2RP2001277	3.11	3.11	7.02	4.91	6.22	10.82
	NT2RP2001290	2.71	2.71	6.46	4.42	5.61	6.01
	NT2RP2001295	5.46	5.46	9.44	5.13	5.98	7.92
20	NT2RP2001297	118.17	118.17	120.73	139.11	97.16	145.76
	NT2RP2001301	9.12	9.12	18.56	15.89	19.62	14.24
	NT2RP2001312	2.7	2.7	5.68	5.6	4.59	6.04
	NT2RP2001327	4.73	4.73	5.69	6.39	8.53	11.86
	NT2RP2001328	8.44	8.44	20.87	16.32	23.25	23.16
25	NT2RP2001341	4.59	4.59	9.22	3.06	7.65	7.21
	NT2RP2001347	3.09	3.09	8.54	5.54	9.55	6.9
	NT2RP2001366	10.33	10.33	48.06	54.83	51.5	52.33
	NT2RP2001378	2.33	2.33	3.77	3.74	4.64	5.02
	NT2RP2001381	2.82	2.82	6.86	5.79	6.62	8.37
30	NT2RP2001388	3.25	3.25	6.71	4.54	5.11	5.2
	NT2RP2001391	443.52	443.52	734.13	742.83	990.71	747.95
	NT2RP2001392	2.98	2.98	6.43	4.58	3.16	4.18
	NT2RP2001394	3.3	3.3	8.55	8.35	6.09	10.15
	NT2RP2001397	5.04	5.04	6.79	7.33	5.68	12.2
35	NT2RP2001400	3.1	3.1	6.4	3.43	6.25	2.92
	NT2RP2001408	3.31	3.31	6.13	4.02	5.97	5.62
	NT2RP2001420	5.63	5.63	12.09	8.09	9.97	9.17
	NT2RP2001423	4.71	4.71	9.71	6.21	8.29	7.19
	NT2RP2001427	2.68	2.68	5.32	3.69	4.61	5.49
40	NT2RP2001428	2.71	2.71	7.13	5.49	3.78	3.03
	NT2RP2001436	4.27	4.27	8.85	5.84	2.85	4.84
	NT2RP2001440	2.89	2.89	7.34	10.24	10.15	11.98 * +
	NT2RP2001445	2.43	2.43	6.75	5.86	5.55	5.89
	NT2RP2001449	4.37	4.37	6.41	5	4.74	5.02
45	NT2RP2001450	3.19	3.19	6.75	2.26	5.4	8.59
	NT2RP2001467	4.53	4.53	10.28	5.32	4.72	6.5
	NT2RP2001469	4.74	4.74	6.79	8.22	11.04	7.18
	NT2RP2001480	6.54	6.54	26.68	14.98	12.63	15.42
50	NT2RP2001495	5.86	5.86	11.96	3.16	9.04	10.39
	NT2RP2001499	8.25	8.25	16.78	10.05	14.46	9.66
	NT2RP2001506	2.79	2.79	7.24	5.32	8.19	5.33
	NT2RP2001508	10.59	10.59	13.66	18.74	20.49	21.92 ** +
	NT2RP2001511	6.41	6.41	9.74	6.08	8.63	6.53
55	NT2RP2001514	7.04	7.04	7.02	7.24	6.44	6.38

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	NT2RP2001520	2.93	2.93	4.84	2.6	3.19	2.87		
	NT2RP2001526	3.88	3.88	8.49	7.01	5.27	3.83		
	NT2RP2001529	9.87	9.87	53.78	44.74	55.72	60.88		
5	NT2RP2001536	1.63	1.63	4.17	3.81	4.52	4.71		
	NT2RP2001538	83.44	83.44	178.68	132.75	146.73	155.87		
	NT2RP2001547	4.96	4.96	14.87	16.77	19.21	17.77	*	+
	NT2RP2001560	6.28	6.28	21.64	25.41	28.19	27.75	*	+
10	NT2RP2001562	5.56	5.56	5.57	5.94	6.75	4.64		
	NT2RP2001566	7.96	7.96	9.24	8.22	7.91	8.56		
	NT2RP2001569	4.26	4.26	8.71	6.09	5.65	8.28		
	NT2RP2001576	3.95	3.95	11.58	13.42	9	12.82		
	NT2RP2001581	47.15	47.15	130.15	121.19	112.28	129.54		
15	NT2RP2001597	3.73	3.73	7.88	8.57	8.3	13.3		
	NT2RP2001601	2.37	2.37	4.81	3.67	4.81	3.34		
	NT2RP2001613	2.74	2.74	4.87	2.83	2.72	4.15		
	NT2RP2001628	3.42	3.42	3.97	3.14	3.04	7.84		
	NT2RP2001634	8.64	8.64	13.94	16.57	23.67	17.67	*	+
20	NT2RP2001635	2.51	2.51	5.92	5.63	5.53	4.72		
	NT2RP2001660	4.27	4.27	16.91	5.9	5.54	10.06		
	NT2RP2001662	1.49	1.49	4.07	4.5	4.44	3.47		
	NT2RP2001663	2.82	2.82	5.09	10.37	8.21	9.74	**	+
	NT2RP2001672	3.28	3.28	3.82	3.88	4.09	4	*	+
25	NT2RP2001675	4.1	4.1	5.01	5.23	4.73	5.06		
	NT2RP2001677	9.58	9.58	18.2	20.9	26.67	19.74	*	+
	NT2RP2001678	4.84	4.84	6.73	4.6	4.83	4.5		
	NT2RP2001683	1.89	1.89	3.12	4.6	4.72	2.78		
	NT2RP2001699	3.15	3.15	6.16	6.5	5.84	4.88		
30	NT2RP2001707	1.24	1.24	3.19	3.42	4.13	4.8	*	+
	NT2RP2001720	1.47	1.47	3.6	3.91	3	2.72		
	NT2RP2001721	2.26	2.26	4.57	5.53	3.96	3.66		
	NT2RP2001740	12	12	60.21	52.38	79.71	54.73		
	NT2RP2001748	6.43	6.43	10.8	8.75	10.25	8.55		
35	NT2RP2001755	5.51	5.51	4.96	3.71	4.62	2.69	*	-
	NT2RP2001762	1.25	1.25	2.01	3.87	2.56	3.52	*	+
	NT2RP2001768	1.91	1.91	4.7	6.7	5.55	4.55		
	NT2RP2001769	3.06	3.06	5.86	10.42	5.06	11.86		
	NT2RP2001784	3.62	3.62	6.23	7.06	6.02	6.91		
40	NT2RP2001805	2.33	2.33	5.61	6.02	4.93	6.6		
	NT2RP2001813	2.75	2.75	3.73	1.84	1.98	1.94	*	-
	NT2RP2001817	3.16	3.16	4.49	4.03	5.32	3.45		
	NT2RP2001818	2.72	2.72	2.45	2.35	3.62	2.66		
	NT2RP2001837	5.13	5.13	13.43	10.29	10.16	12.33		
45	NT2RP2001839	17.02	17.02	83.84	60.14	71.06	82.26		
	NT2RP2001861	2	2	6.37	3.16	3.52	3.87		
	NT2RP2001869	2.64	2.64	6.54	4.35	5.77	8.84		
	NT2RP2001876	12.15	12.15	27.71	24.54	24.93	23.67		
	NT2RP2001878	2.32	2.32	3.96	2.95	3.32	4.95		
50	NT2RP2001881	3.72	3.72	5.4	9.67	12.64	12.16	**	+
	NT2RP2001883	2.63	2.63	6.8	4.33	5.42	6.35		
	NT2RP2001884	13.59	13.59	23.56	15.33	10.54	23.6		
	NT2RP2001885	3.27	3.27	5.49	2.88	4.39	4.82		
55	NT2RP2001898	10.76	10.76	80.37	69.48	88.43	73.46		

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	NT2RP2001900	3.38	3.38	4.03	2.61	4.93	10.26	
	NT2RP2001903	3.73	3.73	7.71	5.57	5.7	8.2	
	NT2RP2001907	3.1	3.1	8.56	5.05	7.56	6.72	
5	NT2RP2001915	2.89	2.89	5.06	4.06	3.08	7.19	
	NT2RP2001921	4.04	4.04	10.3	13.02	12.45	19.33	* +
	NT2RP2001926	2.75	2.75	8.25	3.55	5.3	5.64	
	NT2RP2001933	5.65	5.65	52.55	43.62	43.55	48.58	
10	NT2RP2001936	1.54	1.54	5.03	2.8	2.96	3.8	
	NT2RP2001943	25.33	25.33	49.4	47.71	40.48	51.65	
	NT2RP2001946	3.05	3.05	4.3	3.41	4.51	6.1	
	NT2RP2001947	3.18	3.18	3.44	3.93	3.21	6.88	
	NT2RP2001948	3.59	3.59	10.79	5.71	7.29	19.72	
15	NT2RP2001956	5.24	5.24	12.73	11.54	9.42	9.89	
	NT2RP2001969	4.05	4.05	7.82	3.24	5.7	6	
	NT2RP2001976	2.9	2.9	6.39	5.68	6.95	6.41	
	NT2RP2001978	3.26	3.26	6.08	4.18	4.83	6.03	
	NT2RP2001985	2.14	2.14	3.8	2.56	4.63	2.51	
20	NT2RP2001991	3.34	3.34	5.7	1.53	4.62	5.19	
	NT2RP2001997	3.16	3.16	8.43	5.31	7.47	6.98	
	NT2RP2002015	136.21	136.21	265.98	266.8	340.89	272.43	
	NT2RP2002017	3.24	3.24	6.06	2.06	3.3	2.57	
	NT2RP2002025	6.08	6.08	51.73	31.83	26.94	37.84	
25	NT2RP2002030	6.06	6.06	11.95	9.77	8.07	8.76	
	NT2RP2002032	2.31	2.31	4.95	2.39	3.81	2.55	
	NT2RP2002033	3	3	6.71	3.53	7.57	8.05	
	NT2RP2002041	3.5	3.5	6.37	2.76	3.15	9	
30	NT2RP2002046	3	3	6.88	2.99	7.4	6.01	
	NT2RP2002047	2.71	2.71	3.86	2.06	3.87	3.83	
	NT2RP2002050	7.67	7.67	11.66	9.78	6.47	7.77	
	NT2RP2002052	3.77	3.77	8.39	6.6	3.99	6.28	
	NT2RP2002058	2.07	2.07	4.11	3.1	4.82	3.39	
	NT2RP2002060	1.48	1.48	3.44	2.1	5.9	3.18	
35	NT2RP2002063	3.61	3.61	5.83	3.3	5.2	6.65	
	NT2RP2002066	10.11	10.11	13.47	5.47	9.88	9.73	
	NT2RP2002070	3.74	3.74	6.3	2.15	3.1	3.83	
	NT2RP2002076	3.72	3.72	5.1	3.35	5.58	3.63	
40	NT2RP2002078	13.09	13.09	105.74	73.87	88.51	76.08	
	NT2RP2002079	5.76	5.76	36.34	31.87	32.66	36.54	
	NT2RP2002099	4.19	4.19	5.82	4.7	6.75	6.03	
	NT2RP2002105	2.66	2.66	12.25	11.41	14.04	11.23	
	NT2RP2002115	1.63	1.63	5.21	1.98	3.42	1.52	
45	NT2RP2002124	3.66	3.66	6	4.56	5.38	3.88	
	NT2RP2002137	3.99	3.99	4.83	2.21	2.1	1.76	** -
	NT2RP2002139	24.08	24.08	45.74	51.88	77.99	62.3	* , +
	NT2RP2002154	1.37	1.37	4.13	3.56	2.36	3.2	
	NT2RP2002155	351.63	351.63	869.83	623.53	501.61	620.68	
50	NT2RP2002172	1.5	1.5	3.33	2.78	3.53	5.13	
	NT2RP2002185	3.29	3.29	7.65	7.3	8.56	8.12	
	NT2RP2002188	1.74	1.74	5.95	4.15	4.31	4.95	
	NT2RP2002192	2.9	2.9	7.6	6.65	6.42	5.83	
	NT2RP2002193	5.21	5.21	5.22	4.76	4.95	5.75	
55	NT2RP2002208	5.96	5.96	7.31	4.7	5.67	5.14	

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	NT2RP2002219	2.2	2.2	1.8	2.22	3.2	2.26		
	NT2RP2002231	1.72	1.72	3.1	4.11	2.76	5.76		
	NT2RP2002232	2.59	2.59	5.17	3.93	4.7	6.08		
5	NT2RP2002235	5.62	5.62	15.07	16.26	16.18	15.18		
	NT2RP2002239	37.02	37.02	67.99	72.09	67.21	63.77		
	NT2RP2002252	2.64	2.64	3.66	2.63	2.76	2.94		
	NT2RP2002256	4.62	4.62	15.3	11.37	16.99	12.91		
10	NT2RP2002257	7.01	7.01	22.77	18.65	25.09	20.6		
	NT2RP2002259	1.58	1.58	13.91	9.9	12.15	10.49		
	NT2RP2002264	0.6	0.6	3.14	3.2	3.12	3.92		
	NT2RP2002267	3.66	3.66	8.75	8.95	8.3	11.16		
	NT2RP2002270	4.26	4.26	8.23	15.09	10.47	14.71	*	+
15	NT2RP2002281	2.85	2.85	5.66	8.18	6.48	6.54	*	+
	NT2RP2002288	4.32	4.32	6.6	5.33	5.56	4.23		
	NT2RP2002292	5.42	5.42	8.4	6.64	8.08	6.95		
	NT2RP2002299	9.6	9.6	9.22	11.75	19.42	15.97	*	+
	NT2RP2002304	1.37	1.37	4.78	6.99	5.08	5.52		
20	NT2RP2002312	1.21	1.21	2.33	3.78	5.3	3.28	*	+
	NT2RP2002316	3.28	3.28	5.43	7.57	7.21	8.2	**	+
	NT2RP2002325	1.95	1.95	3.46	2.79	2.22	4.95		
	NT2RP2002333	2.13	2.13	3.03	3.53	4.86	5.69	*	+
	NT2RP2002371	5.43	5.43	9.14	9.72	12.07	11.65	*	+
25	NT2RP2002373	10.65	10.65	40.1	36.72	58.84	33.58		
	NT2RP2002381	4.68	4.68	2.35	2.66	3.19	3.71		
	NT2RP2002385	5.71	5.71	11.84	9.95	11.34	9.47		
	NT2RP2002394	0.94	0.94	1.52	1.24	0.96	1.26		
30	NT2RP2002408	2.7	2.7	5.08	3.89	3.12	4.29		
	NT2RP2002409	3.73	3.73	10.81	10.78	7.95	8.35		
	NT2RP2002424	2.98	2.98	4.22	5.84	6.22	7.85	*	+
	NT2RP2002426	6.44	6.44	11.38	7.59	8.46	8.93		
	NT2RP2002429	17.2	17.2	24.73	27.87	33.96	20.83		
35	NT2RP2002437	4.61	4.61	5.98	4.83	6.47	4.79		
	NT2RP2002439	3.83	3.83	6.69	2.68	3.22	4		
	NT2RP2002442	13.63	13.63	71.65	57.78	63.05	78.84		
	NT2RP2002457	3.27	3.27	5.31	4.35	4.87	5.82		
	NT2RP2002464	2.17	2.17	5.34	3.29	4.59	4.24		
40	NT2RP2002475	3.11	3.11	7.88	5.3	2.83	5.43		
	NT2RP2002479	3.09	3.09	4.25	1.95	2.99	1.93		
	NT2RP2002487	1.73	1.73	5.15	1.98	2.1	3.04		
	NT2RP2002498	1.52	1.52	2.2	2.62	2.82	4.47		
	NT2RP2002503	7.63	7.63	31.85	29.32	32.02	31.84		
45	NT2RP2002504	3.81	3.81	5.73	6	7.23	11.28		
	NT2RP2002510	2.65	2.65	8.92	4.68	6.59	6.85		
	NT2RP2002520	3.57	3.57	7.17	6.26	8.86	6.61		
	NT2RP2002527	5.18	5.18	6.02	9	12.37	11.22	**	+
	NT2RP2002533	3.34	3.34	6.27	4.83	6.94	5.88		
50	NT2RP2002537	3.22	3.22	4.02	4.09	5.91	10.08		
	NT2RP2002542	4.81	4.81	4.64	5.99	5.93	9.73		
	NT2RP2002546	4.31	4.31	5.85	6.5	4.91	5.24		
	NT2RP2002549	4.06	4.06	9.33	7.68	10.49	11.65		
	NT2RP2002564	4.11	4.11	11.18	10.67	9.21	9.29		
55	NT2RP2002591	2.45	2.45	7.03	3.31	4.79	5.79		

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	NT2RP2002595	9.67	9.67	12.41	12.06	13.39	14.79		
	NT2RP2002602	4.19	4.19	7.53	5.68	8.96	10.42		
	NT2RP2002606	1.27	1.27	2.93	2.26	2.97	3.95		
5	NT2RP2002609	6.12	6.12	9.95	4.79	5.48	7.74		
	NT2RP2002618	2.74	2.74	6.83	4.2	6.34	5.44		
	NT2RP2002621	4.24	4.24	10.22	6.58	7.52	9.79		
	NT2RP2002643	1.79	1.79	4.84	3.11	5.98	3.94		
	NT2RP2002672	4.48	4.48	9.23	8.03	9.37	9.87		
10	NT2RP2002673	4.13	4.13	5.01	8	12.88	17.73	*	+
	NT2RP2002674	2.4	2.4	4.06	2.78	2.37	1.84		
	NT2RP2002686	2.73	2.73	4.61	3.17	5.19	6.49		
	NT2RP2002688	10.73	10.73	28.07	22.34	33.34	28.71		
	NT2RP2002695	2.62	2.62	7.03	5.26	4.34	5.52		
15	NT2RP2002701	7.29	7.29	13.37	11.85	5.18	10.04		
	NT2RP2002706	3.02	3.02	5.58	6.47	8.14	6.19	*	+
	NT2RP2002710	11.2	11.2	36.97	39.43	33.9	42.75		
	NT2RP2002721	5.53	5.53	9.42	7.33	7.34	8.45		
20	NT2RP2002727	3.56	3.56	6.87	2.17	3.96	3.52		
	NT2RP2002734	3.59	3.59	6.65	5.71	7.65	7.54		
	NT2RP2002736	5.25	5.25	13.13	13.17	13.59	17.58		
	NT2RP2002740	2	2	5.11	3.18	2.81	3.13		
	NT2RP2002741	2.12	2.12	4.8	4.68	5.39	5.78		
25	NT2RP2002750	2.5	2.5	9.22	7.73	9.57	8.18		
	NT2RP2002752	4.59	4.59	10.39	7.93	7.66	8.03		
	NT2RP2002753	4.49	4.49	9.91	8.66	9.04	14.67		
	NT2RP2002760	4.79	4.79	10.31	3.56	4.5	4.13		
	NT2RP2002769	4.42	4.42	6.06	3.89	5.67	6.43		
30	NT2RP2002778	4.13	4.13	10.59	6.8	8.2	9.12		
	NT2RP2002791	8.89	8.89	54.27	48.75	53.08	50.19		
	NT2RP2002800	1.66	1.66	4.52	4	5.19	5.38		
	NT2RP2002805	3.38	3.38	5.46	4.75	6.44	3.81		
	NT2RP2002811	3.27	3.27	8.23	5.87	8.13	10.61		
35	NT2RP2002824	18.29	18.29	25.05	29.95	34.29	25.05		
	NT2RP2002839	13.26	13.26	31.21	16.09	23.42	16.27		
	NT2RP2002845	5.87	5.87	7.93	4.61	6.12	5.5		
	NT2RP2002857	2.95	2.95	3.6	2.35	4.23	2.99		
	NT2RP2002862	4.56	4.56	12.49	12.55	9.84	11.34		
40	NT2RP2002880	5.27	5.27	13.89	13.5	11.56	11.1		
	NT2RP2002885	8.6	8.6	17.12	7.56	10.07	10.02		
	NT2RP2002891	1.9	1.9	7.78	4.65	6.63	7.56		
	NT2RP2002907	2.95	2.95	6.91	5.95	5.5	4.9		
	NT2RP2002925	5.67	5.67	6.73	10.04	11.6	8.45	*	+
45	NT2RP2002927	10.08	10.08	10.63	19.05	21.85	15.48	**	+
	NT2RP2002928	4.32	4.32	4.56	2.65	2.34	2.51	**	-
	NT2RP2002929	3.96	3.96	9.74	8.09	7.86	9.87		
	NT2RP2002934	1.5	1.5	1.4	2.81	3.01	2.49	**	+
	NT2RP2002939	2.96	2.96	5.09	5.15	6.71	4.91		
50	NT2RP2002942	2.4	2.4	5.06	4.35	5.07	10.81		
	NT2RP2002954	5.41	5.41	11.46	7.21	9.1	8.65		
	NT2RP2002959	8.15	8.15	12.55	13.81	16.28	16.69	*	+
	NT2RP2002974	5.03	5.03	6.53	4.7	3.45	4.54		
55	NT2RP2002976	6.92	6.92	17.08	11.84	14.66	12.42		

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	NT2RP2002979	4.41	4.41	8.12	7.03	8.66	7.6		
	NT2RP2002980	6.44	6.44	15.09	15.56	11	17.45		
	NT2RP2002986	3.87	3.87	7.6	6.68	7.4	7.39		
5	NT2RP2002987	3.52	3.52	8.23	11.1	9.18	9.4	*	+
	NT2RP2002988	14.96	14.96	22.92	30.07	31.87	31.36	**	+
	NT2RP2002993	2.97	2.97	4.18	3.8	3.84	2.84		
	NT2RP2003000	4.88	4.88	8.34	6.97	9.62	9.97		
10	NT2RP2003008	4.85	4.85	5.06	3.34	4.76	4.78		
	NT2RP2003020	4.45	4.45	44.26	28.35	46.52	34.33		
	NT2RP2003032	1.91	1.91	4.02	5.82	6.48	6.59	**	+
	NT2RP2003034	4.21	4.21	13.47	13.16	11.15	16.31		
	NT2RP2003042	2.15	2.15	3.81	4.57	3.65	4.92		
	NT2RP2003050	2.32	2.32	3.56	2.55	2.17	1.83		
15	NT2RP2003060	7.27	7.27	15.51	21.53	18.91	17.46	*	+
	NT2RP2003073	5.61	5.61	8.73	7.06	10.51	8.17		
	NT2RP2003099	5.05	5.05	3.67	3.21	3.73	2.84		
	NT2RP2003108	3.6	3.6	4.23	5.29	3.91	6.62		
20	NT2RP2003115	1.68	1.68	5	7.75	4.69	4.84		
	NT2RP2003117	2.71	2.71	5.69	3.6	4.66	4.13		
	NT2RP2003121	1.83	1.83	3.47	4.03	2.69	3.33		
	NT2RP2003125	4.13	4.13	11.44	15.42	12.55	13.66	*	+
	NT2RP2003127	2.36	2.36	3.94	1.53	1.66	1.75		
25	NT2RP2003129	3.43	3.43	7.09	6.08	6.05	5.42		
	NT2RP2003137	4.49	4.49	6.14	7.58	8.4	6.46	*	+
	NT2RP2003138	4.66	4.66	20.24	16.55	17.45	16.92		
	NT2RP2003146	6.2	6.2	24.78	18.5	23.25	25.96		
	NT2RP2003148	3.09	3.09	6.73	3.06	4.6	4.04		
30	NT2RP2003150	1.45	1.45	5.71	3.98	5.2	4.3		
	NT2RP2003157	6.93	6.93	34.27	34.29	31.85	32.84		
	NT2RP2003158	6.3	6.3	25.32	26.87	28.69	59.31		
	NT2RP2003161	2.73	2.73	3.36	2.51	2.82	6.12		
	NT2RP2003164	1.96	1.96	2.1	1.28	1.87	2.46		
35	NT2RP2003165	2.18	2.18	5.94	3.1	3.69	4.84		
	NT2RP2003177	1.63	1.63	4.37	2.79	3.03	4.42		
	NT2RP2003179	1.23	1.23	4.98	4.08	3.63	7.96		
	NT2RP2003194	4.04	4.04	7.2	5.73	6.29	14.77		
	NT2RP2003206	1.59	1.59	4.47	1.64	3.52	1.44		
40	NT2RP2003210	5.06	5.06	15.15	16.14	12.93	15.9		
	NT2RP2003227	1.62	1.62	3.97	2.04	3.66	6.28		
	NT2RP2003228	6.57	6.57	29.53	29.56	43.94	44.24		
	NT2RP2003230	3.51	3.51	7.91	4.49	8.04	8.46		
45	NT2RP2003231	2.22	2.22	5.59	2.46	3.23	3.83		
	NT2RP2003237	2.52	2.52	4.59	4.59	6.4	6.46	*	+
	NT2RP2003239	2.3	2.3	4.46	2.97	4.46	4.05		
	NT2RP2003243	2.16	2.16	4.13	2.38	3.28	3.98		
	NT2RP2003265	3.93	3.93	5.33	4.22	4.88	4.92		
50	NT2RP2003267	2.73	2.73	3.15	3.24	4.17	7.42		
	NT2RP2003272	6.03	6.03	14.8	16.93	23.85	32.58	*	+
	NT2RP2003277	3.85	3.85	11.29	5.53	8.39	6.39		
	NT2RP2003280	3.47	3.47	9.38	7.67	7.25	6.09		
	NT2RP2003286	2.18	2.18	4.23	4.13	5	9.61		
55	NT2RP2003293	2.98	2.98	6.9	5.66	7.05	7.94		

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	NT2RP2003295	4.67	4.67	8.45	8.73	12.39	6.35	
	NT2RP2003297	3.43	3.43	7.57	4.32	6.89	5.28	
	NT2RP2003300	20.38	20.38	32.04	45.7	53.51	48.07	** +
5	NT2RP2003302	2.88	2.88	4.52	3.46	3.81	7.26	
	NT2RP2003307	0.57	0.57	2.62	1.43	1.49	1.38	
	NT2RP2003308	1.44	1.44	4.5	2.77	4.44	5.44	
	NT2RP2003311	4.18	4.18	5.83	7.35	4.25	8.2	
10	NT2RP2003329	2.99	2.99	4.41	2.63	3.89	4.44	
	NT2RP2003339	3.06	3.06	7.01	3.76	4.92	3.64	
	NT2RP2003345	4.15	4.15	8.38	2.77	3.97	6.33	
	NT2RP2003347	2.55	2.55	4.23	2.08	1.98	3.46	
	NT2RP2003367	2.15	2.15	4.65	2.7	1.98	1.44	
15	NT2RP2003369	1.34	1.34	4.71	2.16	2.36	0.89	
	NT2RP2003383	4.05	4.05	6.75	7.66	7.17	6.99	
	NT2RP2003390	9.1	9.1	17.93	16.66	14.27	12.94	
	NT2RP2003391	9.39	9.39	12.9	11.96	9.91	12.84	
	NT2RP2003393	4.23	4.23	6.99	6.14	5.03	9.44	
20	NT2RP2003394	8.67	8.67	16.21	17.56	21.75	17.23	
	NT2RP2003401	4.39	4.39	5.97	3.52	3.72	2.9	
	NT2RP2003403	3.42	3.42	7.64	6.62	8.55	7.79	
	NT2RP2003433	3.02	3.02	15.54	13.62	13.5	13.08	
	NT2RP2003445	3.2	3.2	4.74	4.08	3.5	3.93	
25	NT2RP2003446	2.67	2.67	6.23	5.06	6.05	4.47	
	NT2RP2003456	2.04	2.04	6.57	4.26	5.89	3.81	
	NT2RP2003466	3.56	3.56	20.09	17.34	25.96	23.53	
	NT2RP2003469	6.2	6.2	5.65	6.19	7.53	6.33	
	NT2RP2003470	5.64	5.64	6.47	5.06	6.11	6.44	
30	NT2RP2003471	2.72	2.72	3.88	3.22	2.78	3.38	
	NT2RP2003480	7.15	7.15	20.74	19.77	19.89	21.14	
	NT2RP2003495	3.99	3.99	6.03	8.07	7.24	10.72	* +
	NT2RP2003499	1.52	1.52	4.58	3.67	4.05	2.75	
	NT2RP2003505	0.98	0.98	3.21	2.62	3.88	1.4	
35	NT2RP2003506	2.54	2.54	6.53	5.65	5.36	4.78	
	NT2RP2003511	3.67	3.67	5.57	4.22	3.1	2.96	
	NT2RP2003513	3.79	3.79	6.01	5.49	5.57	5.71	
	NT2RP2003517	2.9	2.9	2.52	1.32	1.11	0.85	** -
	NT2RP2003522	11.08	11.08	19.77	10.55	11.42	16.52	
40	NT2RP2003525	5.12	5.12	14.93	12.19	10.72	11.79	
	NT2RP2003533	3.36	3.36	10.44	12.12	10.72	12.94	
	NT2RP2003541	6.72	6.72	11.29	12.02	13.42	11.7	
	NT2RP2003543	2.48	2.48	5.96	4.17	3.55	6.54	
	NT2RP2003545	2.59	2.59	4.85	2.22	3.6	1.85	
45	NT2RP2003559	4.92	4.92	4.81	3.97	3.84	3.37	** -
	NT2RP2003564	4.46	4.46	3.93	2.53	1.97	2.42	** -
	NT2RP2003565	4.94	4.94	50.48	41.12	48.32	37.82	
	NT2RP2003567	3.51	3.51	16.65	16.25	19.43	16.05	
	NT2RP2003575	4.44	4.44	18.78	19.56	22.63	20.7	
50	NT2RP2003576	102.12	102.12	203.44	206.62	128.42	171.89	
	NT2RP2003579	11.45	11.45	26.58	38.62	39.51	39.88	* +
	NT2RP2003581	3.85	3.85	6.1	4.33	4.38	3.96	
	NT2RP2003587	8.37	8.37	11.47	13.35	14.11	12.14	* +
55	NT2RP2003590	7.15	7.15	9.08	11.06	13.15	14.91	* +

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	NT2RP2003593	1.58	1.58	4.57	7.84	4.43	8.59		
	NT2RP2003596	4.86	4.86	10.86	14.43	13.12	17.96	*	+
	NT2RP2003599	6.49	6.49	12.46	14.29	10.17	11.98		
5	NT2RP2003600	1.88	1.88	2.95	3.02	3.64	6.36		
	NT2RP2003604	7.09	7.09	8.97	16.39	13.03	16.68	**	+
	NT2RP2003629	3.72	3.72	5.25	3.11	4.56	2.38		
	NT2RP2003630	4.09	4.09	6.66	4.79	6.78	3.84		
	NT2RP2003643	5.49	5.49	4.88	7.15	9.8	8.51	*	+
10	NT2RP2003655	4.27	4.27	11.12	7.52	6.38	7.59		
	NT2RP2003664	12.29	12.29	24.31	17.9	18.07	17.11		
	NT2RP2003668	2.52	2.52	5.01	3.3	3.18	3.62		
	NT2RP2003687	1.61	1.61	2.77	1.63	2.42	1.71		
	NT2RP2003691	3.03	3.03	5.07	3.7	4.21	4.57		
15	NT2RP2003702	3.99	3.99	6.14	2.89	3.02	2.89		
	NT2RP2003704	3.31	3.31	4.12	2.65	3.84	1.99		
	NT2RP2003706	2.44	2.44	1.24	1.72	1.42	1.6		
	NT2RP2003713	4.11	4.11	5.49	4.16	3.89	3.87		
20	NT2RP2003714	3.39	3.39	7.8	5.19	5.31	5.32		
	NT2RP2003727	3.96	3.96	11.63	4.81	6.08	10.46		
	NT2RP2003737	2.52	2.52	8.58	4.88	6.47	4.6		
	NT2RP2003751	1.66	1.66	4.84	1.24	1.67	1.37		
	NT2RP2003760	2.52	2.52	5.47	3.87	4.19	5.45		
25	NT2RP2003764	2.1	2.1	2.81	1.44	1.87	4.62		
	NT2RP2003769	5.52	5.52	11.45	7.41	8.17	10.64		
	NT2RP2003770	7.43	7.43	12.42	7.17	5.67	12.82		
	NT2RP2003777	3.44	3.44	6.78	5.01	5.6	9.57		
	NT2RP2003781	4.93	4.93	15.85	13.04	11.91	13.48		
30	NT2RP2003785	9.69	9.69	13.44	11.1	10.68	8.99		
	NT2RP2003793	9.32	9.32	9.5	8.29	13.22	10.51		
	NT2RP2003806	5.6	5.6	12.03	8.54	8.75	12.97		
	NT2RP2003825	10.73	10.73	62.01	57.88	71.84	82.78		
	NT2RP2003840	3.19	3.19	6.07	3.86	4.44	4.71		
35	NT2RP2003857	4.02	4.02	4.94	3.15	4.61	6.12		
	NT2RP2003859	1.82	1.82	6	3.35	4.16	4.21		
	NT2RP2003871	5.22	5.22	9.43	5.1	4.59	7.79		
	NT2RP2003876	3.82	3.82	8.8	5.92	5.87	7.92		
	NT2RP2003878	3.38	3.38	6.49	3.8	4.9	4.11		
40	NT2RP2003885	2.46	2.46	3.09	1.66	3.29	2.37		
	NT2RP2003898	5.39	5.39	8.91	12.3	12.73	18.25	*	+
	NT2RP2003902	5.09	5.09	10.78	8.24	8.23	10.42		
	NT2RP2003912	3.83	3.83	14.48	5.91	7.43	6.74		
45	NT2RP2003931	1.81	1.81	6.03	3.95	6.86	4.42		
	NT2RP2003940	2.31	2.31	9.51	7.1	6.2	7.3		
	NT2RP2003950	2.81	2.81	5.48	3.84	5.57	2.98		
	NT2RP2003952	1.86	1.86	5.63	2.58	4.23	2.98		
	NT2RP2003968	4.82	4.82	7.38	9.86	11.76	13.51	*	+
50	NT2RP2003976	5.35	5.35	9.56	12.56	12.6	13.2	*	+
	NT2RP2003981	3.27	3.27	7.41	4.62	2.03	4.07		
	NT2RP2003984	5.57	5.57	15.87	10.21	4.25	10.34		
	NT2RP2003986	2.79	2.79	6.22	6.29	6.32	5.17		
	NT2RP2003988	2.36	2.36	6.84	4.51	7.42	5		
55	NT2RP2004013	8.46	8.46	13.75	14.68	13.19	17		

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	NT2RP2004014	4.24	4.24	10.07	4.06	5.12	4.08		
	NT2RP2004036	6.88	6.88	14.85	14.08	19.02	16.03		
	NT2RP2004041	2.77	2.77	5.02	3.96	4.43	5.19		
5	NT2RP2004042	1.99	1.99	4.6	4.41	2.02	4.09		
	NT2RP2004049	4.68	4.68	19.13	14.24	15.5	16.3		
	NT2RP2004060	5.7	5.7	10.41	7.09	8.67	10.84		
	NT2RP2004066	2.17	2.17	4.31	3.05	4.83	3.65		
	NT2RP2004069	3.99	3.99	7.24	3.54	6	4.26		
10	NT2RP2004076	3.73	3.73	5.82	1.92	4.2	3.61		
	NT2RP2004080	4.21	4.21	9.26	4.45	6.47	6.15		
	NT2RP2004081	3.27	3.27	5.39	3.51	3.71	4.5		
	NT2RP2004098	2.32	2.32	6.48	5.4	3.1	5.75		
	NT2RP2004108	3.82	3.82	9.56	7.18	5.89	7.56		
15	NT2RP2004124	3.13	3.13	5.9	3.68	5.82	3.92		
	NT2RP2004130	3.67	3.67	9.32	5.51	9.12	8.4		
	NT2RP2004133	2.05	2.05	6.41	3.69	6.54	6.25		
	NT2RP2004141	5.72	5.72	7.15	5.14	7.05	7.05		
20	NT2RP2004142	5.33	5.33	8.1	4.18	5.45	3.93		
	NT2RP2004152	3.34	3.34	4.78	5.7	7.49	4.39		
	NT2RP2004165	3.71	3.71	8.3	5.87	5.92	6.54		
	NT2RP2004170	1.86	1.86	5.97	5.37	4.17	4.94		
	NT2RP2004172	2.93	2.93	5.24	4.69	5.58	4.26		
25	NT2RP2004176	3.45	3.45	8.4	7.77	10.21	8.98		
	NT2RP2004179	4.01	4.01	9.17	3.94	5.07	4.15		
	NT2RP2004187	3.16	3.16	6.36	3.87	3.88	4.59		
	NT2RP2004190	5.1	5.1	5.46	5.49	7.33	9.98		
	NT2RP2004194	7.54	7.54	14.57	18.5	23.44	19.83	*	+
30	NT2RP2004196	4.28	4.28	13.77	10.02	7.87	14.61		
	NT2RP2004205	2.67	2.67	8.14	8.64	6.62	7.81		
	NT2RP2004207	2.57	2.57	4.38	4.15	4.97	3.59		
	NT2RP2004226	2.09	2.09	4.95	4.11	6.15	5.33		
	NT2RP2004232	2.79	2.79	6.52	6	6.59	5.33		
35	NT2RP2004239	3.57	3.57	4.49	2.71	3.97	5.6		
	NT2RP2004240	7.07	7.07	12.57	13	15.8	8.95		
	NT2RP2004242	3.87	3.87	6.52	5.77	6.94	7.27		
	NT2RP2004245	1.74	1.74	3.47	2.42	3.29	3.15		
	NT2RP2004270	9.77	9.77	33.78	28.39	27.43	29.48		
40	NT2RP2004300	2	2	5.22	4.34	4.52	3.26		
	NT2RP2004304	6.46	6.46	15.37	17.41	12.33	13.9		
	NT2RP2004313	3.17	3.17	3.78	5.51	4.18	4.63	*	+
	NT2RP2004316	3.46	3.46	5.84	4.9	4.96	4.04		
45	NT2RP2004321	4.71	4.71	6.06	6.79	7.43	6.29	*	+
	NT2RP2004336	4.19	4.19	4.97	2.73	4.28	4.53		
	NT2RP2004339	5.3	5.3	20.89	17.11	18.07	15.39		
	NT2RP2004347	1.39	1.39	3.99	4.78	5	4.19		
	NT2RP2004364	2.26	2.26	6.52	5.08	6.72	4.76		
50	NT2RP2004365	3.18	3.18	6.58	6.68	6.34	7.7		
	NT2RP2004366	2.49	2.49	6.06	4.49	4.71	3.08		
	NT2RP2004373	8.17	8.17	14.38	7.1	7.22	5.91		
	NT2RP2004375	9.27	9.27	13.98	20.89	26.85	20.68	**	+
	NT2RP2004389	5.25	5.25	5.62	5.01	6.26	5.61		
55	NT2RP2004392	8.88	8.88	23.7	13.04	19.48	20.89		

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	NT2RP2004396	1.98	1.98	6.27	6.65	4.98	6.17	
	NT2RP2004399	5.24	5.24	8.12	12.56	7.74	9.52	
	NT2RP2004400	2.07	2.07	3.55	2.36	3.47	2	
5	NT2RP2004404	15.79	15.79	46	45.56	40.89	41.74	
	NT2RP2004410	16.64	16.64	24.04	27.99	33.46	32.69	* +
	NT2RP2004412	5.84	5.84	6.74	7.37	9.71	7.37	
	NT2RP2004414	4.27	4.27	5.09	3.81	4.89	3.8	
10	NT2RP2004425	3.71	3.71	6.53	3.73	3.18	4.04	
	NT2RP2004447	1.93	1.93	5.68	2.75	5.22	3.56	
	NT2RP2004463	13.57	13.57	16.23	16.84	16.25	20.26	
	NT2RP2004476	9.11	9.11	12.69	11.89	12.66	15.87	
	NT2RP2004488	3.82	3.82	8.52	4.59	6.02	5.37	
15	NT2RP2004490	2.88	2.88	3.86	2.31	2.96	4.1	
	NT2RP2004495	35.59	35.59	88.76	96.31	109.31	123.5	* +
	NT2RP2004512	4.25	4.25	7.62	5.84	6.41	7.12	
	NT2RP2004523	5.18	5.18	11.04	8.44	7.56	10.21	
	NT2RP2004524	2.19	2.19	6.33	4.97	5.32	5.56	
20	NT2RP2004536	8.99	8.99	16.96	14.1	14.51	17.51	
	NT2RP2004538	8.03	8.03	24.44	20.15	25.59	22.24	
	NT2RP2004548	4.45	4.45	9.92	7.39	9.1	10.51	
	NT2RP2004551	4.95	4.95	5.62	7.17	9.98	6.21	
	NT2RP2004556	83.73	83.73	210.17	226.48	298.92	241.84	
25	NT2RP2004568	5.19	5.19	11.18	6.52	9.16	9.99	
	NT2RP2004580	3.98	3.98	7.71	5.71	7.88	7.04	
	NT2RP2004585	11.28	11.28	49.82	36.69	46.91	64.56	
	NT2RP2004587	1.85	1.85	4.16	2.07	2.89	3	
	NT2RP2004594	4.56	4.56	9.24	11.47	12.21	28.18	
30	NT2RP2004600	3.49	3.49	5.76	2.22	3.22	3.09	
	NT2RP2004602	4.62	4.62	6.32	6	8.49	6.26	
	NT2RP2004606	392.21	392.21	581.19	612.4	897.5	764.63	* +
	NT2RP2004614	2.92	2.92	4.73	2.69	3.63	3.81	
	NT2RP2004648	2.52	2.52	4.96	3.24	5.01	4.12	
35	NT2RP2004655	5.69	5.69	10.1	8.37	6.76	9.46	
	NT2RP2004664	3.64	3.64	5.35	3.59	4.62	5.97	
	NT2RP2004670	1.98	1.98	3.81	1.98	3.71	4.27	
	NT2RP2004675	3.37	3.37	9.29	4.08	5.87	5.33	
	NT2RP2004681	3.46	3.46	7.56	5.72	8.92	7.55	
40	NT2RP2004689	2.63	2.63	5.75	5.75	4.73	7.87	
	NT2RP2004709	3.93	3.93	7.79	4.46	2.89	5.25	
	NT2RP2004710	3.15	3.15	8.37	5.63	4.61	6.88	
	NT2RP2004721	1.79	1.79	5.99	3.39	4.41	2.78	
	NT2RP2004736	3.26	3.26	5.81	6.11	4.79	4.63	
45	NT2RP2004743	4.94	4.94	7.96	5.94	6.67	7.36	
	NT2RP2004750	6.21	6.21	17.46	11.9	15.49	11.01	
	NT2RP2004755	11.65	11.65	19.9	14.84	22.87	19.91	
	NT2RP2004767	3.54	3.54	9	4.05	5.8	4.81	
50	NT2RP2004768	3.48	3.48	29.51	18.48	18.73	19.6	
	NT2RP2004775	4.68	4.68	5.68	7.71	5.62	8.26	
	NT2RP2004791	7.23	7.23	16.58	9.33	10.24	11.68	
	NT2RP2004794	14.01	14.01	25.74	23.04	16.86	22.78	
	NT2RP2004795	5.15	5.15	7.97	6.96	5.67	11.2	
55	NT2RP2004799	6.74	6.74	10.99	5.35	8.58	6.3	

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	NT2RP2004802	6.35	6.35	11.79	6.1	7.62	6.24	
	NT2RP2004810	3.44	3.44	8.83	7.37	7.84	6.03	
	NT2RP2004816	5.58	5.58	12.1	11.22	8.76	11.15	
5	NT2RP2004837	4.13	4.13	9.89	10.43	7.23	12.98	
	NT2RP2004841	0.91	0.91	2.86	3.69	4.03	8.87	
	NT2RP2004847	3.25	3.25	13.75	13.82	13.87	17.16	
	NT2RP2004861	2.3	2.3	5.23	2.33	4.23	2.46	
	NT2RP2004897	3.35	3.35	6.43	4.26	3.27	3.35	
10	NT2RP2004932	6.64	6.64	10.16	7.96	8.53	6.91	
	NT2RP2004933	4.63	4.63	3.41	2.98	2.93	3.2	*
	NT2RP2004936	3.69	3.69	6.41	4.56	4.42	7.53	
	NT2RP2004951	2.98	2.98	10.48	5.09	5.22	19.28	
	NT2RP2004959	3.13	3.13	6.61	6.43	6.26	6.5	
15	NT2RP2004961	2.1	2.1	4.79	4.89	6.49	5.44	
	NT2RP2004962	2.27	2.27	7.28	4.5	5.57	4.47	
	NT2RP2004966	2.26	2.26	6.07	4.1	4.1	2.97	
	NT2RP2004967	3.87	3.87	6.16	4.07	4.82	3.26	
20	NT2RP2004974	5.27	5.27	5.43	3.59	3.47	3.89	**
	NT2RP2004978	2.68	2.68	5.26	4.17	6.39	5.09	
	NT2RP2004982	0.57	0.57	1.82	2.2	1.94	1.72	
	NT2RP2004985	16.03	16.03	45.34	44.65	46.12	54.4	
	NT2RP2004999	2.21	2.21	5.64	4.27	8.86	10.34	
25	NT2RP2005000	3.62	3.62	5.76	4.33	4.76	4.65	
	NT2RP2005001	5.41	5.41	7.91	8.26	9.15	8.32	
	NT2RP2005003	3.8	3.8	7.2	6.11	7.91	6.2	
	NT2RP2005012	6.61	6.61	20.14	18.41	20.96	17.87	
	NT2RP2005018	1.9	1.9	4.24	3.29	2.24	2.91	
30	NT2RP2005020	6.12	6.12	23.58	19.97	19.94	22.96	
	NT2RP2005022	1.65	1.65	5.01	5.09	7.24	4.77	
	NT2RP2005027	5.96	5.96	38.61	42.51	40.08	33.77	
	NT2RP2005031	1.54	1.54	4.99	3.94	4.53	3.92	
	NT2RP2005035	44.19	44.19	94.82	116.52	107.36	106.69	* +
35	NT2RP2005037	4.28	4.28	5.87	7.91	10.26	7.09	* +
	NT2RP2005038	4.86	4.86	4.84	1.85	2.29	3.1	**
	NT2RP2005048	9.92	9.92	30.91	30.14	33.38	32.48	
	NT2RP2005069	16.01	16.01	34.88	21.99	20.63	27.64	
	NT2RP2005073	7.36	7.36	30.35	29.36	28.24	30.33	
40	NT2RP2005097	2.39	2.39	5.6	5.27	5.2	4.6	
	NT2RP2005108	1.76	1.76	3.95	2.84	4.21	7.12	
	NT2RP2005116	3.53	3.53	5.96	6.27	5.42	5.89	
	NT2RP2005126	5.88	5.88	8.31	8.9	14.96	8.51	
	NT2RP2005135	5.08	5.08	5.22	4.65	6.59	5.47	
45	NT2RP2005139	1.94	1.94	2.77	1.87	1.81	2.45	
	NT2RP2005140	3.82	3.82	4.86	12.39	6.72	8.55	* +
	NT2RP2005144	4.04	4.04	6.31	6.69	5.97	9.7	
	NT2RP2005147	2.23	2.23	5.49	5.61	6.15	6.25	
50	NT2RP2005148	2.86	2.86	5.63	3.83	6.65	4.83	
	NT2RP2005159	3.92	3.92	5.6	4.94	6.38	7.41	
	NT2RP2005162	3.23	3.23	5.56	4.57	5.4	4.21	
	NT2RP2005163	9.15	9.15	20.61	24.53	28.92	23.77	* +
	NT2RP2005168	2.87	2.87	6.14	5.24	4.79	4.88	
55	NT2RP2005181	2.64	2.64	5.42	3.4	2.11	1.98	

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	NT2RP2005204	5.4	5.4	7.81	9.08	11.94	11.81	*	+
	NT2RP2005219	4.61	4.61	9.64	7.09	10.28	8.7		
	NT2RP2005227	3.59	3.59	10.43	7.55	5.36	9.97		
5	NT2RP2005237	26.49	26.49	94.81	86.96	105.8	93.92		
	NT2RP2005239	2.24	2.24	6.07	2.62	4.27	4.34		
	NT2RP2005247	10.63	10.63	37.59	35.58	46.1	46.95		
	NT2RP2005254	4.35	4.35	9.14	5.7	6.44	6.93		
	NT2RP2005270	9.06	9.06	17.44	10.82	9.28	17.11		
10	NT2RP2005276	7.19	7.19	11.53	10.88	11.68	15.71		
	NT2RP2005287	7.98	7.98	11.97	8.37	7.7	13.36		
	NT2RP2005288	2.51	2.51	5.14	2.89	5.59	5.22		
	NT2RP2005289	4.26	4.26	8.48	6.68	9.08	7.49		
	NT2RP2005293	5	5	6.93	13.68	14.37	15.66	**	+
15	NT2RP2005315	5.79	5.79	10.64	8.04	12.95	16.68		
	NT2RP2005322	5.05	5.05	15.42	18.91	11.33	22.43		
	NT2RP2005325	8.45	8.45	18.4	15.57	13.63	20.01		
	NT2RP2005336	1.71	1.71	6.68	4.18	5.74	5.3		
20	NT2RP2005343	2.44	2.44	7.48	3.91	4.11	5.89		
	NT2RP2005344	3.39	3.39	4.83	2.37	2.67	3.32		
	NT2RP2005347	3.14	3.14	3.61	3.34	2.96	3.53		
	NT2RP2005354	6.49	6.49	11.79	10.37	13	11.38		
	NT2RP2005358	35.87	35.87	109.04	101.37	134.72	117.96		
25	NT2RP2005360	2.93	2.93	5	3.59	4.97	3.84		
	NT2RP2005378	5.27	5.27	13.12	7.54	8.7	13.93		
	NT2RP2005391	3.06	3.06	5.41	4.21	6.76	7.72		
	NT2RP2005393	1.61	1.61	6.34	4.86	6.16	4.07		
	NT2RP2005407	2.59	2.59	5.71	4.28	5.65	4.64		
30	NT2RP2005419	2.65	2.65	9.05	6.37	8.5	6.77		
	NT2RP2005425	5.63	5.63	18.38	15.27	18.89	15.46		
	NT2RP2005429	3.23	3.23	5.85	5.41	6.65	5.64		
	NT2RP2005436	4.65	4.65	10.5	7.02	4.28	4.97		
	NT2RP2005441	2.28	2.28	5.62	3.36	3.77	5.79		
35	NT2RP2005442	24.92	24.92	40.66	34.62	25.56	41.66		
	NT2RP2005444	10.72	10.72	19.24	21.92	21.07	25.56	*	+
	NT2RP2005453	2.79	2.79	7.44	2.63	4.09	3.15		
	NT2RP2005457	15.12	15.12	23.21	28.69	37.38	31.61	*	+
	NT2RP2005458	2.47	2.47	5.27	3.55	4.16	4.95		
40	NT2RP2005463	7.73	7.73	15.23	15.65	22.11	25.05	*	+
	NT2RP2005464	5.96	5.96	11.91	9.22	4.67	10.35		
	NT2RP2005465	1.81	1.81	6.69	3.86	3.75	3.74		
	NT2RP2005472	10.98	10.98	32.59	28.21	27.9	25.85		
	NT2RP2005476	5.01	5.01	8.99	7.01	6.98	6.08		
45	NT2RP2005490	7.51	7.51	21.09	18.18	25.55	23.45		
	NT2RP2005491	4.99	4.99	12.47	8.63	10.12	8.78		
	NT2RP2005495	3.56	3.56	5.77	3.38	4.55	4.3		
	NT2RP2005496	4.84	4.84	18.25	11.3	13.16	11.28		
	NT2RP2005498	2.92	2.92	7.45	5.18	5.03	4.98		
50	NT2RP2005501	2.04	2.04	5.54	3.12	4.34	2.46		
	NT2RP2005506	124.3	124.3	217.82	139.27	121.83	104.81		
	NT2RP2005509	6.97	6.97	10.45	11.4	9.61	15.73		
	NT2RP2005514	3.93	3.93	6	4.06	7.05	4.39		
55	NT2RP2005520	14.95	14.95	32.39	27.11	39.97	33.03		

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	NT2RP2005525	6.19	6.19	7.01	7.81	7.68	4.79	
	NT2RP2005531	2.18	2.18	3.33	1.67	2.12	1.9	
	NT2RP2005535	4.66	4.66	9.09	9.34	7.79	8.91	
5	NT2RP2005539	3.39	3.39	6.22	6.43	5.84	7.45	
	NT2RP2005540	3.2	3.2	7.15	4.79	5.58	6.59	
	NT2RP2005541	21.25	21.25	39.57	25.85	38.31	39.61	
	NT2RP2005549	2.69	2.69	7.66	6.72	4.85	7.11	
	NT2RP2005555	7.97	7.97	10.1	14.96	16.19	15.37	** +
10	NT2RP2005557	4.89	4.89	8.47	4.03	6.52	6.26	
	NT2RP2005581	3.93	3.93	9.61	6.32	7.95	6.89	
	NT2RP2005586	1.56	1.56	3.18	3.21	2.92	4.74	
	NT2RP2005597	2.77	2.77	2.93	2.98	4.1	3.84	
	NT2RP2005600	1.81	1.81	3.71	4.03	4.29	4.44	* +
15	NT2RP2005605	4.93	4.93	14.29	13.17	15.14	15.75	
	NT2RP2005614	3.06	3.06	5.62	3.68	4.11	2.45	
	NT2RP2005620	3.47	3.47	6.26	3.6	3.92	3.11	
	NT2RP2005622	6.14	6.14	5.07	6.21	7.43	4.61	
20	NT2RP2005632	5.72	5.72	10.95	11.57	10.42	14.89	
	NT2RP2005635	2.22	2.22	19.06	18.14	23.77	18.14	
	NT2RP2005637	1.53	1.53	8	3.73	3.71	4.14	
	NT2RP2005640	1.72	1.72	7.22	7.49	8.73	6.06	
	NT2RP2005645	4.68	4.68	11.8	10.61	11.47	9.67	
25	NT2RP2005651	3.45	3.45	7.88	7.64	6.78	10.15	
	NT2RP2005654	4.08	4.08	4.14	3.02	2.52	3.8	
	NT2RP2005666	4.91	4.91	5.27	4.34	7.7	4.74	
	NT2RP2005669	7.15	7.15	7.95	7.05	11.14	8.21	
	NT2RP2005670	2.35	2.35	6.91	7.77	5.04	5.2	
30	NT2RP2005671	3.12	3.12	7.83	10.77	8.9	9.78	* +
	NT2RP2005675	7.32	7.32	37.84	34.46	40.94	40.02	
	NT2RP2005683	2.56	2.56	7.01	7.16	5.19	7.16	
	NT2RP2005690	2.84	2.84	4.48	2.82	3.74	3.4	
	NT2RP2005694	4.07	4.07	5.49	3.77	6.26	3.54	
35	NT2RP2005701	5.97	5.97	8.82	10.39	10.35	9.52	* +
	NT2RP2005712	5.67	5.67	5.28	4.83	7.94	6.33	
	NT2RP2005719	1.86	1.86	3.26	4.42	3.8	3.76	* +
	NT2RP2005722	4.16	4.16	11.13	13.39	15.7	15.94	* +
	NT2RP2005723	2.71	2.71	4.2	3.65	4.58	3.67	
40	NT2RP2005726	2.55	2.55	4.13	2.86	4.01	3.22	
	NT2RP2005729	4.64	4.64	9.94	10.21	10.7	10.62	
	NT2RP2005731	3.05	3.05	3.39	2.51	2.16	1.27	*
	NT2RP2005732	9.41	9.41	57.73	48.37	75.21	41.64	
45	NT2RP2005737	10.75	10.75	22.28	27.16	25.02	17.59	
	NT2RP2005741	3.03	3.03	5.35	3.68	3.31	3.37	
	NT2RP2005748	1.86	1.86	5.94	3.8	3.72	2.95	
	NT2RP2005752	2.46	2.46	5.55	3.27	4.37	3.8	
	NT2RP2005753	8.45	8.45	14.76	11.12	11.69	14.45	
50	NT2RP2005763	3	3	8.03	4.22	4.77	5	
	NT2RP2005767	3.72	3.72	7.79	5.55	6.75	6.29	
	NT2RP2005773	8.11	8.11	10.02	10.6	11.59	13.37	* +
	NT2RP2005774	4.25	4.25	12.72	6.86	12.24	14.61	
	NT2RP2005775	3.75	3.75	7.2	3.35	4.83	5.63	
55	NT2RP2005781	5.11	5.11	9.88	9.82	7.19	12.94	

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	NT2RP2005784	5.41	5.41	11.51	7.68	12.12	14.06	
	NT2RP2005789	3.98	3.98	11.24	7.89	9.52	8.86	
	NT2RP2005799	2.45	2.45	6.35	2.64	4.67	3.7	
5	NT2RP2005804	9.01	9.01	25	27.85	27.32	30.57	
	NT2RP2005812	2.63	2.63	4.83	2.9	3.89	5.21	
	NT2RP2005815	2.48	2.48	3.15	2.38	3.21	5.2	
	NT2RP2005835	5.99	5.99	11.26	7.13	13.74	11.69	
10	NT2RP2005841	2.32	2.32	10.04	4.89	7.43	11.23	
	NT2RP2005853	1.29	1.29	4.44	2.71	4.6	4.96	
	NT2RP2005857	7.37	7.37	9.87	13.46	7.93	20.27	
	NT2RP2005859	2.76	2.76	5	2.91	6.14	4.78	
	NT2RP2005860	1.41	1.41	3.54	1.45	1.89	2.22	
15	NT2RP2005863	3.03	3.03	6.55	10.76	18.29	15.94	* +
	NT2RP2005868	3.86	3.86	5.85	5.1	6.3	7.77	
	NT2RP2005876	5.7	5.7	12.31	7.84	8.29	8.2	
	NT2RP2005878	2.26	2.26	8.44	5.25	4.95	6.32	
	NT2RP2005883	13.54	13.54	21.06	23.75	9.57	28.09	
20	NT2RP2005886	7.18	7.18	50.05	51.13	62.09	50.14	
	NT2RP2005887	3.76	3.76	6.51	4.74	8.05	4.81	
	NT2RP2005890	4.17	4.17	9.77	11.87	17.13	12.15	* +
	NT2RP2005901	3.19	3.19	5.69	3.91	6.18	5.14	
	NT2RP2005902	3.17	3.17	4.33	4.78	4.77	6.25	
25	NT2RP2005908	3.09	3.09	7.86	4.89	3.7	6.34	
	NT2RP2005927	1.77	1.77	2.66	2.25	4.36	3.07	
	NT2RP2005933	2.5	2.5	5.59	6.4	4.77	6.42	
	NT2RP2005941	2.09	2.09	5.2	3.31	4.41	3.9	
	NT2RP2005942	4	4	6.86	3.08	4.59	4.64	
30	NT2RP2005946	4.63	4.63	9.49	5.33	7.06	6.24	
	NT2RP2005970	5.44	5.44	14	16.16	22.05	18.9	* +
	NT2RP2005980	3.71	3.71	5.25	2.69	3.46	2.37	
	NT2RP2005994	2.99	2.99	6.76	4.28	3.28	5.14	
	NT2RP2006004	1.31	1.31	2.89	2.07	6.09	2.58	
35	NT2RP2006013	1.38	1.38	4.91	3.1	5.07	4.92	
	NT2RP2006023	8.37	8.37	17.77	20	21.43	21.14	* +
	NT2RP2006028	5.03	5.03	10.23	7.47	9.89	9.71	
	NT2RP2006038	4.67	4.67	5.86	2.79	5.4	1.09	
40	NT2RP2006042	8.3	8.3	7.22	6.63	5.89	6.3	* -
	NT2RP2006043	5.65	5.65	7.59	7.6	10.99	8.29	
	NT2RP2006052	1.48	1.48	4.48	4.13	3.12	4.54	
	NT2RP2006057	3.73	3.73	6.23	5.69	3.83	4.95	
	NT2RP2006064	4.16	4.16	7.73	5.86	6.81	9.08	
45	NT2RP2006068	2.76	2.76	6.75	6.8	7.81	5.81	
	NT2RP2006069	1.46	1.46	4.94	3.56	3.95	3.3	
	NT2RP2006071	8.37	8.37	7.8	9.28	10.48	9.11	* +
	NT2RP2006090	6.62	6.62	5.78	3.27	3.55	3.64	** -
	NT2RP2006092	3.78	3.78	8.3	6.18	8.04	7.07	
50	NT2RP2006097	14.05	14.05	40.38	31.2	25.81	40.02	
	NT2RP2006098	1.94	1.94	4.27	4.52	4.61	7.65	
	NT2RP2006099	3.84	3.84	11.02	10.65	10.99	13.34	
	NT2RP2006100	2.87	2.87	5.78	3.63	7.31	5.19	
	NT2RP2006103	2.39	2.39	5.54	2.6	3.93	1.71	
55	NT2RP2006106	6.48	6.48	21.51	18.05	24.81	22.3	

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	NT2RP2006127	3.17	3.17	4.92	1.62	1.26	1.21	*	-
	NT2RP2006134	4.25	4.25	4.41	6.08	6.7	5.47	**	+
	NT2RP2006141	3.91	3.91	7.94	7.45	6.04	9.08		
5	NT2RP2006166	3.1	3.1	10.65	9.01	8.94	7.85		
	NT2RP2006176	2.15	2.15	4.26	3.95	5.73	4.69		
	NT2RP2006181	1.68	1.68	2.84	3.21	3.14	2.45		
	NT2RP2006184	8.85	8.85	17.16	20.8	19.95	17.1		
10	NT2RP2006186	3.01	3.01	4.57	2.77	2.29	4.33		
	NT2RP2006196	5.24	5.24	7.21	5.25	5.23	4.16		
	NT2RP2006199	5.06	5.06	4.38	3.81	3.65	3.64	**	-
	NT2RP2006200	0.87	0.87	3.43	4.37	4.52	2.17		
	NT2RP2006210	20.08	20.08	59.85	75.37	70.55	96.59	*	+
15	NT2RP2006219	2.88	2.88	6.26	5.97	5.11	7.36		
	NT2RP2006224	3.7	3.7	7.55	9	7.7	8.93		
	NT2RP2006237	1.97	1.97	4.79	3.45	2.74	4.14		
	NT2RP2006238	3.9	3.9	6.33	4.2	4.69	3.93		
	NT2RP2006258	4.5	4.5	6.73	3.07	4.27	4.39		
20	NT2RP2006261	7.32	7.32	3.98	2.04	3.19	7.69		
	NT2RP2006269	4.11	4.11	7.96	9.52	5.46	9.06		
	NT2RP2006275	3.67	3.67	30.36	23.46	35.36	25.14		
	NT2RP2006282	3.16	3.16	8.89	8.85	8.4	7.05		
	NT2RP2006302	5.69	5.69	12.68	13.12	12.4	11.87		
25	NT2RP2006312	4.88	4.88	8.22	8.47	9.13	9.8		
	NT2RP2006320	4.27	4.27	9.87	6.42	9.32	9.69		
	NT2RP2006321	3.27	3.27	4.23	2.79	4.99	4.13		
	NT2RP2006323	4.1	4.1	2.59	2.39	3.6	1.83		
	NT2RP2006333	0.67	0.67	1.82	1.7	1.04	1.17		
30	NT2RP2006334	2.24	2.24	4.02	4.57	2.72	3.54		
	NT2RP2006338	2.4	2.4	5.26	4.73	5.11	4.04		
	NT2RP2006339	2.24	2.24	2.94	2.47	1.93	2.06		
	NT2RP2006355	3.61	3.61	4.59	3.14	3.39	2.22		
	NT2RP2006365	3.3	3.3	4.44	2.42	2.6	1.3	*	-
35	NT2RP2006374	16.34	16.34	111.62	108.73	174.7	73.65		
	NT2RP2006393	4.93	4.93	7.68	7.38	8	6.95		
	NT2RP2006394	8.59	8.59	17.91	11.3	11.18	15.38		
	NT2RP2006400	2.25	2.25	4.51	2.08	3.58	1.95		
40	NT2RP2006411	27.71	27.71	42.11	23.61	17.25	37.31		
	NT2RP2006429	2.22	2.22	7.3	2.82	5.3	2.21		
	NT2RP2006435	1.46	1.46	5.29	1.76	2.65	1.98		
	NT2RP2006436	2.33	2.33	6.43	4.33	5.28	3.75		
	NT2RP2006441	4.69	4.69	8.19	7.76	8.89	8.37		
45	NT2RP2006447	2.41	2.41	4.78	3.18	2.63	3.87		
	NT2RP2006454	2.58	2.58	5.38	4.39	3.37	4.03		
	NT2RP2006455	3.79	3.79	7.14	2.91	4.62	9.23		
	NT2RP2006456	1.96	1.96	5.99	2.51	4.49	3.17		
	NT2RP2006464	5.44	5.44	8.28	4.47	8.85	7.9		
50	NT2RP2006467	4.17	4.17	10	8.56	12.47	12.58		
	NT2RP2006472	5.05	5.05	6.84	7.24	6.92	7.37		
	NT2RP2006474	4.69	4.69	16.3	18.19	32.31	21.3		
	NT2RP2006475	2.5	2.5	9.54	6.14	6.86	7.66		
	NT2RP2006476	5.34	5.34	14.94	7.62	13.82	17.24		
55	NT2RP2006501	2.44	2.44	7.28	4.6	7.45	7.74		

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	NT2RP2006512	10.25	10.25	19.79	16.72	7.89	29.01	
	NT2RP2006526	2.09	2.09	5.19	2.24	2.78	2.31	
	NT2RP2006527	3.61	3.61	7.05	4.56	6.14	6.46	
5	NT2RP2006534	2.24	2.24	4.49	2.08	2.95	2.73	
	NT2RP2006537	6.08	6.08	15.7	11.72	17.73	12.82	
	NT2RP2006543	7.83	7.83	14.8	6.52	5.4	6.88	
	NT2RP2006554	1.33	1.33	3.71	1.79	3.76	2.2	
	NT2RP2006565	3.78	3.78	8.91	5.79	8.42	7.55	
10	NT2RP2006571	1.38	1.38	3.88	2.77	4.01	2.29	
	NT2RP2006573	2.1	2.1	4.02	3.05	3.6	2.41	
	NT2RP2006598	2.25	2.25	7.04	4.34	6.56	4.78	
	NT2RP2006601	24.92	24.92	35.13	38.45	45.47	31.69	
	NT2RP3000002	5.04	5.04	6.09	4.7	5.04	8.18	
15	NT2RP3000011	1.82	1.82	5.9	2.59	1.85	2.22	
	NT2RP3000014	3.29	3.29	7.66	4.22	3.06	4.95	
	NT2RP3000016	3.42	3.42	7	5.29	6.56	6.11	
	NT2RP3000022	1.71	1.71	3.93	1.72	4.68	0.59	
20	NT2RP3000024	3.74	3.74	7.03	4.31	4.92	4.06	
	NT2RP3000031	4.66	4.66	8.66	4	6.75	4.86	
	NT2RP3000034	3.76	3.76	6.24	4.44	7.13	3.23	
	NT2RP3000037	2.76	2.76	6.5	9.41	13.44	11.06	* +
	NT2RP3000040	2.04	2.04	5.96	3.21	3.46	3.56	
25	NT2RP3000041	2.15	2.15	7.35	3.71	3.01	3.16	
	NT2RP3000046	1.95	1.95	4.42	3.67	7.11	3.84	
	NT2RP3000047	3.25	3.25	5.55	5.85	6.2	5.94	
	NT2RP3000049	2.54	2.54	6.94	5.26	7.78	3.58	
	NT2RP3000050	4.99	4.99	9.03	3.76	8.5	6.22	
30	NT2RP3000051	5.99	5.99	10.69	8.51	11.19	9.72	
	NT2RP3000054	4.31	4.31	6.5	4.38	5.35	3.22	
	NT2RP3000055	1.98	1.98	4.76	3.81	2.67	3.96	
	NT2RP3000056	2.87	2.87	7.09	5.59	3.32	3.91	
	NT2RP3000059	2.54	2.54	5.1	1.89	4.07	1.6	
35	NT2RP3000063	2.18	2.18	5.51	3.34	5.19	2.27	
	NT2RP3000068	3.76	3.76	24.22	25.83	37.88	23.13	
	NT2RP3000069	17.44	17.44	20.58	22	28.87	18.2	
	NT2RP3000072	5.9	5.9	6.18	4.96	5.39	4.19	*
	NT2RP3000080	4.38	4.38	6.72	3.78	5.28	3.93	
40	NT2RP3000085	1.9	1.9	4.84	5.13	4.66	5.5	
	NT2RP3000087	3.77	3.77	9.1	6.22	5.61	6	
	NT2RP3000092	1.92	1.92	3.6	2.72	3.2	2.52	
	NT2RP3000109	1.74	1.74	5.05	5.63	7.94	4.24	
45	NT2RP3000119	4.66	4.66	14.27	11.29	13.7	14.28	
	NT2RP3000125	3.02	3.02	5.56	3.42	4.53	2	
	NT2RP3000131	7.84	7.84	14.37	16.23	19.96	12.93	
	NT2RP3000134	5.96	5.96	9.01	6.61	7.25	6.46	
	NT2RP3000137	3.88	3.88	6.48	5.58	6.3	6.11	
50	NT2RP3000142	2.87	2.87	7.77	7.28	5.03	5.31	
	NT2RP3000148	1.84	1.84	6.28	4.9	5.04	5.34	
	NT2RP3000149	2.51	2.51	6.97	6.14	7.77	8.24	
	NT2RP3000163	2.16	2.16	6.17	3.27	3.9	2.5	
	NT2RP3000168	5.53	5.53	14.55	12.8	11.65	11.73	
55	NT2RP3000169	3.74	3.74	6.01	6.03	8.47	5.72	

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	NT2RP3000171	10.86	10.86	16.71	28.33	38.98	25.93	*	+
	NT2RP3000172	0.86	0.86	1.53	1.66	1.2	1.46		
	NT2RP3000186	4.32	4.32	10.6	19.18	15.43	15.82	*	+
5	NT2RP3000197	1.22	1.22	3.66	4.03	4.29	3.39		
	NT2RP3000201	2.4	2.4	7.2	10.49	8.4	7.88		
	NT2RP3000204	2.16	2.16	4.44	3.88	4.1	4.25		
	NT2RP3000207	2.87	2.87	4.71	3	2.6	2.45		
10	NT2RP3000216	5.38	5.38	10.1	5.87	9.5	5.73		
	NT2RP3000220	5.14	5.14	5.66	3.68	5.69	2.92		
	NT2RP3000221	2.18	2.18	5.45	6.26	6.63	5.93		
	NT2RP3000232	2.7	2.7	8.01	7.1	5.52	5.92		
	NT2RP3000233	1.55	1.55	6.01	6.9	5.91	4.06		
15	NT2RP3000234	3.23	3.23	9.09	12.89	10.4	11.41	*	+
	NT2RP3000235	1.57	1.57	3.3	2.35	2.92	1.38		
	NT2RP3000239	4.61	4.61	11.11	9.51	9.71	14.92		
	NT2RP3000247	3.25	3.25	5.82	2.92	4.04	1.96		
	NT2RP3000251	6.11	6.11	6.52	5.22	5.82	3.25		
20	NT2RP3000252	3.73	3.73	7.99	7.61	8.53	8.4		
	NT2RP3000255	2.18	2.18	2.96	3.26	3.13	1.97		
	NT2RP3000262	6.72	6.72	9.43	11.67	7.95	9.13		
	NT2RP3000266	6.47	6.47	15.5	13.38	10.83	12.64		
	NT2RP3000267	2.71	2.71	4.04	2.9	2.64	3.03		
25	NT2RP3000271	4.38	4.38	5.57	5.11	4.84	3.72		
	NT2RP3000278	7.84	7.84	56.85	48.55	82.07	42.57		
	NT2RP3000281	4.94	4.94	10.72	8.19	8.22	7.27		
	NT2RP3000292	5.63	5.63	14.1	9.17	6.77	6.93		
	NT2RP3000299	2.31	2.31	4.92	3.73	4.89	4.98		
30	NT2RP3000304	2.15	2.15	3.48	2.85	3.36	1.64		
	NT2RP3000310	7.24	7.24	24.22	18.94	23.07	19.88		
	NT2RP3000312	2.99	2.99	8.16	3.31	5.25	3.87		
	NT2RP3000320	7.06	7.06	6.17	5.25	4.74	4.74	**	-
35	NT2RP3000322	11.05	11.05	18.76	32.59	45.13	46.95	**	+
	NT2RP3000324	6.91	6.91	46.42	36.64	43.53	39.68		
	NT2RP3000326	1.95	1.95	6.17	4.02	5.75	3.53		
	NT2RP3000329	2.5	2.5	5.96	4.97	8.84	5.9		
	NT2RP3000330	4.1	4.1	6.18	4.62	5.53	6.12		
40	NT2RP3000333	3.23	3.23	7.45	4.36	5.28	4.52		
	NT2RP3000341	8.8	8.8	12.85	14.81	18.59	14.41	*	+
	NT2RP3000344	2.73	2.73	3.75	2.69	3.54	2.29		
	NT2RP3000345	3.09	3.09	3.57	1.65	1.97	2.66	*	-
	NT2RP3000348	444.59	444.59	802.63	824.62	1016.01	909.68		
45	NT2RP3000350	4.25	4.25	10.34	4.57	9.28	6.4		
	NT2RP3000359	9.53	9.53	24.44	8.54	11.36	16.62		
	NT2RP3000361	7.5	7.5	11.12	7.89	7.81	8.95		
	NT2RP3000366	7.38	7.38	14.27	9.52	11.84	16.13		
	NT2RP3000378	2.67	2.67	5.75	3.92	4.78	2.47		
50	NT2RP3000384	5.42	5.42	10.88	9.52	13.1	9.28		
	NT2RP3000389	12.54	12.54	21.49	23.95	35.02	27.32	*	+
	NT2RP3000393	3.74	3.74	6.16	5.03	4.53	4.77		
	NT2RP3000395	110.27	110.27	212	108.33	38.18	148.45		
	NT2RP3000397	2.83	2.83	5.28	2.51	5.26	3.31		
55	NT2RP3000398	3.39	3.39	10.12	11.46	11.18	12.26		

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	NT2RP3000403	3.22	3.22	9.39	10.1	8.2	8.44	
	NT2RP3000418	3.4	3.4	10.22	7.12	11.08	13.42	
	NT2RP3000424	2.86	2.86	9.43	6.25	9.52	6.86	
5	NT2RP3000427	4.65	4.65	9.05	11.55	13.43	12.35	* +
	NT2RP3000431	2.05	2.05	4.93	3.43	3.26	3.93	
	NT2RP3000433	2.63	2.63	8.65	5.65	7.09	6.65	
	NT2RP3000436	11.39	11.39	20.93	18.76	9.35	18.86	
10	NT2RP3000439	1.4	1.4	3.61	2.54	3.56	2	
	NT2RP3000441	3.88	3.88	7.4	7.56	7.92	6.39	
	NT2RP3000444	3.31	3.31	7.29	2.36	3.25	2.2	
	NT2RP3000448	4.45	4.45	10.15	4.05	6.54	3.93	
	NT2RP3000449	2.84	2.84	4.59	3.1	3.94	2.93	
15	NT2RP3000451	1.76	1.76	5.12	3.7	5	2.96	
	NT2RP3000456	1.69	1.69	5.48	4.23	6.67	4.21	
	NT2RP3000460	18.87	18.87	36.67	24.52	25.24	26.25	
	NT2RP3000471	3.14	3.14	6.49	2.74	4.98	5.84	
20	NT2RP3000477	19.96	19.96	23.67	28.98	17.78	32.78	
	NT2RP3000478	5.86	5.86	8.95	5.21	8.98	2.6	
	NT2RP3000481	5.48	5.48	5.76	2.76	3.61	1.52	** -
	NT2RP3000484	3.51	3.51	4.26	2.32	2.55	1.76	* -
	NT2RP3000487	1.77	1.77	7.4	5.07	4.03	4.97	
25	NT2RP3000512	3.29	3.29	17.7	15.17	15.9	14.52	
	NT2RP3000523	13.05	13.05	30.74	31.75	27.83	34.4	
	NT2RP3000526	3.07	3.07	7.38	5.18	6.31	4.64	
	NT2RP3000527	2.83	2.83	6.5	3.76	7.25	5.03	
	NT2RP3000531	2.9	2.9	7.71	5.11	5.51	4.69	
30	NT2RP3000532	5.74	5.74	5.6	5.75	8.39	4.26	
	NT2RP3000542	6.23	6.23	8.1	7.21	7.3	6.39	
	NT2RP3000554	8.81	8.81	15.22	13.78	10.56	14.95	
	NT2RP3000561	1.21	1.21	3.51	3.11	2.76	2.25	
	NT2RP3000562	1.84	1.84	3.5	3.7	3.87	3.23	
35	NT2RP3000578	1.56	1.56	2.54	2.54	3.37	2.36	
	NT2RP3000582	1.26	1.26	4.66	2.24	2.52	0.41	
	NT2RP3000584	2.82	2.82	6.52	3.2	2.5	2.02	
	NT2RP3000586	4.08	4.08	4.59	3.28	3.9	2.87	
	NT2RP3000590	5.69	5.69	4.61	3.78	4.35	2.57	
40	NT2RP3000592	1.8	1.8	2.99	2.97	2.75	3.15	
	NT2RP3000596	2.27	2.27	4.89	4.5	3.33	3.03	
	NT2RP3000599	1.67	1.67	3.07	3.88	4.98	3.82	* +
	NT2RP3000603	6.09	6.09	39.25	40.43	44.88	35.89	
45	NT2RP3000605	2.84	2.84	6.66	4.56	4.23	2.56	
	NT2RP3000607	5.35	5.35	7.59	5.74	8.46	7.55	
	NT2RP3000616	3.26	3.26	5.45	2.56	2.38	1.21	
	NT2RP3000621	5.18	5.18	8.48	10.28	10.29	6.01	
	NT2RP3000622	2.36	2.36	8.76	5.85	6.21	4.72	
	NT2RP3000624	1.53	1.53	3.19	3.97	3.06	2.78	
50	NT2RP3000628	2.44	2.44	8.04	10.27	7.85	5.58	
	NT2RP3000631	4.71	4.71	14.95	22.82	16.45	14.2	
	NT2RP3000632	2.35	2.35	5.5	7.78	8.91	5.91	* +
	NT2RP3000638	6.95	6.95	17.93	11.8	11.6	9.97	
55	NT2RP3000644	25.72	25.72	48.41	57.98	72.01	52.49	* +
	NT2RP3000645	5.85	5.85	10.48	9.84	12.55	8.43	

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	NT2RP3000652	3.39	3.39	5.34	6.22	5.9	7.74	*	+
	NT2RP3000658	2.26	2.26	5.01	6.16	4.24	4.86		
	NT2RP3000660	2.34	2.34	6.25	6.98	6.91	5.14		
5	NT2RP3000661	1.98	1.98	4.49	4.06	3.87	3.1		
	NT2RP3000665	4.79	4.79	12.26	11.83	11.92	7		
	NT2RP3000676	4.46	4.46	7.55	6.65	7.81	5.42		
	NT2RP3000677	2.87	2.87	4.13	2.44	3.07	1.54		
10	NT2RP3000681	19.85	19.85	30.12	32.94	41.51	34.34	*	+
	NT2RP3000683	2.68	2.68	9.67	6.69	7.09	6.69		
	NT2RP3000685	1.7	1.7	2.5	3.63	2.36	3.44		
	NT2RP3000690	2.77	2.77	3.29	3.82	3.75	2.72		
	NT2RP3000698	10	10	22.49	25.66	17.08	27.43		
15	NT2RP3000708	3.45	3.45	5.5	8.17	9.22	8.56	**	+
	NT2RP3000719	2.83	2.83	2.83	1.16	1.7	1.91	**	-
	NT2RP3000721	5.63	5.63	24.61	23.43	39.76	21.55		
	NT2RP3000728	3.33	3.33	2.57	1.4	1.64	1.05	**	-
	NT2RP3000730	2.06	2.06	5.04	2.76	4.23	1.86		
20	NT2RP3000733	2.87	2.87	6.32	3.48	4.47	4.25		
	NT2RP3000735	1.74	1.74	4.22	1.81	2.22	1.26		
	NT2RP3000736	2.71	2.71	6.35	3.29	5.05	3.65		
	NT2RP3000739	13.76	13.76	12.16	18.05	9.37	20.19		
	NT2RP3000742	3.89	3.89	10.06	4.54	4.97	4.43		
25	NT2RP3000753	2.29	2.29	3.9	2.17	2.65	6.3		
	NT2RP3000759	9.07	9.07	15.99	11.11	17.14	23.05		
	NT2RP3000789	1.58	1.58	5.76	4.89	4.23	3.69		
	NT2RP3000815	1.91	1.91	5.92	4.49	5.57	3.08		
30	NT2RP3000818	4.35	4.35	11.29	6.64	10.49	8.27		
	NT2RP3000820	9.01	9.01	18.49	18.58	20.1	16.9		
	NT2RP3000821	2.13	2.13	4.83	3.28	5.19	2.02		
	NT2RP3000825	1.87	1.87	4.94	1.92	1.47	2.27		
	NT2RP3000826	4.04	4.04	13.59	10.86	13.8	12.94		
	NT2RP3000836	5.33	5.33	11.61	11.55	14.11	13.3		
35	NT2RP3000838	319.2	319.2	741.74	710.2	743.55	1049.86		
	NT2RP3000839	2.35	2.35	6.67	4.53	6.38	4.36		
	NT2RP3000841	2.17	2.17	4.32	3.79	5.55	4.72		
	NT2RP3000845	3.96	3.96	8.89	5.76	6.71	7.85		
	NT2RP3000847	3.7	3.7	7.94	4.48	5.94	5.28		
40	NT2RP3000848	2.84	2.84	8.34	5.36	6.81	6.3		
	NT2RP3000850	5.67	5.67	7.04	6.58	11.29	7.47		
	NT2RP3000852	3.27	3.27	3.17	4.02	5.23	5.8	*	+
	NT2RP3000859	2.76	2.76	7.12	4.46	7.11	8.43		
45	NT2RP3000861	2.58	2.58	10.51	6.13	10.36	6.43		
	NT2RP3000862	15.29	15.29	24.16	16.36	9.81	23.13		
	NT2RP3000865	1.58	1.58	4.26	2.54	4.21	1.83		
	NT2RP3000866	2.08	2.08	5.03	2.37	3.59	5.22		
	NT2RP3000868	2.2	2.2	7.09	3.04	3.84	2.28		
50	NT2RP3000869	3.54	3.54	11.36	9.61	15.76	7.9		
	NT2RP3000871	1.75	1.75	3.79	1.81	3.24	1.94		
	NT2RP3000875	0.99	0.99	4.25	2.57	2.71	3.64		
	NT2RP3000895	2.54	2.54	5.56	2.84	3.55	4.93		
	NT2RP3000900	6.01	6.01	11.86	11.3	7.7	14.58		
55	NT2RP3000901	3.67	3.67	7.03	4.11	6.39	5.3		

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	NT2RP3000903	3.76	3.76	7.87	3.12	5.92	3.93	
	NT2RP3000904	3.83	3.83	8.67	3.05	4.87	3.16	
	NT2RP3000907	5.66	5.66	10.03	8.94	10.67	10.14	
5	NT2RP3000913	6.04	6.04	15.01	17.87	25.57	17.37	* +
	NT2RP3000917	7.64	7.64	16.58	7.66	6.56	13.51	
	NT2RP3000919	1.99	1.99	5.15	3.5	4.3	2.68	
	NT2RP3000921	2.26	2.26	7.67	4.88	4.07	6.51	
	NT2RP3000942	2.66	2.66	3.89	2.68	4.12	2.63	
10	NT2RP3000968	70.24	70.24	87.55	105.89	110.05	115.38	** +
	NT2RP3000974	5.36	5.36	9.06	3.21	4.48	2.64	
	NT2RP3000980	5.77	5.77	5.77	2.09	4.14	2.26	* -
	NT2RP3000984	3.17	3.17	7.65	6.33	6.68	4.58	
15	NT2RP3000994	2.09	2.09	4.88	2.4	3.14	3.37	
	NT2RP3001001	1.46	1.46	3.45	3.75	4.14	1.31	
	NT2RP3001004	3.37	3.37	6.52	3.51	5.63	5.01	
	NT2RP3001007	4.46	4.46	9.87	10.02	10.62	6.81	
	NT2RP3001012	2.78	2.78	5.4	4.99	6.83	3.65	
20	NT2RP3001042	4.74	4.74	5.52	2.99	5.18	1.38	
	NT2RP3001044	6.26	6.26	7.12	7.16	6.76	4.92	
	NT2RP3001048	2.52	2.52	3.01	3.5	3.93	2.42	
	NT2RP3001050	1.79	1.79	4.99	4.68	5.94	4.7	
	NT2RP3001055	6.55	6.55	15.6	16.48	12.44	20.49	
25	NT2RP3001057	2.79	2.79	10.84	5.57	6.05	5.67	
	NT2RP3001061	3.18	3.18	6.57	5.03	7.85	5.42	
	NT2RP3001069	6.03	6.03	14.95	18.49	17.53	15.08	
	NT2RP3001074	4.2	4.2	7.22	8.72	10	6.64	
	NT2RP3001078	5.11	5.11	7.29	7.51	8.72	5.18	
30	NT2RP3001081	4	4	5.72	4.65	5.19	3.52	
	NT2RP3001084	2.7	2.7	7.92	6.85	6.71	6.23	
	NT2RP3001095	1.57	1.57	3.88	3.69	3.68	3.42	
	NT2RP3001096	2.52	2.52	7.33	16.78	8.08	18.7	* +
35	NT2RP3001097	3.65	3.65	4.28	6.42	8.11	8.5	** +
	NT2RP3001107	3.69	3.69	4.79	3.77	4.03	2.37	
	NT2RP3001109	3.2	3.2	5.5	6.01	9.56	7.26	* +
	NT2RP3001111	4.58	4.58	4.19	3.41	3.51	2.29	* -
	NT2RP3001112	12.61	12.61	18.48	25.73	29.85	24.61	** +
40	NT2RP3001113	1.21	1.21	2.59	2.47	3.24	2.19	
	NT2RP3001115	1.51	1.51	3.32	2.57	3.77	2.19	
	NT2RP3001116	1.01	1.01	2.66	2.55	4.4	2.91	
	NT2RP3001119	3.69	3.69	6.75	9.07	6.67	5.44	
	NT2RP3001120	5.02	5.02	8.24	8.85	7.87	6.71	
45	NT2RP3001126	6.16	6.16	12.34	17.84	19.66	17.49	** +
	NT2RP3001127	6.93	6.93	6.76	4.79	7.63	6.36	
	NT2RP3001133	3.95	3.95	4.95	3.95	4.16	3.62	
	NT2RP3001140	1.46	1.46	2.43	3.21	2.38	6.71	
	NT2RP3001147	3.16	3.16	6.96	16.08	14.49	13.84	** +
50	NT2RP3001150	1.99	1.99	4.32	4.06	5.68	3.76	
	NT2RP3001152	1.7	1.7	3.29	3.15	3.62	2.51	
	NT2RP3001155	2.95	2.95	4.35	3.68	4.35	3.58	
	NT2RP3001156	4.38	4.38	6.57	2.91	5.72	5.67	
	NT2RP3001159	5.38	5.38	10.5	7.87	10.86	7.25	
55	NT2RP3001170	7.38	7.38	5.96	6.12	8.01	4.56	

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	NT2RP3001176	3.49	3.49	10.75	6.27	8.23	9.49		
	NT2RP3001195	2.35	2.35	4.81	6.79	5.79	6.22	*	+
	NT2RP3001209	3.47	3.47	5.98	5.96	4.64	5.22		
5	NT2RP3001214	1.63	1.63	4.91	3.44	3.87	3.81		
	NT2RP3001216	3.58	3.58	6.38	6.25	4.33	3.6		
	NT2RP3001221	3.33	3.33	4.27	3.07	3.06	1.79		
	NT2RP3001226	5.96	5.96	29.04	21.93	31.45	17.76		
	NT2RP3001230	3.17	3.17	2.41	3.09	3.14	1.56		
10	NT2RP3001232	1.8	1.8	4.72	2.36	3.7	2.85		
	NT2RP3001236	1.68	1.68	4.3	1.7	3.26	1.47		
	NT2RP3001239	1.58	1.58	5.21	2.81	4.31	2.01		
	NT2RP3001240	12.83	12.83	22.18	23.01	24.3	14.46		
	NT2RP3001245	3.53	3.53	9.88	4.08	6.36	3.39		
15	NT2RP3001253	2.79	2.79	4.87	3.34	4.53	5.21		
	NT2RP3001259	6.62	6.62	11.97	12.33	15.62	11.83		
	NT2RP3001260	3.74	3.74	5.15	3.45	5.44	3.97		
	NT2RP3001264	2.2	2.2	10.29	5.99	6.92	6.38		
20	NT2RP3001268	2.25	2.25	7.18	4.93	4.72	4.35		
	NT2RP3001271	7.06	7.06	16.29	13.07	12.27	14.24		
	NT2RP3001272	3.73	3.73	12.45	9.43	11.09	10.15		
	NT2RP3001274	6.08	6.08	8.09	6.72	6.35	5.11		
	NT2RP3001275	9.78	9.78	11.58	21.56	26.84	22.59	**	+
25	NT2RP3001280	3.39	3.39	5.5	3.58	5.24	4.18		
	NT2RP3001281	3.15	3.15	3.89	3.08	4.48	5.14		
	NT2RP3001288	49.31	49.31	103.24	124.07	142.92	164.41	*	+
	NT2RP3001297	6.39	6.39	42.01	37.04	42.75	41.14		
	NT2RP3001300	5.23	5.23	15.92	16.78	17.41	17.76		
30	NT2RP3001301	2.91	2.91	6.59	3.96	4.58	3.9		
	NT2RP3001307	1.76	1.76	7.67	2.07	2.81	2.06		
	NT2RP3001310	11.55	11.55	17.04	25.54	26.07	28.13	**	+
	NT2RP3001318	2.11	2.11	3.4	2.49	3.37	2.37		
	NT2RP3001322	3.58	3.58	5.23	2.62	3.84	5.48		
35	NT2RP3001325	2.7	2.7	8.39	5.82	6.82	5.58		
	NT2RP3001338	2.67	2.67	6.19	4.1	4.21	3.5		
	NT2RP3001339	2.53	2.53	5.64	3.08	4.89	2.91		
	NT2RP3001340	2.9	2.9	8.42	6.36	7.07	5.79		
	NT2RP3001341	2.26	2.26	6.97	5.1	5.62	4.73		
40	NT2RP3001354	3.22	3.22	9.77	4.28	6.93	9.35		
	NT2RP3001355	1.9	1.9	5.41	2.65	3.82	2.74		
	NT2RP3001356	2	2	5.34	2.59	3.2	3.55		
	NT2RP3001359	1.09	1.09	4.05	1.63	2.5	1.75		
	NT2RP3001364	2.34	2.34	5.31	3.26	6.67	2.67		
45	NT2RP3001373	1.12	1.12	3.22	2.1	3.74	1.71		
	NT2RP3001374	1.9	1.9	4.17	3.18	3.92	3.1		
	NT2RP3001383	3.84	3.84	8.96	3.92	6.65	3.85		
	NT2RP3001384	4.11	4.11	9.47	3.54	4.46	2.41		
50	NT2RP3001388	3.98	3.98	8.79	9.48	10.99	9.4		
	NT2RP3001392	4.61	4.61	6.19	3.91	6.14	3.23		
	NT2RP3001396	1.7	1.7	6.39	4.04	4.66	4.53		
	NT2RP3001398	2.51	2.51	6.55	3.85	7.05	2.94		
	NT2RP3001399	4.91	4.91	20.67	15.86	16.12	12.44		
55	NT2RP3001402	6.46	6.46	36.36	33.37	41.61	39.66		

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	NT2RP3001407	6.96	6.96	19.16	13.69	17.65	12.35	
	NT2RP3001416	7.92	7.92	15.88	13.02	18.3	14.72	
	NT2RP3001420	5.33	5.33	6.4	3.27	3.64	1.8	*
5	NT2RP3001425	3.73	3.73	4.92	4.74	5.67	3.15	
	NT2RP3001426	2.39	2.39	6.08	5.45	4.45	5.11	
	NT2RP3001427	1.82	1.82	5.61	3.46	2.89	3.59	
	NT2RP3001428	2.42	2.42	6.29	5.69	4.81	3.77	
	NT2RP3001429	3.08	3.08	5.91	4.15	7.37	4.73	
10	NT2RP3001432	2.14	2.14	6.61	3.72	4.44	3.58	
	NT2RP3001439	4.14	4.14	6.39	5.87	7.27	4.41	
	NT2RP3001441	6.45	6.45	12.63	11.13	14.61	11.2	
	NT2RP3001446	4.99	4.99	4.99	4.64	5.22	4.39	
	NT2RP3001447	2.72	2.72	5.21	6.64	5.14	6.33	
15	NT2RP3001449	3.95	3.95	11.85	16.9	14.57	13.16	* +
	NT2RP3001453	1.84	1.84	3.66	3.5	4.4	2.81	
	NT2RP3001457	3.86	3.86	7.71	6.06	6.93	5.5	
	NT2RP3001459	2.39	2.39	6.03	2.64	2.78	1.17	
20	NT2RP3001463	2.77	2.77	6.74	5.93	5.94	3.98	
	NT2RP3001466	2.87	2.87	3.56	1.19	1.43	0.78	** -
	NT2RP3001472	5.74	5.74	4.02	3.7	4.85	4.32	
	NT2RP3001475	3.54	3.54	7.61	6.91	6.65	7.39	
	NT2RP3001479	2.54	2.54	6.66	4.37	5.69	5.16	
25	NT2RP3001490	3.18	3.18	9.26	4.4	6.02	5.21	
	NT2RP3001492	4.36	4.36	7.84	7.59	7.08	5.72	
	NT2RP3001495	4.14	4.14	3.85	2.75	2.92	1.76	* -
	NT2RP3001497	5.8	5.8	6.32	7.47	9.96	6.8	
	NT2RP3001501	5.36	5.36	5.52	3.12	4.49	3.43	* -
30	NT2RP3001527	4.89	4.89	6.71	4.9	5.14	3.52	
	NT2RP3001529	1.51	1.51	3.5	4.12	3.95	4.18	* +
	NT2RP3001538	1.78	1.78	6.2	6.93	7.81	6.23	
	NT2RP3001539	5.81	5.81	14.5	15.19	14.15	16.47	
	NT2RP3001542	1.52	1.52	5.26	4.23	4.38	2.13	
35	NT2RP3001549	4.75	4.75	11.12	14.57	11.37	13.44	
	NT2RP3001554	3.06	3.06	6.16	6.37	7.5	5.05	
	NT2RP3001560	4.96	4.96	5.73	4.67	6.35	2.36	
	NT2RP3001561	8.85	8.85	20.77	20.38	27.2	17.15	
	NT2RP3001564	1.54	1.54	8.24	6.43	4.53	5.96	
40	NT2RP3001568	2.1	2.1	7.68	11.84	10.29	8.49	* +
	NT2RP3001575	3.94	3.94	7.24	6.39	6.97	6.16	
	NT2RP3001580	1.78	1.78	4.49	4.35	3.8	3.11	
	NT2RP3001587	4.38	4.38	8.74	10.75	10.04	7.77	
45	NT2RP3001589	3.17	3.17	8.21	5.6	7.79	4.36	
	NT2RP3001592	4.52	4.52	21.6	19	32.62	14.54	
	NT2RP3001607	3.42	3.42	1.86	1.59	2.8	1	
	NT2RP3001608	1.05	1.05	3.59	2.41	1.73	2.31	
	NT2RP3001613	3.08	3.08	2.77	3.89	2.91	3.99	
50	NT2RP3001619	4.31	4.31	8.15	7.69	6.45	7.62	
	NT2RP3001621	1.18	1.18	2.69	2.39	2.28	2.02	
	NT2RP3001629	2.58	2.58	3.28	2.68	2.41	1.7	
	NT2RP3001630	3.39	3.39	4.56	1.67	2.02	1.17	** -
	NT2RP3001631	9.01	9.01	14.34	18.65	21.16	15.24	* +
55	NT2RP3001634	4	4	5.29	4.51	6.89	5.11	

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	NT2RP3001642	3.71	3.71	7.45	5.77	4.41	5.09	
	NT2RP3001646	1.56	1.56	3.7	0.89	2.79	0.95	
	NT2RP3001650	2.06	2.06	5.81	4.86	7.03	2.08	
5	NT2RP3001667	4.66	4.66	11.91	6.93	9.95	5.13	
	NT2RP3001671	2.28	2.28	7.98	7.7	4.69	5.99	
	NT2RP3001672	1.33	1.33	4.55	1.66	1.47	1.72	
	NT2RP3001676	2.18	2.18	5.02	2.35	3.14	2.24	
	NT2RP3001678	2.86	2.86	9.24	5.12	5.14	6.03	
10	NT2RP3001679	6.12	6.12	9.19	6.74	4.73	6.91	
	NT2RP3001682	1.82	1.82	5.09	4.45	6.18	3.35	
	NT2RP3001685	3.02	3.02	6.74	3.52	6.53	3.01	
	NT2RP3001688	3.01	3.01	9.42	5.46	8.21	6.43	
	NT2RP3001690	3.21	3.21	4.87	2.91	3.54	2.99	
15	NT2RP3001693	5.69	5.69	10.93	16.59	18.34	16.12	** +
	NT2RP3001696	2.28	2.28	3.63	1.77	3.68	3.39	
	NT2RP3001698	35.35	35.35	79.65	85.09	91.88	105.32	
	NT2RP3001708	4.82	4.82	8.78	6.34	6.95	9.01	
20	NT2RP3001712	8.69	8.69	16.06	10.22	14.19	13	
	NT2RP3001716	1.44	1.44	5.45	2.14	3.42	2.31	
	NT2RP3001724	2.75	2.75	6	4.08	4.54	2.63	
	NT2RP3001727	11.73	11.73	38.73	39.17	49.36	31.26	
	NT2RP3001729	3.36	3.36	4.7	5.69	6.55	3.06	
25	NT2RP3001730	12.54	12.54	26.52	12.53	19.94	16.4	
	NT2RP3001733	1.46	1.46	3.04	2.09	3.7	1.62	
	NT2RP3001737	3.02	3.02	7.12	4.62	5.49	2.78	
	NT2RP3001738	1.59	1.59	8.22	3.38	6.01	3.03	
	NT2RP3001739	3.26	3.26	5.25	5.63	6.1	2.51	
30	NT2RP3001742	2.54	2.54	5.36	3.86	4.55	4.03	
	NT2RP3001751	3.61	3.61	11.54	9.94	12.82	8.76	
	NT2RP3001752	2.58	2.58	7.01	2.1	3.59	2.76	
	NT2RP3001753	5.73	5.73	9.48	10.83	15.3	13.69	* +
	NT2RP3001754	4.63	4.63	9.08	5.86	3.73	5.33	
35	NT2RP3001756	4.66	4.66	7.36	9.37	5.75	8.03	
	NT2RP3001764	2.1	2.1	3.76	2.54	4.25	2.49	
	NT2RP3001771	2.63	2.63	3.2	1.52	4.14	1.22	
	NT2RP3001777	2.59	2.59	5.99	3.25	5.19	3.26	
	NT2RP3001782	3.52	3.52	14.68	6.47	6.63	6.47	
40	NT2RP3001792	2.27	2.27	4.35	2.91	4.09	1.35	
	NT2RP3001799	1.76	1.76	5.18	5.71	6.36	5.68	
	NT2RP3001819	1.36	1.36	4.54	1.7	1.52	2.06	
	NT2RP3001829	21.63	21.63	43.14	35.64	17.14	24.87	
	NT2RP3001836	7.31	7.31	10.67	15.24	7.26	11.37	
45	NT2RP3001839	18.86	18.86	31.77	31.97	19.23	17.53	
	NT2RP3001844	4.15	4.15	11.37	8.33	9.59	8.54	
	NT2RP3001848	9.61	9.61	52.04	44.52	74.75	43.87	
	NT2RP3001854	6.41	6.41	11.29	12.86	16.75	13.26	* +
50	NT2RP3001855	2.27	2.27	3.94	1.87	1	1.74	
	NT2RP3001857	3.1	3.1	5.22	5.13	5.6	3.33	
	NT2RP3001858	1.53	1.53	4.45	4.41	6.04	2.97	
	NT2RP3001861	7.35	7.35	16.34	11.85	14.46	10.42	
	NT2RP3001866	4.35	4.35	9.63	5.52	10.42	7.93	
55	NT2RP3001871	4.82	4.82	6.34	5.55	6.38	4.55	

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	NT2RP3001874	6.8	6.8	9.73	7.72	11.19	6.14		
	NT2RP3001878	5.98	5.98	6.35	4.59	6.89	5.02		
	NT2RP3001885	3.21	3.21	5.3	5.65	5.25	4.42		
5	NT2RP3001896	1.64	1.64	3.49	3.37	2.13	2.02		
	NT2RP3001898	9.03	9.03	17.69	14.71	8.69	11.94		
	NT2RP3001899	3.21	3.21	7.33	4.52	6.9	5.81		
	NT2RP3001901	4.58	4.58	9.18	8.19	9.44	9.21		
10	NT2RP3001915	4.84	4.84	11.12	14.09	15.67	14.04	*	+
	NT2RP3001926	2.8	2.8	4.88	2.47	2.45	1.65		
	NT2RP3001929	3.74	3.74	4.06	2.56	3.38	0.86		
	NT2RP3001931	4.63	4.63	5.26	3.9	5.62	2.98		
	NT2RP3001938	2.27	2.27	5.53	4.93	3.93	4.75		
15	NT2RP3001943	3.27	3.27	5.36	5.77	6.5	5.56		
	NT2RP3001944	1.77	1.77	3.72	4.08	5.91	4.34		
	NT2RP3001945	4.25	4.25	12.2	11.86	11.78	6.11		
	NT2RP3001947	2.94	2.94	5.89	4.06	5.41	3.4		
	NT2RP3001949	4.21	4.21	8.9	10.49	11.08	8.08		
20	NT2RP3001952	23.54	23.54	43.64	48.59	88.56	41.86		
	NT2RP3001954	5.06	5.06	3.68	4.34	4.79	1.85		
	NT2RP3001956	4.97	4.97	9.44	7.76	8.22	6.29		
	NT2RP3001967	3.78	3.78	7.74	6.7	5.37	5.66		
	NT2RP3001969	1.71	1.71	2.91	4.05	4.39	3.62	*	+
25	NT2RP3001976	2.25	2.25	4.67	6.22	6.25	4.84	*	+
	NT2RP3001986	3.55	3.55	3.88	3.43	2.82	2.19		
	NT2RP3001989	3.76	3.76	5.23	2.86	3.58	2.54		
	NT2RP3002002	6.68	6.68	9.47	6.25	8.85	3.86		
	NT2RP3002004	5.02	5.02	6.23	3.79	5.74	3.55		
30	NT2RP3002007	1.29	1.29	2.3	3.46	4.05	1.69		
	NT2RP3002014	1.38	1.38	6.23	6.04	6.24	4.21		
	NT2RP3002015	3.61	3.61	10.33	14.17	9.94	8.85		
	NT2RP3002033	1.54	1.54	5.03	7.29	5.03	3.65		
	NT2RP3002045	1.89	1.89	5.29	4.67	4.36	2.5		
35	NT2RP3002054	5.26	5.26	8.12	6.27	9.17	5.42		
	NT2RP3002056	5.67	5.67	5.52	4.24	4.24	2.7	*	-
	NT2RP3002057	4.35	4.35	3.5	2.87	2.41	0.81	*	-
	NT2RP3002061	4.71	4.71	13.94	8.64	8.9	10.74		
40	NT2RP3002062	0.8	0.8	2.42	3.58	3.26	1.11		
	NT2RP3002063	5.61	5.61	10.31	9.29	9.3	7.31		
	NT2RP3002064	2.6	2.6	3.37	2.72	3.74	2.52		
	NT2RP3002071	1.6	1.6	3.91	1.99	3.29	1.45		
	NT2RP3002073	6.47	6.47	9.55	10.45	11.13	8.64		
45	NT2RP3002074	4.2	4.2	7.25	6.33	7.82	4.24		
	NT2RP3002075	7.58	7.58	11.93	21.64	30.17	18.15	*	+
	NT2RP3002077	3.81	3.81	5.95	2.48	3.05	2.78		
	NT2RP3002081	4.25	4.25	7.55	13.22	12.62	11.13	**	+
	NT2RP3002086	3.86	3.86	9.77	5.59	8.66	6.95		
50	NT2RP3002094	7.34	7.34	10.28	13.84	14.79	11.67	*	+
	NT2RP3002096	1.98	1.98	4.53	1.28	3.12	1.73		
	NT2RP3002097	3.77	3.77	6.16	6.1	8.34	6.88		
	NT2RP3002098	1.61	1.61	4.3	1.04	1.8	1.46		
	NT2RP3002102	2	2	4.86	3.11	3.4	3.16		
55	NT2RP3002106	2.74	2.74	4.98	2.83	4.9	2.51		

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	NT2RP3002108	3.69	3.69	7.8	3.11	3.39	3.15
	NT2RP3002109	12.49	12.49	32.04	31.61	27.15	25.12
	NT2RP3002110	36.38	36.38	54.93	55.24	58.94	46.55
5	NT2RP3002113	11.15	11.15	13.99	10.66	15.22	11.44
	NT2RP3002120	2.22	2.22	4.42	2.31	4.13	2.7
	NT2RP3002121	5.93	5.93	14.39	13.38	14.39	15.06
	NT2RP3002126	34.03	34.03	108.96	121.18	130.55	142.49 * +
	NT2RP3002128	4.06	4.06	8.23	3.36	6.87	3.92
10	NT2RP3002130	8.29	8.29	18.59	11.69	10.7	14.03
	NT2RP3002133	14.24	14.24	18.31	10.06	8.3	19.51
	NT2RP3002136	10.32	10.32	15.42	12.49	17.64	17.49
	NT2RP3002140	3.13	3.13	6.35	6.15	3.9	4.16
15	NT2RP3002142	16.86	16.86	50.85	56.54	81.25	62.65 * +
	NT2RP3002146	4	4	7.22	5.14	9.31	6.56
	NT2RP3002147	3.8	3.8	10.45	6.06	7.4	6.2
	NT2RP3002151	5.62	5.62	10.64	6.27	4.43	7.33
	NT2RP3002155	1.62	1.62	3.27	2.01	4.98	0.8
20	NT2RP3002156	3.15	3.15	4.82	2.55	4.08	2.42
	NT2RP3002160	1.57	1.57	3.43	1.36	3.43	1.56
	NT2RP3002163	20.86	20.86	55.1	35.13	44.03	32.6
	NT2RP3002165	4.17	4.17	3.67	6.21	8.31	4.86
	NT2RP3002166	4.04	4.04	10.53	7.76	8.79	5.58
25	NT2RP3002173	2.24	2.24	5.75	2.95	3.34	3.53
	NT2RP3002174	8.41	8.41	15.8	13.21	7.82	14.77
	NT2RP3002181	1.1	1.1	3.46	1.87	3.51	1.61
	NT2RP3002185	2.69	2.69	4.51	2.94	4.35	2.61
	NT2RP3002193	5.51	5.51	13.38	16.39	15.35	11.36
30	NT2RP3002204	5.66	5.66	12.49	17.04	24.14	18.95 * +
	NT2RP3002244	4.03	4.03	8.29	5.28	6.11	4.8
	NT2RP3002248	5.42	5.42	11.1	3.19	11.78	6.52
	NT2RP3002253	2.61	2.61	9.3	9.66	11.26	6.18
	NT2RP3002255	11.07	11.07	26.56	22.78	11.53	20.93
35	NT2RP3002264	3.06	3.06	5.54	5.88	7.37	4.07
	NT2RP3002267	1.26	1.26	4.33	3.1	4.65	1.82
	NT2RP3002273	7.51	7.51	12.98	10.15	13.8	12.11
	NT2RP3002276	5.22	5.22	7.89	3.08	7.68	3.48
	NT2RP3002281	6.37	6.37	6.83	7.45	8.46	3.44
40	NT2RP3002286	3	3	4.79	3.54	4.34	3.88
	NT2RP3002297	10.62	10.62	29.36	22.26	20.57	23.93
	NT2RP3002301	5.73	5.73	13.24	9.47	7.55	6.21
	NT2RP3002303	3.01	3.01	6.39	5.29	6.65	4.58
	NT2RP3002304	2.66	2.66	7.17	6.3	7.3	4.91
45	NT2RP3002309	2.3	2.3	7.18	9.26	13	4.39
	NT2RP3002311	4.54	4.54	6.67	3.17	4.02	1.83
	NT2RP3002315	15.27	15.27	20.91	25.82	33.13	21.82
	NT2RP3002319	2.37	2.37	5.06	3.07	3.51	2.38
50	NT2RP3002324	8.97	8.97	61.42	49.85	51.23	55.4
	NT2RP3002330	4.74	4.74	8.33	10.31	8.24	8.15
	NT2RP3002333	5.13	5.13	14.32	13.14	13.65	8.12
	NT2RP3002337	2.61	2.61	5.14	4.8	5.57	4.87
	NT2RP3002342	5.16	5.16	11.56	5.52	7.51	6.43
55	NT2RP3002343	3.38	3.38	7.29	5.8	7.03	4.13

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	NT2RP3002351	4.32	4.32	4.55	4.38	3.9	2.55	
	NT2RP3002352	6.3	6.3	8.01	4.4	6.76	4.31	
	NT2RP3002353	3	3	4.85	4.87	6.18	5.9	
5	NT2RP3002362	5	5	11.74	15.86	11.03	10.49	
	NT2RP3002363	2.41	2.41	3.67	5.53	6.17	2.32	
	NT2RP3002377	2.61	2.61	5.47	6.8	7.31	4.73	
	NT2RP3002377	4.47	4.47	7.73	11.4	5.31	7.09	
	NT2RP3002394	5.58	5.58	7.35	7.82	10.17	4.46	
10	NT2RP3002397	3.77	3.77	4.81	2.7	3.12	1.68	*
	NT2RP3002399	4.61	4.61	7.69	14.65	13.02	16.16	** +
	NT2RP3002402	2.84	2.84	6.99	8.94	8.7	6.99	
	NT2RP3002404	2.88	2.88	5.6	3.12	3.73	1.83	
15	NT2RP3002410	4.85	4.85	15.65	17.05	14.13	10.65	
	NT2RP3002411	2.98	2.98	5.68	3.7	5.29	2.85	
	NT2RP3002414	5.62	5.62	9.35	10.28	6.81	7.92	
	NT2RP3002430	5.11	5.11	14.63	18.24	19.29	14.51	
	NT2RP3002448	5.4	5.4	4.6	4.35	5.25	3.62	
20	NT2RP3002454	7.3	7.3	15.31	12.9	12.71	9.32	
	NT2RP3002455	4.62	4.62	12.11	14.31	9.11	13.25	
	NT2RP3002456	3.21	3.21	7.75	7.09	6.57	5.9	
	NT2RP3002462	2.79	2.79	4.16	4.94	6.17	4.79	* +
	NT2RP3002469	3.84	3.84	6.38	9.24	6.78	8.07	* +
25	NT2RP3002470	6.7	6.7	14.71	17.86	16.99	13.48	
	NT2RP3002484	4.01	4.01	6.86	6.81	8.01	4.59	
	NT2RP3002491	3.62	3.62	4.1	2.05	2.51	1.46	** -
	NT2RP3002494	79.24	79.24	131.02	118.47	163.2	105.2	
	NT2RP3002497	1.07	1.07	1.57	2.37	1.39	1.37	
30	NT2RP3002500	1.23	1.23	1.13	2.72	2.02	2.07	** +
	NT2RP3002501	5.25	5.25	8.49	8.45	8.11	9.69	
	NT2RP3002512	2.85	2.85	3.97	3.3	2.74	3.57	
	NT2RP3002529	3.94	3.94	7.5	6.59	5.14	5.85	
35	NT2RP3002533	7.95	7.95	10.26	9.79	10.51	8.18	
	NT2RP3002539	4.39	4.39	4.32	5.66	6.61	2.85	
	NT2RP3002540	5.24	5.24	5.5	3.48	4.76	3.65	* -
	NT2RP3002543	3.44	3.44	7.17	4.93	6.21	5.31	
	NT2RP3002545	7.34	7.34	7.46	5.17	5.52	6.8	* -
40	NT2RP3002549	3.27	3.27	7.8	4.98	6.11	4.54	
	NT2RP3002552	3.05	3.05	6.04	4.17	5.81	4.06	
	NT2RP3002558	9.54	9.54	9.39	9.93	4.26	11.27	
	NT2RP3002565	1.94	1.94	4.83	1.73	2.48	1.52	
	NT2RP3002566	3.62	3.62	7.02	4.03	8.51	3.65	
45	NT2RP3002571	2.53	2.53	4.85	3.77	5.41	3.74	
	NT2RP3002572	2.98	2.98	5.28	4.75	4.74	5.21	
	NT2RP3002573	4.31	4.31	11.38	7.06	9.48	7.06	
	NT2RP3002577	1.57	1.57	4.61	2.71	2.32	1.9	
	NT2RP3002579	3.92	3.92	6.41	4.03	7.75	11.16	
50	NT2RP3002582	5.02	5.02	7.17	11.51	14.07	8.45	* +
	NT2RP3002587	1.9	1.9	3.13	2.68	3.04	1.97	
	NT2RP3002590	3.16	3.16	5.65	9.06	10.39	8.06	** +
	NT2RP3002602	3.02	3.02	4.24	3.95	5.85	3.77	
	NT2RP3002603	71.53	71.53	214.41	268.41	257.84	298.26	* +
55	NT2RP3002621	1.95	1.95	3.42	2.13	5.13	1.85	

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	NT2RP3002622	2.63	2.63	7.38	3.7	7.36	4.67	
	NT2RP3002624	2.29	2.29	7.4	4.04	4.9	3.64	
	NT2RP3002628	6.36	6.36	16.17	19.57	22.15	16.21	
5	NT2RP3002629	8.96	8.96	13.58	15.4	18.26	15.57	* +
	NT2RP3002631	1.95	1.95	1.67	0.91	1.65	1.69	
	NT2RP3002647	4.04	4.04	4.01	5.44	7.16	4.6	
	NT2RP3002649	2.99	2.99	5.99	2.15	5.84	3.23	
	NT2RP3002650	3.32	3.32	11.62	4.98	8.53	6.88	
10	NT2RP3002652	2.27	2.27	6.59	4.91	6.83	4.25	
	NT2RP3002654	3.05	3.05	7.5	5.58	5.4	4.2	
	NT2RP3002657	14.14	14.14	13.87	17.27	26.08	18.87	
	NT2RP3002659	1.92	1.92	6.01	3.91	5.78	3.47	
	NT2RP3002660	3.09	3.09	4.84	3.77	7.72	3.52	
15	NT2RP3002663	2.39	2.39	3.33	2.54	3.13	2.84	
	NT2RP3002664	2.74	2.74	7.28	3.65	2.56	2.13	
	NT2RP3002667	2.92	2.92	6.59	6.63	5.46	5.35	
	NT2RP3002671	2.37	2.37	5.02	3.91	5.52	4.11	
	NT2RP3002682	6.34	6.34	20.62	14.37	17.64	21.7	
20	NT2RP3002684	4	4	6.34	3.32	6.16	3.18	
	NT2RP3002687	3.25	3.25	6.22	2.7	3.87	6.41	
	NT2RP3002688	3.22	3.22	4.98	2.63	3.91	2.61	
	NT2RP3002698	2.2	2.2	3.99	3.07	4.28	2.38	
	NT2RP3002701	2.93	2.93	6.73	3.45	3.07	3.6	
25	NT2RP3002705	2.17	2.17	8.01	4.36	8.76	4.72	
	NT2RP3002708	3.69	3.69	9.88	5.64	7.34	4.9	
	NT2RP3002711	6.67	6.67	7.85	7.77	7.56	6.69	
	NT2RP3002712	55.99	55.99	75.28	146.74	168.42	130.64	** +
30	NT2RP3002713	4.31	4.31	7.06	2.66	2.19	1.87	* -
	NT2RP3002721	5.77	5.77	10.06	11.06	16.94	8.96	
	NT2RP3002722	7.11	7.11	10.08	7.8	6.45	6.62	
	NT2RP3002723	42.31	42.31	75.85	60.39	46.74	58.76	
	NT2RP3002737	8.35	8.35	18.1	10.97	11.6	9.37	
35	NT2RP3002738	1.9	1.9	6.13	3.09	5.23	3.54	
	NT2RP3002742	14.11	14.11	23.22	30.39	28.27	27.66	* +
	NT2RP3002744	4.09	4.09	5.24	3.92	4.92	1.71	
	NT2RP3002756	5.8	5.8	5.8	3.19	2.68	1.55	** -
	NT2RP3002757	12	12	17.79	19.76	24.24	19.75	* +
40	NT2RP3002758	21.11	21.11	42.35	44.47	63.91	36.38	
	NT2RP3002762	5.07	5.07	8.82	7.21	7.43	7.76	
	NT2RP3002763	1.62	1.62	4.86	3.76	4.99	2.18	
	NT2RP3002770	1.78	1.78	5.14	3.46	3.7	2.93	
	NT2RP3002771	17.04	17.04	39.53	24.93	40.21	34.4	
45	NT2RP3002785	2.42	2.42	5.45	3.36	4.09	2.66	
	NT2RP3002790	4.65	4.65	4.22	3.16	3.57	2.33	* -
	NT2RP3002799	4.73	4.73	6.33	3.42	2.7	1.43	* -
	NT2RP3002801	4.14	4.14	3.59	3.6	3.22	2.49	
	NT2RP3002802	2.31	2.31	6.3	6.78	5.43	4.4	
50	NT2RP3002810	2.98	2.98	5.41	7.44	12.32	13.27	* +
	NT2RP3002818	1.5	1.5	2.44	2.18	4.16	2.47	
	NT2RP3002821	12.8	12.8	33.14	26.1	35.81	23.02	
	NT2RP3002823	3.85	3.85	8.98	4.65	5.92	3.87	
55	NT2RP3002825	5.47	5.47	13.04	13.47	19.19	7.12	

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	NT2RP3002829	5.37	5.37	6.25	4.75	4.89	3.8	
	NT2RP3002831	4.01	4.01	6.13	9.07	8.77	5.19	
	NT2RP3002836	7.33	7.33	19.42	11.56	16.91	20.66	
5	NT2RP3002845	4.17	4.17	6.63	7.87	8.6	8.45	*
	NT2RP3002852	3.37	3.37	7.57	7.8	8.72	8.21	+
	NT2RP3002861	3.82	3.82	6.4	7.34	7.35	4.63	
	NT2RP3002869	3.66	3.66	3.26	2.49	1.86	0.49	*
	NT2RP3002874	11.25	11.25	21.44	25.33	31.95	25.54	*
10	NT2RP3002876	6.98	6.98	11.06	12.8	14.93	14.39	*
	NT2RP3002877	4.7	4.7	5.96	3.3	5.24	2.53	+
	NT2RP3002887	0.47	0.47	3.42	2.81	3.53	3.91	
	NT2RP3002900	6.46	6.46	19.64	21.86	21.54	22.3	
15	NT2RP3002902	4.01	4.01	10.25	11.72	8.52	8.06	
	NT2RP3002909	2.61	2.61	6.19	6.67	5.38	3.93	
	NT2RP3002911	3.05	3.05	3.68	3.09	3.73	2.24	
	NT2RP3002948	4.09	4.09	4.81	2.73	4.44	2.07	
	NT2RP3002953	3.85	3.85	3.6	2.27	2.52	0.84	*
20	NT2RP3002955	6.55	6.55	3.78	1.93	2.47	0.86	*
	NT2RP3002958	5.85	5.85	11.4	16.5	10.57	16.64	-
	NT2RP3002969	4.28	4.28	8.27	12.91	7.49	7.33	
	NT2RP3002972	3.55	3.55	4.82	4.41	6.18	2.29	
	NT2RP3002978	1.48	1.48	2.99	2.61	3.7	1.49	
25	NT2RP3002983	2.89	2.89	4.69	4.46	6.12	4.37	
	NT2RP3002985	4.23	4.23	17.87	13.64	20.26	11.12	
	NT2RP3002988	3.97	3.97	4.6	4.12	5.64	4.13	
	NT2RP3003000	3.11	3.11	3.46	2.46	3.2	1.51	
	NT2RP3003008	3.26	3.26	5.87	3.95	4.55	2.96	
30	NT2RP3003012	3.43	3.43	6.06	3.9	4.96	2.79	
	NT2RP3003015	1.35	1.35	4.9	1.5	2.5	0.54	
	NT2RP3003018	2.15	2.15	6.09	3.45	7.24	2.59	
	NT2RP3003028	3.53	3.53	7.23	3.5	5.05	4.01	
	NT2RP3003029	111.75	111.75	149.73	175.13	159.77	181.4	*
35	NT2RP3003032	7.06	7.06	9.05	11.87	18.84	9.94	+
	NT2RP3003041	2.07	2.07	1.88	1.61	1.41	0.69	
	NT2RP3003044	3.06	3.06	7.45	5.72	6.11	7.57	
	NT2RP3003047	3.09	3.09	5.16	2.4	4.67	2.06	
	NT2RP3003050	5.96	5.96	12.03	6.74	10.3	8.42	
40	NT2RP3003053	7.46	7.46	18	14.42	17.14	13.72	
	NT2RP3003059	1.93	1.93	4.76	2.88	4.41	3.06	
	NT2RP3003061	2.8	2.8	8.59	5.49	5.68	5.16	
	NT2RP3003068	5.99	5.99	11.77	9.41	8.75	10.04	
45	NT2RP3003071	7.22	7.22	10.77	10.39	14.52	10.39	
	NT2RP3003076	2.67	2.67	9.49	5.57	6.57	4.01	
	NT2RP3003078	1.5	1.5	4.12	2.09	4.52	2.43	
	NT2RP3003081	6.21	6.21	10.54	9.94	9.6	9.97	
	NT2RP3003090	1.49	1.49	5.95	3.28	3.57	3.25	
50	NT2RP3003097	2.42	2.42	7.15	2.71	3.72	2.93	
	NT2RP3003098	2.75	2.75	4.22	2.73	3.43	1.73	
	NT2RP3003101	5.56	5.56	7.24	7.73	10.35	7.18	
	NT2RP3003109	16.11	16.11	27.38	27.36	41.03	21.91	
	NT2RP3003121	3.39	3.39	11.03	4.61	8	2.44	
55	NT2RP3003133	2.09	2.09	5.78	4.93	8.58	3.96	

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	NT2RP3003137	3.42	3.42	5.74	6.32	7.59	5.29	
	NT2RP3003138	2.36	2.36	5.27	5.26	5.7	3.74	
	NT2RP3003139	2.53	2.53	7.8	3.15	5.74	2.7	
5	NT2RP3003145	5.08	5.08	32.56	25.8	29.74	19.72	
	NT2RP3003150	2.03	2.03	5.17	3.56	3.76	1.97	
	NT2RP3003157	2.52	2.52	8.34	6.4	10.1	4.94	
	NT2RP3003185	1.77	1.77	3.88	1.91	3.34	2.62	
10	NT2RP3003193	2.62	2.62	5.75	6.03	4.59	2.65	
	NT2RP3003197	2.38	2.38	3.8	3.11	4.02	2.2	
	NT2RP3003203	11.82	11.82	14.35	16.85	10.17	15.27	
	NT2RP3003204	3.76	3.76	7.93	4.04	6.17	3.79	
	NT2RP3003210	14.48	14.48	75.3	58.97	84.6	68.66	
15	NT2RP3003212	5.15	5.15	9.44	9.21	10.67	7.36	
	NT2RP3003213	4.16	4.16	5.68	5.15	7.02	5.44	
	NT2RP3003224	1.7	1.7	4.75	2.43	2.11	2.64	
	NT2RP3003226	3.25	3.25	5.68	5.57	5.94	3.63	
	NT2RP3003230	7.79	7.79	11.47	12.39	8.89	6.72	
20	NT2RP3003235	7.61	7.61	10.79	7.77	7.73	6.89	
	NT2RP3003242	12.17	12.17	23.49	26.68	32.03	19.25	
	NT2RP3003251	5.61	5.61	9.47	3.73	4.95	4.08	
	NT2RP3003252	3.95	3.95	5.95	2.19	3.7	2.42	
	NT2RP3003258	4.92	4.92	7.89	19.94	24.95	15.47	** +
25	NT2RP3003260	4.54	4.54	12.34	13.46	11.52	12.68	
	NT2RP3003264	1.64	1.64	5.99	3.18	4.32	1.86	
	NT2RP3003273	2.18	2.18	4.93	4.57	3.58	1.72	
	NT2RP3003278	1.33	1.33	4	1.31	5.12	0.63	
	NT2RP3003280	9.85	9.85	23.11	18.18	19.52	18.19	
30	NT2RP3003282	5.29	5.29	6.25	3.62	3.97	3.48	** -
	NT2RP3003290	6.64	6.64	9.09	4.8	5.38	3.78	* -
	NT2RP3003301	4.01	4.01	5.73	4.31	4.59	3.23	
	NT2RP3003302	1.45	1.45	2.31	2.91	2.64	1.91	
	NT2RP3003311	2.45	2.45	6.76	15.72	13.09	11.55	** +
35	NT2RP3003312	1.81	1.81	3.35	3.73	3.87	2.41	
	NT2RP3003313	1.61	1.61	4.2	2.91	5.4	2.87	
	NT2RP3003327	1.62	1.62	6.24	4.81	4.95	3.34	
	NT2RP3003330	5.13	5.13	8.01	15.68	16.13	12.78	** +
	NT2RP3003344	3.36	3.36	4.14	2.92	3.74	2.6	
40	NT2RP3003346	3.81	3.81	4.83	4.38	4.05	1.24	
	NT2RP3003349	4.04	4.04	6.93	9.96	9.41	9.65	** +
	NT2RP3003353	1.95	1.95	3.24	4.06	5.37	2.45	
	NT2RP3003354	5.09	5.09	13.72	16.29	12.02	13.5	
	NT2RP3003368	3.03	3.03	4.73	4.04	4.08	2.63	
45	NT2RP3003375	4.1	4.1	7.4	7.41	9.67	6.62	
	NT2RP3003377	4.16	4.16	3.98	2.57	3.58	1.65	
	NT2RP3003384	5.77	5.77	4.55	2.83	3.43	2.56	** -
	NT2RP3003385	4.55	4.55	3.12	1.9	2.36	1.47	* -
	NT2RP3003396	3.93	3.93	13.63	16.4	8.38	12.32	
50	NT2RP3003403	1.62	1.62	2.54	3.24	4.73	1.92	
	NT2RP3003409	1.18	1.18	2.97	3.3	4.48	3.03	
	NT2RP3003411	4.59	4.59	15.42	14.11	15.42	10.96	
	NT2RP3003420	3.79	3.79	4.36	3.68	2.13	1.85	
55	NT2RP3003425	3.25	3.25	6.71	5.85	7.25	5.49	

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	NT2RP3003426	9.11	9.11	16.3	10.88	11.12	17.45	
	NT2RP3003427	5.95	5.95	10.09	9.15	13.58	8.03	
	NT2RP3003433	2.55	2.55	6.26	8.42	9.57	4.87	
5	NT2RP3003437	22.12	22.12	49.85	51.81	44	38.77	
	NT2RP3003448	1.88	1.88	4.24	3.5	3.83	2.63	
	NT2RP3003455	5.23	5.23	12.16	11.8	9.96	8.44	
	NT2RP3003462	4.96	4.96	10.07	10.76	8.25	7.08	
10	NT2RP3003464	3.79	3.79	5.03	3.01	4.76	1.2	
	NT2RP3003469	4.1	4.1	7.77	6.62	7.56	5.07	
	NT2RP3003473	22.06	22.06	36.6	54.82	69.25	56.46	** +
	NT2RP3003474	8.26	8.26	23.04	13.23	12.04	13.52	
	NT2RP3003475	2.84	2.84	4.04	4.55	4.45	3.28	
15	NT2RP3003490	2.7	2.7	5.81	4.21	4.43	3.12	
	NT2RP3003491	2.26	2.26	3	2.14	2.75	1.26	
	NT2RP3003493	11.75	11.75	30.77	34.59	28.9	34.45	
	NT2RP3003500	4.93	4.93	5.26	4.99	7.46	3.65	
	NT2RP3003527	2.73	2.73	3.09	2.42	2.92	1.72	
20	NT2RP3003532	2.7	2.7	1.81	2.14	3.33	2.13	
	NT2RP3003535	3.14	3.14	4.37	1.92	3.4	2.19	
	NT2RP3003536	3.04	3.04	5.95	3.45	5.2	4.97	
	NT2RP3003543	2.61	2.61	6.24	3.21	4.81	3.83	
25	NT2RP3003549	1.43	1.43	6.66	2.18	4.07	1.55	
	NT2RP3003552	1.8	1.8	5.76	0.64	0.84	1.58	
	NT2RP3003555	4.4	4.4	14.14	12.16	17.43	16.23	
	NT2RP3003559	2.81	2.81	6.7	3.88	5.11	5.49	
	NT2RP3003564	3.11	3.11	5.9	2.24	4.6	5.25	
30	NT2RP3003572	2.1	2.1	4.21	1.88	3.02	2.32	
	NT2RP3003576	5.88	5.88	10.15	11.32	8.98	9.22	
	NT2RP3003587	7.39	7.39	12.41	10.01	12.71	12.75	
	NT2RP3003589	15.33	15.33	22.45	23.89	23.75	26.58	
	NT2RP3003592	7.77	7.77	10.4	8.42	14.48	9.74	
35	NT2RP3003593	8.16	8.16	13.62	13.47	13.84	110.49	
	NT2RP3003614	2.66	2.66	8.18	3.11	4.48	7.09	
	NT2RP3003621	1.64	1.64	3.91	2.1	3.68	2.96	
	NT2RP3003625	1.54	1.54	6.94	3.79	5.09	4.96	
	NT2RP3003627	6.73	6.73	20.05	16.23	13.97	25.71	
40	NT2RP3003636	3.3	3.3	7.74	5.99	3.79	10.4	
	NT2RP3003642	7.12	7.12	12.2	12.85	13.15	15.83	
	NT2RP3003645	2.91	2.91	6.07	2.23	2.42	3.53	
	NT2RP3003648	2.88	2.88	3.71	2.17	2.44	3.13	
	NT2RP3003649	2.7	2.7	9.28	6.36	5.11	12.04	
45	NT2RP3003650	2.65	2.65	4.25	4.38	3.16	4.09	
	NT2RP3003656	1.69	1.69	3.23	1.94	4.12	3	
	NT2RP3003659	2.76	2.76	4.56	2.14	4.8	4.88	
	NT2RP3003662	31.39	31.39	53.28	34.35	14.68	34.64	
50	NT2RP3003664	3.56	3.56	6.5	6.18	5.45	6.55	
	NT2RP3003665	1.89	1.89	4.83	2.07	2.8	4.96	
	NT2RP3003671	2.88	2.88	4.33	3.03	2.6	4.29	
	NT2RP3003672	4.78	4.78	9.8	10.69	14.73	16.35	* +
	NT2RP3003673	4.98	4.98	9.42	5.35	3.05	4.12	
55	NT2RP3003679	40.1	40.1	95.75	69.92	23.86	83.88	
	NT2RP3003680	3.13	3.13	5.38	3.96	4.58	5.88	

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	NT2RP3003686	2.22	2.22	4.43	2.84	4.85	2.25
	NT2RP3003689	4.05	4.05	9.69	5.94	5.63	8.27
	NT2RP3003697	13.79	13.79	120.74	108.93	77.49	68.74
5	NT2RP3003701	2.7	2.7	5.17	2.58	3.05	2.57
	NT2RP3003704	2.99	2.99	6.96	7.09	7.61	6.96
	NT2RP3003714	1.39	1.39	4.25	1.68	0.89	1.14
	NT2RP3003716	2.05	2.05	4.23	3	2.29	2.24
10	NT2RP3003721	1.83	1.83	3.27	1.85	3.45	2.18
	NT2RP3003722	3.45	3.45	8.18	8.08	7.79	5.45
	NT2RP3003726	3.5	3.5	4.9	2.77	4.51	2.32
	NT2RP3003729	4.1	4.1	8.53	4.22	5.44	4.6
	NT2RP3003731	5.06	5.06	6.98	4.19	3.54	7.45
15	NT2RP3003740	2.58	2.58	5.08	2.42	2.48	2.94
	NT2RP3003746	3.63	3.63	8.14	6.7	5.94	6.59
	NT2RP3003749	0.67	0.67	2.58	1.55	2.08	1.73
	NT2RP3003754	3.32	3.32	7.31	4.66	5.87	5.81
	NT2RP3003759	1.16	1.16	4.44	2.49	4.41	1.43
20	NT2RP3003764	3.97	3.97	7.08	6.85	7.41	5.06
	NT2RP3003766	6.93	6.93	7.84	3.3	5.87	3.79 *
	NT2RP3003767	11.19	11.19	16.8	14.83	21.08	16.97
	NT2RP3003778	3.36	3.36	4.89	4.46	5.55	4.27
25	NT2RP3003779	4.05	4.05	15.26	13.02	8.74	10.52
	NT2RP3003783	9.25	9.25	21.72	22.42	13.65	18.76
	NT2RP3003787	2.15	2.15	4.65	4.41	4.74	6.37
	NT2RP3003789	5.12	5.12	10.16	11.63	12.19	14.96 * +
	NT2RP3003795	1.48	1.48	6.48	4.09	2.82	2.24
30	NT2RP3003799	2.67	2.67	5.5	3.08	2.38	1.75
	NT2RP3003800	4.36	4.36	5.92	4.14	4.57	6.91
	NT2RP3003805	8.15	8.15	6.78	8.4	5.48	5.89
	NT2RP3003809	1.94	1.94	7.2	5.83	5.4	4.82
	NT2RP3003819	3.39	3.39	6.07	7.3	5.97	6.35
35	NT2RP3003824	5.69	5.69	10.69	14.08	14.85	13.32 * +
	NT2RP3003825	9.06	9.06	16.31	12.87	16.88	16.75
	NT2RP3003828	4.7	4.7	14.38	13.36	15.69	14.55
	NT2RP3003831	4.01	4.01	6.38	5.77	6.54	7.23
	NT2RP3003833	5.12	5.12	7.5	6.44	8.88	6.96
40	NT2RP3003836	6.37	6.37	5.05	5.74	6.47	4.31
	NT2RP3003842	2.7	2.7	9.08	6.84	6.51	7.09
	NT2RP3003843	9.26	9.26	26.77	16.67	12.71	16.2
	NT2RP3003844	20.38	20.38	46.56	42.84	27.94	44.32
45	NT2RP3003846	4.04	4.04	8.45	8.94	7.18	8.05
	NT2RP3003849	2.27	2.27	2.68	2.67	2.73	1.68
	NT2RP3003862	28.91	28.91	45.63	32	37.58	44.88
	NT2RP3003870	4.76	4.76	4.81	2.54	2.93	2.05 ** -
	NT2RP3003874	21.46	21.46	20.88	33.11	47.25	36.44 * +
50	NT2RP3003876	1.62	1.62	8.08	5.45	7.49	6.81
	NT2RP3003880	1.74	1.74	4.63	5.31	4.66	4.73
	NT2RP3003889	1.69	1.69	3.04	3.41	3.53	9.53
	NT2RP3003891	1.88	1.88	2.98	2.56	3.19	1.37
	NT2RP3003914	3.1	3.1	7.35	6.88	5.15	7.39
55	NT2RP3003915	5.03	5.03	8.44	9.52	11.35	8.6
	NT2RP3003918	6.79	6.79	10.39	10.04	13.71	12.42

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	NT2RP3003920	6.9	6.9	9.13	8.31	10.22	8.96	
	NT2RP3003924	2.25	2.25	9.57	6.49	5.34	6.91	
	NT2RP3003932	1.41	1.41	3.85	5.17	5.26	3.85	
5	NT2RP3003939	3.48	3.48	11.88	9.86	14.05	11.09	
	NT2RP3003940	11.34	11.34	27.33	23.54	20.59	23.06	
	NT2RP3003943	2.6	2.6	2.83	2.85	2.78	3.88	
	NT2RP3003959	3.52	3.52	6.96	6.54	5.93	5.49	
10	NT2RP3003963	4.83	4.83	7.59	4.01	4.61	2.52	
	NT2RP3003965	11.14	11.14	13.85	18.75	20.67	17.22	** +
	NT2RP3003972	26.1	26.1	40.32	22.13	17.98	38.48	
	NT2RP3003973	2.85	2.85	4.33	1.96	3.6	3.96	
	NT2RP3003979	5.89	5.89	12.53	6.92	8.49	8.84	
15	NT2RP3003980	3.52	3.52	9.41	9.34	8.89	7.92	
	NT2RP3003982	4.2	4.2	4.63	2.44	1.6	4.61	
	NT2RP3003989	6.24	6.24	4.69	9.61	5.62	16.05	
	NT2RP3003992	2.13	2.13	4.89	2.47	5.12	4.8	
20	NT2RP3004000	2.81	2.81	6	1.72	3.22	2.62	
	NT2RP3004001	11.38	11.38	19.94	11.62	11.37	21.11	
	NT2RP3004005	2.89	2.89	7.79	4.7	4.48	6.84	
	NT2RP3004013	2.23	2.23	7.2	2.66	4.87	3.57	
	NT2RP3004016	1.5	1.5	7.1	2.22	3.14	2.88	
25	NT2RP3004025	4.02	4.02	7.69	7.48	12.19	9.01	
	NT2RP3004030	7.05	7.05	12.64	13.97	15.8	17.66	* +
	NT2RP3004041	5.65	5.65	11.38	10.48	9.57	19.81	
	NT2RP3004042	15.22	15.22	102.33	97.27	103.6	99.67	
	NT2RP3004044	2.13	2.13	6.51	5.14	7.21	4.22	
30	NT2RP3004051	2.6	2.6	5.79	2.23	5.51	4.69	
	NT2RP3004052	7.1	7.1	11.22	5.63	4.98	9.78	
	NT2RP3004053	15.87	15.87	35.04	23.12	40.67	40.17	
	NT2RP3004055	2.38	2.38	5.33	2.98	3.3	4.47	
	NT2RP3004059	4.05	4.05	8.8	8.15	7.03	11	
35	NT2RP3004063	5.13	5.13	11.23	8.78	11.27	12.33	
	NT2RP3004067	4.24	4.24	8.4	6.62	6.42	4.47	
	NT2RP3004070	3.58	3.58	9.92	6.26	4.4	5.47	
	NT2RP3004075	4.16	4.16	11.23	12.62	11.88	13.3	
	NT2RP3004078	2.6	2.6	5.25	4.94	4.19	2.79	
40	NT2RP3004083	2.93	2.93	6.23	4.57	6.8	11.37	
	NT2RP3004084	4.65	4.65	20.29	6.18	8.56	5.32	
	NT2RP3004087	4.2	4.2	7.86	7.14	10.81	9.03	
	NT2RP3004090	4.11	4.11	6.42	9	8.19	8.61	** +
45	NT2RP3004093	2.38	2.38	7.49	4.07	3.51	4.47	
	NT2RP3004095	5.02	5.02	13.11	11.57	10.17	18.55	
	NT2RP3004102	3.32	3.32	5.59	5.25	4.27	3.21	
	NT2RP3004110	12.74	12.74	18.66	22.12	14.31	19.97	
	NT2RP3004119	3.3	3.3	7.71	3.91	4.08	3.73	
50	NT2RP3004125	5.55	5.55	12.05	8.13	10.88	8.38	
	NT2RP3004129	4.62	4.62	7.38	3.36	2.95	6.08	
	NT2RP3004130	11.81	11.81	28.12	21.92	31.13	21.05	
	NT2RP3004133	4.51	4.51	12.95	14.62	8.94	16.81	
	NT2RP3004145	1.43	1.43	4.17	2.62	4.87	3.59	
55	NT2RP3004148	2.67	2.67	7.07	5.26	6.24	4.5	
	NT2RP3004155	2.37	2.37	4.82	4.7	4.57	6.59	

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	NT2RP3004165	17.94	17.94	29.96	29.58	31.82	39.18	
	NT2RP3004179	7.34	7.34	6.72	2.71	5.41	3.3 *	-
	NT2RP3004185	5.2	5.2	5.53	2.76	2.76	1.95 **	-
5	NT2RP3004188	4.77	4.77	10.82	7.74	11.35	7	
	NT2RP3004189	4.23	4.23	5.91	4.97	4.82	6.28	
	NT2RP3004190	2.6	2.6	5.57	5.84	4.36	5.26	
	NT2RP3004191	14.09	14.09	23.4	31.41	29.45	30.09 *	+
10	NT2RP3004202	2.04	2.04	4.56	4.16	4.42	2.3	
	NT2RP3004205	8.75	8.75	21.54	21.27	25.35	20.28	
	NT2RP3004206	4.5	4.5	9.74	5.14	6.37	9	
	NT2RP3004207	5.19	5.19	4.99	3.09	3.25	1.77 **	-
	NT2RP3004209	4.74	4.74	7.74	8.2	11.23	9.08 *	+
15	NT2RP3004215	1.86	1.86	6.7	3.96	2.41	4.55	
	NT2RP3004219	5.15	5.15	11.25	10.04	8.81	13.65	
	NT2RP3004242	4.65	4.65	10.36	9.8	10.19	14.56	
	NT2RP3004246	4.5	4.5	9.39	9.18	10.95	3.8	
	NT2RP3004253	1.89	1.89	4.85	3.64	4.99	2.8	
20	NT2RP3004258	5.45	5.45	10.89	12.77	11.07	11.39	
	NT2RP3004262	4.26	4.26	5.71	2.63	2.99	2.01 *	-
	NT2RP3004275	5.59	5.59	3.43	1.4	2.97	2.34 *	-
	NT2RP3004282	5.45	5.45	68.08	51.29	52.72	53.57	
	NT2RP3004289	1.79	1.79	2.95	1.9	2.18	3.99	
25	NT2RP3004294	2.74	2.74	6.02	6.95	6.93	7.24 *	+
	NT2RP3004298	8.76	8.76	48.63	46.33	60.89	50.83	
	NT2RP3004309	3.3	3.3	6.46	5.2	5.22	5.31	
	NT2RP3004321	3.71	3.71	6.11	3.29	3.74	3.34	
30	NT2RP3004322	5.61	5.61	6.86	6.06	6.43	6.56	
	NT2RP3004332	11.69	11.69	100.11	78.54	102.41	76.72	
	NT2RP3004334	1.49	1.49	6.97	8.56	6.06	9.06	
	NT2RP3004336	2.11	2.11	6.24	6.02	4.44	5.63	
	NT2RP3004338	3.09	3.09	8.41	10.22	9.52	16.47	
35	NT2RP3004341	1.81	1.81	4.56	6.13	5.17	9.13	
	NT2RP3004345	4.1	4.1	8.68	9.3	9.63	8.48	
	NT2RP3004348	5.06	5.06	11.25	13.04	10.79	12.54	
	NT2RP3004349	5	5	7.5	4.89	7.75	5.76	
	NT2RP3004355	5.57	5.57	7.09	7.55	7.07	7.18	
40	NT2RP3004356	5.76	5.76	21.51	11.29	15.14	15.56	
	NT2RP3004360	3.4	3.4	5.26	6.01	5.32	7.85	
	NT2RP3004361	2.6	2.6	6.26	7.67	7.3	8.87 *	+
	NT2RP3004374	3.06	3.06	10.09	8.8	6.6	5.75	
45	NT2RP3004378	10.48	10.48	18.57	28.26	24.09	34.81 *	+
	NT2RP3004399	3.88	3.88	5.77	3.53	3.17	9.06	
	NT2RP3004405	4.07	4.07	6.77	3.03	5.52	3.93	
	NT2RP3004406	5.36	5.36	6.23	5.19	6.03	6.12	
	NT2RP3004411	5.93	5.93	13.28	8.08	6.39	9.51	
50	NT2RP3004424	1.53	1.53	2.43	3.27	1.81	2.83	
	NT2RP3004428	3.03	3.03	5.36	5.07	3.82	4.09	
	NT2RP3004432	3.3	3.3	3.52	3.61	3.11	4.38	
	NT2RP3004434	3.42	3.42	8.41	7.28	9.09	7.99	
	NT2RP3004446	3.29	3.29	4.6	3.29	4.1	2.63	
55	NT2RP3004451	3.2	3.2	6.01	3.89	3.38	2.48	
	NT2RP3004454	2.96	2.96	4.16	2.69	3.5	2.5	

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	NT2RP3004466	3.5	3.5	7.89	5.25	3.85	5.61	
	NT2RP3004470	7.42	7.42	24.53	18.4	16.35	24.72	
	NT2RP3004472	2.49	2.49	4.4	3.97	3.84	3.88	
5	NT2RP3004475	1.71	1.71	5.52	2.72	5.93	3.9	
	NT2RP3004480	14.12	14.12	17.04	18.94	10.5	18.82	
	NT2RP3004481	5.42	5.42	11.37	5.04	7.37	12.39	
	NT2RP3004490	2.66	2.66	8.45	3.92	7.03	8.25	
10	NT2RP3004496	4.8	4.8	14.38	7.22	9.3	11.08	
	NT2RP3004498	6.39	6.39	21.39	16.86	15.11	18.92	
	NT2RP3004503	2.78	2.78	9.34	4.85	6.23	5.88	
	NT2RP3004504	3.91	3.91	11.09	6.05	10.67	11.52	
	NT2RP3004505	17.38	17.38	28.56	37.35	26.72	37.82	
15	NT2RP3004507	1.57	1.57	6.6	2.52	5.52	1.68	
	NT2RP3004519	4.9	4.9	7.73	4.93	8.36	8.75	
	NT2RP3004524	10.04	10.04	29.21	26.88	26.43	29.62	
	NT2RP3004527	3.03	3.03	3.22	1.29	2.23	2.08	*
	NT2RP3004534	3.08	3.08	10.44	5.58	12	7.38	
20	NT2RP3004539	4.45	4.45	12.17	9.8	8.97	12	
	NT2RP3004541	2.65	2.65	11.06	5.48	9.44	8.25	
	NT2RP3004544	3.54	3.54	8.89	6.62	5.24	9.48	
	NT2RP3004551	3.46	3.46	6.75	6.6	6.6	6.98	
	NT2RP3004552	2.76	2.76	4.33	2.84	3.22	4.98	
25	NT2RP3004557	5.68	5.68	8.73	9.74	15.44	13.16	* +
	NT2RP3004561	1.96	1.96	3.77	2.55	4.46	4.1	
	NT2RP3004566	3.09	3.09	11.55	7.2	10.05	8.79	
	NT2RP3004569	2.21	2.21	7.09	4.63	5.36	6.91	
30	NT2RP3004572	4.37	4.37	6.83	7.08	5.55	7.07	
	NT2RP3004578	2.35	2.35	5.38	4.15	4.27	3.24	
	NT2RP3004584	4.76	4.76	28.36	34.99	37.13	30.29	
	NT2RP3004588	2.38	2.38	4.89	1.6	3.7	3.28	
	NT2RP3004594	2.25	2.25	5.9	5.67	6.49	8.94	
35	NT2RP3004603	34.16	34.16	99.64	80.2	102.6	97.27	
	NT2RP3004612	4.71	4.71	12.17	5.3	3.36	5.34	
	NT2RP3004617	1.09	1.09	2.32	2.49	3.3	2.39	
	NT2RP3004618	4.61	4.61	5.9	2.49	5.21	5.9	
	NT2RP3004625	3.97	3.97	8.17	4.55	6.92	7.1	
40	NT2RP3004635	4.76	4.76	7.83	1.52	2.86	3.47	
	NT2RP3004640	10.61	10.61	62.15	59.33	67.97	48.32	
	NT2RP3004642	8.04	8.04	29.31	22.82	26.12	25.12	
	NT2RP3004647	3.5	3.5	5.65	5.89	7.35	6.88	* +
	NT2RP3004652	1.76	1.76	10.37	4.2	3.71	4.34	
45	NT2RP3004669	2.01	2.01	5.36	4.01	5.33	3.46	
	NT2RP3004670	5.04	5.04	10.58	12.4	9.19	14.23	
	NT2RP4000008	45.17	45.17	71.24	49.77	32.43	48.77	
	NT2RP4000018	11.64	11.64	14.61	11.69	14.8	14.87	
	NT2RP4000023	6.96	6.96	8.91	4.86	7.38	5.98	
50	NT2RP4000025	16.2	16.2	22.16	26.22	29.89	24.7	* +
	NT2RP4000035	6.3	6.3	12.01	11.28	15.33	11.01	
	NT2RP4000041	14.46	14.46	34.8	22.01	17.41	23.68	
	NT2RP4000049	2.64	2.64	6.34	6.59	6.88	5.3	
55	NT2RP4000050	2.24	2.24	6.87	3.54	4.48	4.05	
	NT2RP4000051	4.66	4.66	10.5	10.58	10.02	8.96	

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	NT2RP4000063	20.51	20.51	33.5	26.77	31	18.33		
	NT2RP4000065	7.54	7.54	9.24	11.85	15.01	11.47	*	+
	NT2RP4000070	6.63	6.63	5.29	3.79	4.54	3.84	*	-
5	NT2RP4000074	6.55	6.55	13.63	10.29	15.39	9.52		
	NT2RP4000078	3.41	3.41	9.55	12.2	11.66	12.56	*	+
	NT2RP4000080	3.52	3.52	7.01	5.06	6.84	6.81		
	NT2RP4000099	128.86	128.86	236.22	149.44	161.1	211.56		
10	NT2RP4000102	3.55	3.55	6.48	5.27	4.97	5.54		
	NT2RP4000103	2	2	5.47	2.57	2.85	3.96		
	NT2RP4000108	4.66	4.66	7.91	9.33	10.73	10.61	*	+
	NT2RP4000109	18.89	18.89	22.84	19.87	24.15	16.14		
	NT2RP4000111	4.56	4.56	6.38	4.87	5.27	4.85		
15	NT2RP4000112	5.62	5.62	10.14	12.45	8.7	11.81		
	NT2RP4000115	2.94	2.94	3.62	4.95	7.82	10.93		
	NT2RP4000129	2.18	2.18	4.58	3.02	5.04	5.03		
	NT2RP4000137	3.36	3.36	10.05	5.34	8.72	11.4		
	NT2RP4000138	7.21	7.21	10.91	17.75	20.19	19.17	**	+
20	NT2RP4000141	3.25	3.25	6.1	5.22	4.9	3.57		
	NT2RP4000147	6.21	6.21	4.49	4.27	5.2	3.47		
	NT2RP4000150	5.96	5.96	6.93	7.33	10.41	7.06		
	NT2RP4000151	2.82	2.82	7.82	5.69	6.24	5.05		
	NT2RP4000157	73.27	73.27	222.87	169.53	97.5	173.8		
25	NT2RP4000159	2.02	2.02	5.03	3.38	5.03	2.92		
	NT2RP4000163	5.21	5.21	8.74	10.89	9.18	6.63		
	NT2RP4000167	3.26	3.26	4.35	4.32	3.22	3.69		
	NT2RP4000171	5.72	5.72	7	5.72	7.45	5.03		
30	NT2RP4000175	62.48	62.48	94.56	144.06	214.73	147.88	*	+
	NT2RP4000180	17.17	17.17	106.15	88.61	123.6	81.8		
	NT2RP4000185	7.64	7.64	31.76	31.82	23.23	34.01		
	NT2RP4000192	1.04	1.04	4.78	4.19	3.6	3.05		
	NT2RP4000194	3.13	3.13	7.53	7.58	4.98	6.36		
35	NT2RP4000196	6.81	6.81	43.94	35.57	46.56	41.91		
	NT2RP4000210	5.63	5.63	9.71	9.96	8.35	9.27		
	NT2RP4000212	5.59	5.59	8.88	8.57	8.41	9.08		
	NT2RP4000214	5.53	5.53	10.21	5.72	6.68	11.29		
	NT2RP4000216	8.89	8.89	7.36	7	12.63	10.08		
40	NT2RP4000218	3.45	3.45	9.78	7.25	6.07	5.77		
	NT2RP4000223	21.18	21.18	177.28	121.8	125.75	125.3		
	NT2RP4000243	16.52	16.52	54.51	42.94	41.61	51.74		
	NT2RP4000246	17.75	17.75	37.97	26.43	11.42	27.5		
	NT2RP4000250	16.86	16.86	31.23	24.92	23.85	26.39		
45	NT2RP4000256	4.38	4.38	8.45	4.99	6.44	4.67		
	NT2RP4000257	32.45	32.45	44.22	48.67	57.52	39.19		
	NT2RP4000259	7.07	7.07	6.96	8.48	13.07	9.08		
	NT2RP4000261	4.18	4.18	8.13	4.07	4.55	6.48		
	NT2RP4000262	8.36	8.36	11.02	7.11	10.05	7.64		
50	NT2RP4000263	2.6	2.6	5.14	3.47	3.67	3.78		
	NT2RP4000280	5.84	5.84	11.62	9.05	11.58	14.23		
	NT2RP4000286	4.73	4.73	10.16	4.38	6.77	11.94		
	NT2RP4000290	5.77	5.77	5.42	3.18	3.19	5.5		
	NT2RP4000291	42.53	42.53	73.59	62.12	70.23	70.61		
55	NT2RP4000301	3.31	3.31	20.59	22.93	34.62	26.63	*	+

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	NT2RP4000312	7.76	7.76	45.27	39.01	43.59	45.92	
	NT2RP4000321	3.73	3.73	8.16	7.88	7.14	9.75	
	NT2RP4000323	1.44	1.44	4.26	2.27	2.55	2.12	
5	NT2RP4000324	7.77	7.77	16.76	8.33	10.2	11.08	
	NT2RP4000334	20.97	20.97	77.78	63.81	71.76	68.24	
	NT2RP4000343	2.48	2.48	5.54	1.57	3.16	2.38	
	NT2RP4000348	3.4	3.4	10.81	8.38	6.75	13.2	
10	NT2RP4000349	1.78	1.78	0.83	0.37	0.72	2.48	
	NT2RP4000355	3.98	3.98	14.84	7.18	9.13	9.04	
	NT2RP4000356	8.3	8.3	22.64	9.22	11.44	21.13	
	NT2RP4000360	3.04	3.04	6.98	5.06	5.43	4.73	
	NT2RP4000367	2.18	2.18	3.72	2.04	2.58	2.83	
15	NT2RP4000370	4.21	4.21	7.51	3.62	7.12	5.99	
	NT2RP4000373	3.33	3.33	5.18	3.19	5.23	2.95	
	NT2RP4000376	4.2	4.2	5.5	4.85	5.53	6.5	
	NT2RP4000381	1.97	1.97	6.46	4.31	7.01	5.59	
	NT2RP4000388	85.82	85.82	204.63	128.93	93.38	116.03	
20	NT2RP4000390	12.16	12.16	94.1	78.97	76.6	82.02	
	NT2RP4000393	8.66	8.66	9.77	9.09	5.99	10.79	
	NT2RP4000398	5.51	5.51	26.52	22.08	28.3	26.61	
	NT2RP4000406	6.68	6.68	15.61	12.95	15.02	10.08	
	NT2RP4000407	6.17	6.17	11.52	9.41	14.74	9.13	
25	NT2RP4000413	1.79	1.79	3.63	1.15	2.35	2.12	
	NT2RP4000415	7.59	7.59	26.11	18.6	21.68	21.68	
	NT2RP4000417	7.76	7.76	26.64	14.47	12.79	19.19	
	NT2RP4000423	3.52	3.52	7.56	7	6.98	6.46	
30	NT2RP4000424	2.51	2.51	7.2	3.07	5.03	3.27	
	NT2RP4000447	10.3	10.3	64.21	64.91	71.82	68.48	
	NT2RP4000448	5.59	5.59	6.67	4.32	3.56	6.27	
	NT2RP4000449	5.67	5.67	20.48	14.2	19.45	14.67	
	NT2RP4000453	3.53	3.53	6.32	9.02	10.32	10.12 ** +	
35	NT2RP4000455	2.64	2.64	3.98	1.81	1.75	2.4	
	NT2RP4000456	12.57	12.57	21.7	14.7	9.86	13.58	
	NT2RP4000457	1.54	1.54	7.12	3.9	7.55	2.98	
	NT2RP4000461	5.7	5.7	9.84	7.65	6.41	4.6	
	NT2RP4000462	11.76	11.76	15.32	11.86	11.53	17.37	
40	NT2RP4000463	10.2	10.2	52.59	50.66	69.3	48.36	
	NT2RP4000471	6.36	6.36	10.74	5.74	6.23	4.98	
	NT2RP4000472	3.97	3.97	4.41	1.27	1.27	1.66 ** -	
	NT2RP4000476	27.14	27.14	52.56	74.95	94.93	65.35 * +	
	NT2RP4000480	11.56	11.56	29.27	19.08	9.95	26.66	
45	NT2RP4000481	2.29	2.29	4.76	3.73	4.16	4.33	
	NT2RP4000483	1.38	1.38	7.59	7.58	7.85	6.26	
	NT2RP4000487	1.54	1.54	4.9	2.26	3.17	0.91	
	NT2RP4000496	2.16	2.16	4.98	2.95	4.07	3.65	
	NT2RP4000497	17.15	17.15	22.33	34.9	44.46	29.9 * +	
50	NT2RP4000498	10.46	10.46	21.39	20.15	30.33	24.49	
	NT2RP4000500	2.43	2.43	3.21	2.03	1.49	1.39 * -	
	NT2RP4000507	5.63	5.63	9.02	12.49	10.62	17.51 * +	
	NT2RP4000515	12.85	12.85	88.89	90.3	101.29	96.12	
55	NT2RP4000516	8.77	8.77	26.09	19.63	21.76	21.82	
	NT2RP4000517	3.22	3.22	5.73	4.69	5.89	4.79	

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	NT2RP4000518	3.42	3.42	7.4	4.47	6.05	3.82	
	NT2RP4000519	2.9	2.9	5.76	2.18	2.22	1.77	
	NT2RP4000524	4.2	4.2	3.44	2.05	1.72	1.3 **	-
5	NT2RP4000528	3.67	3.67	3.06	3.01	3.27	8.01	
	NT2RP4000537	35.4	35.4	62.6	36.23	30.93	44.52	
	NT2RP4000541	2.04	2.04	2.45	3.34	4.33	3.09 *	+
	NT2RP4000543	2.93	2.93	8.94	7.96	9.72	8.75	
10	NT2RP4000545	4.03	4.03	6.38	4.99	6.43	4.78	
	NT2RP4000546	3.34	3.34	5.93	5.53	4.9	6.03	
	NT2RP4000549	23.81	23.81	56.43	41.6	51.57	38.82	
	NT2RP4000556	7.36	7.36	13.04	14.69	15.54	12.07	
	NT2RP4000557	6.1	6.1	4.53	1.82	3.97	6.27	
15	NT2RP4000558	30.12	30.12	94.23	68.16	57.01	73.2	
	NT2RP4000560	14.8	14.8	52.31	49.75	58.69	56.12	
	NT2RP4000568	1.72	1.72	3.83	5.6	6.08	4.46 *	+
	NT2RP4000583	11.61	11.61	20.2	23.65	14.97	20.56	
	NT2RP4000585	3.04	3.04	4.14	3.12	2.55	3.24	
20	NT2RP4000588	8.65	8.65	12.77	14.58	16.96	13.55 *	+
	NT2RP4000590	24.89	24.89	41.97	41.86	50.81	32.65	
	NT2RP4000599	4.29	4.29	3.24	2.44	2.23	3.59	
	NT2RP4000603	14.08	14.08	33.32	31.06	21.01	29.12	
25	NT2RP4000607	2.41	2.41	10.04	4.45	7.87	15.35	
	NT2RP4000614	6.14	6.14	15.21	15.57	12.53	15.19	
	NT2RP4000634	6.61	6.61	11	7.78	9.84	10.31	
	NT2RP4000638	3.59	3.59	7.77	8.45	5.8	4.73	
	NT2RP4000648	3.13	3.13	4.26	2.54	2.69	2.19	
30	NT2RP4000657	9.94	9.94	15.38	15.95	18.93	14.49	
	NT2RP4000691	5.76	5.76	5.82	4.92	7.47	7.73	
	NT2RP4000697	3.74	3.74	8.5	5.55	6.56	6.12	
	NT2RP4000704	8.91	8.91	47.2	44.17	54.81	38.14	
	NT2RP4000710	40.22	40.22	98.85	90.4	59.28	83.71	
35	NT2RP4000713	4.35	4.35	19.92	16.67	20.85	15.52	
	NT2RP4000724	6.29	6.29	12.5	8.19	9.81	7.83	
	NT2RP4000725	3.61	3.61	4	1.88	1.74	2.33 **	-
	NT2RP4000728	10.13	10.13	41.12	43.53	66.46	39.83	
	NT2RP4000737	4.07	4.07	2.15	3.63	3.09	3.28	
40	NT2RP4000739	5.07	5.07	7.71	4.61	3.63	5.84	
	NT2RP4000749	2.4	2.4	5.29	2.59	3.97	1.68	
	NT2RP4000769	4.93	4.93	10.12	4.67	6.27	6.2	
	NT2RP4000774	3.34	3.34	8.87	5.12	6.63	4.27	
	NT2RP4000781	2.15	2.15	5.12	2.06	2.26	1.55	
45	NT2RP4000783	6.81	6.81	15.16	13.48	15.44	12.67	
	NT2RP4000787	1.45	1.45	2.27	0.31	0.51	0.54 *	-
	NT2RP4000788	3.58	3.58	23.26	16	18.3	18.73	
	NT2RP4000792	3.68	3.68	5.64	5.5	5.8	9.45	
50	NT2RP4000809	43.7	43.7	56.09	46.75	50.47	81.62	
	NT2RP4000817	3.65	3.65	7.83	7.92	7.25	5.82	
	NT2RP4000821	31.34	31.34	38.66	28.32	33.11	25.22	
	NT2RP4000822	2.46	2.46	5.91	4.29	6.19	2.6	
	NT2RP4000823	697.74	697.74	1127.48	923.16	1026.8	947.85	
55	NT2RP4000831	9.98	9.98	61.97	44.37	68.47	50.69	
	NT2RP4000833	3.19	3.19	11.26	6.73	7.19	11.91	

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	NT2RP4000837	1.41	1.41	4.03	1.56	3.65	2.29	
	NT2RP4000839	12.23	12.23	97.13	79.71	85.74	86.06	
	NT2RP4000846	3.8	3.8	10.13	4.65	3.46	6.65	
5	NT2RP4000848	4.63	4.63	10.74	8.65	8.58	6.07	
	NT2RP4000855	2.91	2.91	4.7	4	3.85	3.43	
	NT2RP4000863	3.08	3.08	4.33	3.11	5.3	3.78	
	NT2RP4000865	6.43	6.43	25.36	20.09	39.64	21.24	
10	NT2RP4000873	9.64	9.64	88.25	63.22	69.65	71.33	
	NT2RP4000874	1.76	1.76	3.98	2.37	3.67	2.03	
	NT2RP4000875	3.31	3.31	9.24	6.88	6.52	7.19	
	NT2RP4000878	24.17	24.17	42.53	28.01	16.35	29.04	
	NT2RP4000879	2.56	2.56	5.1	2.95	5.29	2.62	
15	NT2RP4000880	5.17	5.17	21.59	20.97	27.22	16.8	
	NT2RP4000891	81.07	81.07	192.57	252.29	351.53	221.08	* +
	NT2RP4000894	5.16	5.16	9.81	8.53	4.8	6.97	
	NT2RP4000898	0.86	0.86	2.74	1.88	2.14	1.64	
	NT2RP4000899	9.63	9.63	29.48	24.01	20.85	23.95	
20	NT2RP4000907	2.14	2.14	3.58	1.74	4.04	0.81	
	NT2RP4000908	4.62	4.62	9.67	7.51	5.9	5.87	
	NT2RP4000910	14.4	14.4	104.68	124.04	197.74	160.9	* +
	NT2RP4000918	2.85	2.85	4.76	4.73	4.26	5.35	
	NT2RP4000925	3.9	3.9	5.53	2.81	3.15	1.86	
25	NT2RP4000927	1.99	1.99	2.5	0.46	1.08	0.6	** -
	NT2RP4000928	3.11	3.11	6.8	4.48	4.22	5.18	
	NT2RP4000929	1.44	1.44	3.68	1.94	2.86	0.84	
	NT2RP4000946	0.92	0.92	3.41	1.78	3.22	1.47	
30	NT2RP4000947	1.71	1.71	3.51	1.94	3.31	1.79	
	NT2RP4000949	4.94	4.94	7.84	3.88	5.48	2.38	
	NT2RP4000955	4.17	4.17	6.34	2.07	2.86	0.54	* -
	NT2RP4000959	20.55	20.55	28.14	36.21	42.82	36.14	* +
	NT2RP4000962	3.4	3.4	4.24	8.33	10.09	4.53	
35	NT2RP4000973	8.6	8.6	16.04	10.31	8.92	9.03	
	NT2RP4000975	2.18	2.18	5.84	3.29	3.05	2.62	
	NT2RP4000979	3.83	3.83	8.67	5.55	8.13	7.1	
	NT2RP4000984	1.61	1.61	4.31	3.15	3.93	1.85	
	NT2RP4000986	7.32	7.32	13.27	12.66	12.35	2.52	
40	NT2RP4000988	5.74	5.74	8.37	4	5.2	2.63	
	NT2RP4000989	6.24	6.24	6.55	4.05	3.48	2.89	** -
	NT2RP4000990	3.16	3.16	4	1.92	1.69	2.16	** -
	NT2RP4000994	4.04	4.04	7.67	16.48	10.13	15.95	* +
	NT2RP4000996	3.54	3.54	7.49	6.77	6.52	7.38	
45	NT2RP4000997	21.59	21.59	36.81	28.52	15.18	34.38	
	NT2RP4001001	5.53	5.53	9.17	16.66	18.38	15.09	** +
	NT2RP4001004	1.71	1.71	4.88	2.84	3.09	1.37	
	NT2RP4001006	3.46	3.46	8.12	6.85	6.52	6.13	
	NT2RP4001009	9.3	9.3	10.45	15.44	20.46	8.25	
50	NT2RP4001010	7.33	7.33	9.13	7.38	9.75	6.68	
	NT2RP4001013	23.29	23.29	50.15	30.87	28.1	30.91	
	NT2RP4001029	2.49	2.49	5.95	4.05	2.84	3.63	
	NT2RP4001036	7.55	7.55	13.55	9.11	11.51	13.16	
	NT2RP4001041	6.57	6.57	14.4	9.89	12.3	6.35	
55	NT2RP4001042	4.34	4.34	8.11	9.44	12.5	8.79	

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	NT2RP4001046	6.98	6.98	9.95	13.24	16.28	15.36	**	+
	NT2RP4001050	5.28	5.28	4.81	3.79	4.64	3.35	*	-
	NT2RP4001051	6.48	6.48	8.44	5.43	6.82	5.26		
5	NT2RP4001057	0.76	0.76	2.19	2.34	2.43	1.87		
	NT2RP4001063	1.48	1.48	4.39	3.34	3.53	1.8		
	NT2RP4001064	3.51	3.51	9.18	12.02	9.13	11.57		
	NT2RP4001067	4.42	4.42	9.77	10.96	9.63	6.6		
10	NT2RP4001078	2.12	2.12	3.43	2.67	2.53	1.82		
	NT2RP4001079	5.3	5.3	9.35	8.51	8.02	8.98		
	NT2RP4001080	4.1	4.1	5.27	3.52	4.52	2.3		
	NT2RP4001086	5.08	5.08	4.19	3.93	6.64	2.85		
	NT2RP4001095	2.49	2.49	7.25	7.96	6.49	6.85		
15	NT2RP4001098	0.92	0.92	3.38	3.87	2.95	3.41		
	NT2RP4001100	6.47	6.47	24.34	20.89	20.64	16.99		
	NT2RP4001105	3.13	3.13	7.23	6.51	5.58	4.61		
	NT2RP4001110	1.75	1.75	3.5	7.07	8.35	5.29	*	+
	NT2RP4001115	9.95	9.95	17.68	20.6	18.48	15.31		
20	NT2RP4001117	19.81	19.81	30.49	35.35	42.53	27.5		
	NT2RP4001122	6.06	6.06	6.09	5.17	6.25	3.27		
	NT2RP4001123	3.62	3.62	7.76	7.95	5.96	6.27		
	NT2RP4001126	4.36	4.36	11.28	10.87	9.09	8.04		
	NT2RP4001127	3.25	3.25	4.59	3.39	3.08	2.17		
25	NT2RP4001138	2.46	2.46	5.8	3.41	2.56	1.62		
	NT2RP4001143	2.73	2.73	5.98	6.44	6.54	5.66		
	NT2RP4001148	3.72	3.72	6.76	3.77	3.03	2.05		
	NT2RP4001149	5.07	5.07	7.28	6.76	9.03	6.37		
	NT2RP4001150	3.8	3.8	3.17	3.15	3.7	2.88		
30	NT2RP4001159	7.08	7.08	11.61	7.69	5.58	10.46		
	NT2RP4001162	3.77	3.77	6.14	4.07	6.06	3.41		
	NT2RP4001170	1.15	1.15	4.53	1.28	3.2	2.15		
	NT2RP4001174	4.16	4.16	12.27	7.91	11.95	5.02		
	NT2RP4001175	9.65	9.65	19.14	15.72	21.29	13.28		
35	NT2RP4001176	99.19	99.19	161.51	174.03	241.92	194	*	+
	NT2RP4001184	4.83	4.83	27.1	25.76	32.51	22.85		
	NT2RP4001198	21.66	21.66	48.22	29.54	29.17	38.54		
	NT2RP4001199	2.52	2.52	6.45	2.59	4.74	3.71		
40	NT2RP4001206	8.25	8.25	33.2	25.92	32.07	25.48		
	NT2RP4001207	2.38	2.38	5.15	2.21	3.11	4.01		
	NT2RP4001210	2.73	2.73	5.2	3.62	4.26	2.64		
	NT2RP4001213	3.42	3.42	5.11	3.99	4.23	3.63		
	NT2RP4001214	3.34	3.34	4.3	3.51	3.76	2.16		
45	NT2RP4001219	7.4	7.4	12.05	14.35	19.28	13.39	*	+
	NT2RP4001228	5.26	5.26	9.63	12.15	15.74	20.07	*	+
	NT2RP4001235	2.42	2.42	7.45	3.46	6.02	4.48		
	NT2RP4001256	2.11	2.11	4.24	1.66	3.41	2.66		
	NT2RP4001257	2.48	2.48	7.27	4.05	4.35	4.05		
50	NT2RP4001260	3.16	3.16	5.79	2.52	3.86	2.92		
	NT2RP4001261	3.84	3.84	6.63	8.42	6.47	5		
	NT2RP4001274	22.92	22.92	38.08	25.02	31.56	21.25		
	NT2RP4001276	5.24	5.24	10.03	11.38	15.97	11.63	*	+
	NT2RP4001283	20.72	20.72	122.55	87.44	93.43	86.47		
55	NT2RP4001299	9.62	9.62	15.14	14.95	10.52	15.18		

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	NT2RP4001313	1.45	1.45	3.26	1.72	2.96	0.97	
	NT2RP4001315	6.06	6.06	11.14	7.45	9.92	7.74	
	NT2RP4001320	14.6	14.6	42.74	32.02	38.13	29.24	
5	NT2RP4001325	32.53	32.53	146.14	142.88	178.36	128.89	
	NT2RP4001336	6.69	6.69	40.75	38.55	46.66	32.11	
	NT2RP4001339	4.12	4.12	5.6	3.35	5.56	2.76	
	NT2RP4001343	10.46	10.46	83.37	54.71	61.01	60.06	
10	NT2RP4001344	6.7	6.7	60.08	49.79	55.21	42.62	
	NT2RP4001345	1.65	1.65	6.68	5.64	5.7	3.87	
	NT2RP4001351	4.1	4.1	15.97	10.01	20.05	11.42	
	NT2RP4001353	2.8	2.8	5.91	1.63	2.94	1.86	
	NT2RP4001355	2.57	2.57	8.67	1.83	3.12	2.08	
15	NT2RP4001367	10.64	10.64	17.66	11.92	17.06	13.16	
	NT2RP4001372	2.26	2.26	3.82	2.1	2.06	2.07	
	NT2RP4001373	8.86	8.86	16.4	10.99	8.59	11.48	
	NT2RP4001375	2.71	2.71	6.06	4.91	7.42	2.94	
	NT2RP4001379	1.74	1.74	3.52	2.34	4.67	1.38	
20	NT2RP4001381	5.6	5.6	12.51	12.8	12.66	8.27	
	NT2RP4001386	6.39	6.39	14.52	14.77	20.11	12.32	
	NT2RP4001389	7.28	7.28	8.66	5.43	9.25	4.09	
	NT2RP4001396	5.76	5.76	6.42	2.83	4.61	2.12	*
	NT2RP4001407	2.92	2.92	2.98	3.07	2.04	1.76	
25	NT2RP4001409	13.6	13.6	28.28	8.87	5.85	8.84	
	NT2RP4001410	33.56	33.56	61.26	40.57	18.92	37.8	
	NT2RP4001414	16.59	16.59	37.89	14.29	21.3	16.8	
	NT2RP4001424	3.55	3.55	8.85	7.99	10.45	7.41	
30	NT2RP4001433	3.85	3.85	6	8.39	9.79	3.38	
	NT2RP4001438	9.95	9.95	27.94	46.22	53.63	30.76	* +
	NT2RP4001442	4.33	4.33	4.97	3.3	3.41	2.64	*
	NT2RP4001447	4.42	4.42	4.69	5.08	5.51	3.41	
	NT2RP4001466	3.74	3.74	5.45	7.38	3.23	5.57	
35	NT2RP4001467	21.67	21.67	58.89	54.18	44.07	55.8	
	NT2RP4001472	8.05	8.05	12.19	11.7	11.76	11.97	
	NT2RP4001474	2.83	2.83	4.81	3.2	5.73	1.98	
	NT2RP4001483	1.48	1.48	4.33	2.61	3.7	1.19	
	NT2RP4001488	21.03	21.03	32.41	39.07	46.9	33.42	
40	NT2RP4001492	4.18	4.18	6.73	3.21	3.81	1.91	
	NT2RP4001498	4.3	4.3	2.43	2.95	3.52	2.13	
	NT2RP4001502	28.2	28.2	57.38	27.65	34.81	41.83	
	NT2RP4001503	3.83	3.83	6.74	5.51	4.1	3.37	
	NT2RP4001507	2.39	2.39	3.69	5.03	5.95	5.18	** +
45	NT2RP4001510	1.74	1.74	4.63	5.64	5.05	3.02	
	NT2RP4001516	3.54	3.54	4.16	2.52	1.9	1.27	*
	NT2RP4001520	25.33	25.33	70.64	73.93	107.21	85.05	
	NT2RP4001523	5.57	5.57	9.99	8.4	7.79	6.19	
	NT2RP4001524	6.1	6.1	10.17	8.92	11.45	5.98	
50	NT2RP4001529	29.8	29.8	74.89	59.39	60.69	55.29	
	NT2RP4001531	2.88	2.88	10.96	8.63	11.05	7.81	
	NT2RP4001546	143.48	143.48	388.31	316.63	215.6	309.45	
	NT2RP4001547	9.05	9.05	26.31	28.76	23.06	18.81	
	NT2RP4001551	2.27	2.27	3.93	3.87	4.08	2.02	
55	NT2RP4001555	2.95	2.95	5.8	4.14	3.58	1.74	

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	NT2RP4001567	6.54	6.54	6.88	5.82	7.12	5.68	
	NT2RP4001568	7.58	7.58	11.65	10.02	19.33	12.97	
	NT2RP4001569	15.49	15.49	41.42	32.56	40.11	27.18	
5	NT2RP4001571	5.75	5.75	13.28	9.06	7.43	8.13	
	NT2RP4001574	8.5	8.5	19.03	15.54	17.52	15.29	
	NT2RP4001575	2.46	2.46	5.86	5.71	5.53	4.24	
	NT2RP4001578	17.21	17.21	45.64	52.76	53.63	40.92	
10	NT2RP4001592	9.76	9.76	13.68	14.13	19.64	11.68	
	NT2RP4001593	9.4	9.4	18.11	22.12	27.3	18.04	
	NT2RP4001605	5.97	5.97	4.78	4.1	7.77	4.66	
	NT2RP4001606	2.9	2.9	8.34	6.01	3.51	6.75	
	NT2RP4001607	2.04	2.04	5.24	4.57	3.26	3.78	
15	NT2RP4001610	1.74	1.74	2.42	2.6	2.48	1.7	
	NT2RP4001614	2.17	2.17	7.19	5.38	4.34	6.86	
	NT2RP4001623	2.38	2.38	5.26	2.43	2.65	2.02	
	NT2RP4001626	9.48	9.48	11.67	18.67	23.9	19.44	** +
	NT2RP4001634	2.74	2.74	4.93	3.67	5.24	4.26	
20	NT2RP4001638	3.41	3.41	3.03	2.36	2.11	1.87	** -
	NT2RP4001644	7.86	7.86	33.73	24.36	26.04	24.99	
	NT2RP4001646	11.61	11.61	15.02	7.42	10.74	11.21	
	NT2RP4001656	3.75	3.75	5.23	2.89	4.51	2.07	
	NT2RP4001666	1.99	1.99	4.68	3.26	6.25	2.02	
25	NT2RP4001670	11.74	11.74	15.51	12.45	7.09	8.31	
	NT2RP4001677	28.27	28.27	42.75	42.01	45.48	47.53	
	NT2RP4001679	8.82	8.82	33.83	33.23	51.5	29.78	
	NT2RP4001695	7.71	7.71	12.76	15.66	20.35	12.87	
30	NT2RP4001696	2.64	2.64	5.45	3.13	3.92	3.72	
	NT2RP4001699	3.58	3.58	8.03	3.18	4.12	4.42	
	NT2RP4001717	2.79	2.79	7.03	3.29	5.84	4.15	
	NT2RP4001719	3.59	3.59	9.11	7.6	9.27	6.28	
	NT2RP4001725	2.27	2.27	4.79	2.28	5.07	1.43	
35	NT2RP4001726	7.07	7.07	11.18	5.85	6.91	4.98	
	NT2RP4001730	3.11	3.11	12.82	11.96	19.81	16.3	
	NT2RP4001739	2.83	2.83	5.83	5.79	6.55	4.98	
	NT2RP4001741	7.25	7.25	15.93	9.28	12.42	10.97	
	NT2RP4001753	3.04	3.04	8.4	4.39	4.64	6.64	
40	NT2RP4001760	4.32	4.32	6.6	7.79	7.73	12.96	
	NT2RP4001787	67.61	67.61	173.05	169.17	187.1	193.22	
	NT2RP4001790	2	2	5.29	3.42	2.97	2.58	
	NT2RP4001795	9.31	9.31	12.31	14.38	19.76	12.34	
	NT2RP4001803	3.35	3.35	3.6	3.94	4.78	3.67	
45	NT2RP4001805	2.64	2.64	3.57	3.64	2.47	2.95	
	NT2RP4001809	4.84	4.84	26.35	18.18	23.17	11.33	
	NT2RP4001817	11.55	11.55	19.09	9.5	10.78	12.71	
	NT2RP4001822	2.09	2.09	5.36	3.73	5.11	3.33	
	NT2RP4001823	1.91	1.91	3.95	1.14	3.34	1.24	
50	NT2RP4001827	14.88	14.88	25.96	35.78	40.37	29.5	* +
	NT2RP4001828	9.76	9.76	34.37	27.78	34.21	26.3	
	NT2RP4001836	7.74	7.74	33.26	27.19	39.14	26.78	
	NT2RP4001838	1.59	1.59	7.49	2.09	4.5	2.71	
	NT2RP4001841	8.75	8.75	80.37	61.67	50.27	56.46	
55	NT2RP4001849	1.9	1.9	4.55	2.51	5.08	1.58	

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	NT2RP4001861	7.27	7.27	34.6	36.09	41.9	34.39	
	NT2RP4001877	6.59	6.59	8.44	12.87	9.04	14.1	* +
	NT2RP4001879	9.64	9.64	15.47	11.58	14.24	10.73	
5	NT2RP4001889	5.09	5.09	10.66	6.68	11.25	8.91	
	NT2RP4001893	3.97	3.97	7.34	3.19	6.11	2.72	
	NT2RP4001896	3.18	3.18	6.86	5.38	7.87	4.92	
	NT2RP4001898	7.83	7.83	26.41	22.98	20.13	20.15	
10	NT2RP4001901	1.73	1.73	4.69	4.08	5.87	2.69	
	NT2RP4001910	39.51	39.51	58.21	53.45	33.59	45.93	
	NT2RP4001925	4.1	4.1	10.21	6.69	6.32	6.12	
	NT2RP4001926	6.41	6.41	7.22	7.1	9.54	5.52	
	NT2RP4001927	6.26	6.26	9.97	5.83	8.13	2.82	
15	NT2RP4001931	8.64	8.64	14.16	15.49	17.54	11.89	
	NT2RP4001933	38.49	38.49	87.13	96.81	133.51	91.22	
	NT2RP4001938	2.93	2.93	4.53	4.27	3.31	3.55	
	NT2RP4001942	13.44	13.44	27.12	31.34	24.8	18.71	
	NT2RP4001945	1.41	1.41	4	1.55	3.67	1.77	
20	NT2RP4001946	1.97	1.97	5.67	3.04	3.96	1.66	
	NT2RP4001947	4.42	4.42	8.93	5.92	9.81	5.16	
	NT2RP4001950	4.13	4.13	5	2.25	2.84	1.34	* -
	NT2RP4001953	10.44	10.44	14.15	13.81	19.4	14.36	
25	NT2RP4001966	2.44	2.44	2.41	2.51	4.26	1.52	
	NT2RP4001970	2.26	2.26	5.32	3.91	3.4	2.88	
	NT2RP4001975	8.56	8.56	20.03	18.32	13.05	12.02	
	NT2RP4001988	6.72	6.72	18.78	22.92	24.78	29.44	* +
	NT2RP4001996	5.27	5.27	12.83	10.65	16.35	12.42	
30	NT2RP4002014	3.4	3.4	8.14	43.19	37.87	33.17	** +
	NT2RP4002018	6.19	6.19	13.71	10.47	11.39	10.36	
	NT2RP4002035	5.35	5.35	5.95	5.4	4.17	2.54	
	NT2RP4002043	7.1	7.1	10.8	9.64	12.2	6.5	
	NT2RP4002046	9.74	9.74	20.08	21.94	15.28	17.11	
35	NT2RP4002047	8.37	8.37	19.18	22.28	24.07	28.83	* +
	NT2RP4002052	5.78	5.78	10.36	9.02	9.36	9.37	
	NT2RP4002056	32.58	32.58	71.49	58.09	76.58	49.75	
	NT2RP4002057	6.37	6.37	11.06	12.13	13.58	7.41	
	NT2RP4002058	3.85	3.85	6.6	4.1	4.2	3.22	
40	NT2RP4002064	5.93	5.93	4.39	2.6	4.16	2.07	* -
	NT2RP4002071	6.67	6.67	7.07	6.95	10.06	6.27	
	NT2RP4002075	1.16	1.16	2.11	2.27	2.35	1.27	
	NT2RP4002078	2.25	2.25	8.63	6.86	8.24	4.97	
	NT2RP4002081	8.11	8.11	26.15	18.73	18.78	19.42	
45	NT2RP4002083	1.39	1.39	5.25	3.36	3.16	1.88	
	NT2RP4002099	3.26	3.26	4.73	2.84	3.56	2.51	
	NT2RP4002106	10.35	10.35	20.34	22.36	25.93	20.55	
	NT2RP4002111	11.7	11.7	12.37	19.77	30.44	17.72	
	NT2RP4002112	6.15	6.15	10.97	8.9	8.34	3.22	
50	NT2RP4002116	12.6	12.6	47.19	37.43	41.25	28.65	
	NT2RP4002122	5.34	5.34	9.29	14.84	14.86	12.67	** +
	NT2RP4002126	6.42	6.42	14.44	16.82	14.35	10.42	
	NT2RP4002133	7.56	7.56	20.82	29.17	26.14	21	
	NT2RP4002136	3.63	3.63	5.74	4.89	5.38	2.69	
55	NT2RP4002139	26.89	26.89	31.12	60.65	61.92	32.88	

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	NT2RP4002174	139.27	139.27	232.64	240.71	275.01	193.19
	NT2RP4002185	7.77	7.77	13.2	12.36	19.06	11.58
	NT2RP4002186	4.5	4.5	9.83	7.82	4.72	6.78
5	NT2RP4002187	15.42	15.42	32.13	26.94	19.84	21.17
	NT2RP4002188	3.01	3.01	8.34	8.3	7.75	6.41
	NT2RP4002199	1.85	1.85	3.73	2.6	2.91	3.78
	NT2RP4002206	2.08	2.08	3.39	2.48	2.34	1.29
10	NT2RP4002210	3.13	3.13	4.75	2.02	2.86	0.98
	NT2RP4002222	4.2	4.2	6.63	5.56	6.28	4.16
	NT2RP4002241	7.97	7.97	8.24	10.82	11.75	7.19
	NT2RP4002248	5.08	5.08	16.69	10.74	8.9	8.13
	NT2RP4002250	1.54	1.54	3.22	0.73	1.69	0.56
15	NT2RP4002259	4.86	4.86	9.82	3.21	4.85	1.75
	NT2RP4002268	16.62	16.62	29.54	28.9	28.18	25.68
	NT2RP4002288	6.42	6.42	12.57	13.29	14.36	11.97
	NT2RP4002290	7.55	7.55	7.61	7.96	7.67	5.87
	NT2RP4002298	3.92	3.92	4.18	5.54	5.03	4.18
20	NT2RP4002306	2.38	2.38	5.79	2.97	5.77	2.64
	NT2RP4002308	2.04	2.04	6.03	5.31	5.23	4.1
	NT2RP4002336	2.71	2.71	6.33	3.71	4.19	4.63
	NT2RP4002340	1.09	1.09	3.96	1.28	2.75	0.49
	NT2RP4002361	2.77	2.77	5.78	3.73	4.03	2.48
25	NT2RP4002367	2.27	2.27	5.84	3.23	2.48	2.77
	NT2RP4002368	9.87	9.87	17.2	18.26	19.27	16
	NT2RP4002377	3.3	3.3	23.8	25.46	30.75	23.93
	NT2RP4002408	2.22	2.22	3.87	3.75	6.37	4.11
	NT2RP4002425	2.84	2.84	5.81	8.24	7.98	5.23
30	NT2RP4002432	12.33	12.33	85.4	61.06	72.53	67.82
	NT2RP4002447	2.97	2.97	7.68	3.96	5.4	4.59
	NT2RP4002451	5.48	5.48	6.2	5.84	5.85	6.83
	NT2RP4002461	9.8	9.8	32.09	32.76	38.91	29.04
35	NT2RP4002486	3.5	3.5	6.71	2.47	4.15	2.87
	NT2RP4002517	3.65	3.65	9.11	7.02	8.53	7.18
	NT2RP4002556	4.29	4.29	3.91	5.68	10.03	6.41
	NT2RP4002569	3.36	3.36	7.36	4.93	5.29	3.42
	NT2RP4002587	2.26	2.26	4.19	2.8	3.4	2.02
40	NT2RP4002591	2.21	2.21	4.89	2.89	4.5	3.08
	NT2RP4002607	1.43	1.43	3.34	2.87	4.63	1.58
	NT2RP4002627	17.83	17.83	61.9	55.9	76.17	65.3
	NT2RP4002628	7.28	7.28	15.48	14.53	23.95	12.54
	NT2RP4002630	4.19	4.19	5.25	6.72	9.4	7.16 * +
45	NT2RP4002639	9.43	9.43	70.25	52.38	77.24	57.28
	NT2RP4002641	1.58	1.58	9.03	3.94	4.07	4.1
	NT2RP4002658	114.62	114.62	166.93	76.49	34.96	109.83
	NT2RP4002669	3.5	3.5	5.67	5.4	5.33	4.68
	NT2RP4002677	6.24	6.24	9.41	10.14	7.99	13.62
50	NT2RP4002715	8.42	8.42	34.92	40.1	48.46	32.3
	NT2RP4002750	2.6	2.6	8.29	1.68	2.04	1.33
	NT2RP4002784	3.71	3.71	9.51	9.44	11.22	7.06
	NT2RP4002791	4.91	4.91	9.44	4.88	9.76	5.33
	NT2RP4002811	1.63	1.63	6.38	3.17	2.95	3.43
55	NT2RP4002830	4.26	4.26	7.45	3.9	5.9	5.46

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	NT2RP4002832	2.12	2.12	3.13	2.38	5.59	2.54	
	NT2RP4002850	5.07	5.07	12.04	14.36	12.63	8.06	
	NT2RP4002874	5.17	5.17	6.67	3.41	5.14	1.96	
5	NT2RP4002884	28.81	28.81	49.75	43.57	74.75	52.87	
	NT2RP4002888	5.55	5.55	4.83	3.67	4.32	3.08	*
	NT2RP4002891	5.48	5.48	15.79	13.16	19.42	11.91	
	NT2RP4002894	12.04	12.04	24.47	18.44	12.76	16.4	
10	NT2RP4002896	5.54	5.54	12.2	8.96	6.18	7.78	
	NT2RP4002905	1.71	1.71	4.27	2.32	3.58	1.28	
	NT2RP4002907	5.11	5.11	7.62	6.94	10.72	1.41	
	NT2RP5003459	68.11	68.11	133.25	154.61	146.15	164.37	* +
	NT2RP5003461	7.34	7.34	10.14	10.85	14.36	8	
15	NT2RP5003471	106.6	106.6	168.71	124.4	148.85	112.14	
	NT2RP5003477	2.71	2.71	2.62	2.59	2.33	1.9	
	NT2RP5003487	157.44	157.44	424.89	292.71	256.56	354.93	
	NT2RP5003492	3.1	3.1	4.91	5.25	6.17	5.91	* +
	NT2RP5003500	1.5	1.5	3.28	2.38	2.54	2.59	
20	NT2RP5003506	4.96	4.96	9.3	7.83	10.37	9.04	
	NT2RP5003512	2.21	2.21	4.35	2.63	3.46	2.15	
	NT2RP5003522	4.1	4.1	5.97	4.62	4.19	2.34	
	NT2RP5003524	4.38	4.38	3.86	1.61	1.54	0.84	**
	NT2RP5003527	24.72	24.72	71.27	76.81	87.24	60.59	
25	NT2RP5003531	7.16	7.16	17.2	15.58	14.06	14.11	
	NT2RP5003534	2.68	2.68	5.49	5.54	6.82	4.55	
	NT2RP6000020	8.69	8.69	19.96	14.65	15.13	16.29	
	NT2RP6000022	3.19	3.19	4.05	4.06	3.96	2.44	
	NT2RP6000050	3.95	3.95	3.99	4.98	5.82	2.88	
30	NT2RP6000063	3.91	3.91	6.04	3.61	2.52	2.56	
	NT2RP6000074	5.38	5.38	4.88	3.41	3.27	2.17	**
	NT2RP6000083	7.76	7.76	11.18	11.49	16	9.91	
	NT2RP6000100	2.49	2.49	4.58	4.04	4.71	3.3	
	NT2RP6000123	1.94	1.94	3.29	5.1	4.26	4.22	* +
35	NT2RP6000129	1.9	1.9	4.47	4.06	4.27	2.74	
	NT2RP6000147	3.75	3.75	11.74	10.8	11.03	7.48	
	NT2RP6000163	2.62	2.62	4.23	2.28	1.95	1.71	
	NT2RP6000181	8.03	8.03	12.4	9.44	13.25	9.01	
40	NT2RP6000182	5.44	5.44	6.42	4.82	5.56	3.88	
	OVARC1000001	4.97	4.97	5.24	6.04	7.48	2.35	
	OVARC1000003	3.21	3.21	8.31	8.51	7.66	7.05	
	OVARC1000004	9.87	9.87	116.19	88.04	109.99	85.44	
	OVARC1000006	3.57	3.57	6.58	9.04	7.88	4.73	
45	OVARC1000013	6.51	6.51	9.19	7.32	8.36	8.33	
	OVARC1000014	3.39	3.39	5.02	4.23	5.02	4.17	
	OVARC1000017	3.11	3.11	6.81	4.2	4.45	2.72	
	OVARC1000026	24.79	24.79	32.1	56.82	69.34	44.53	* +
	OVARC1000035	11.11	11.11	20.26	20.41	23.65	15.36	
50	OVARC1000037	8.73	8.73	19.12	15.64	9.13	15.9	
	OVARC1000058	6.06	6.06	11.69	13.84	7.56	10.6	
	OVARC1000060	1.89	1.89	6.28	5.98	5.24	5.13	
	OVARC1000068	2.38	2.38	5.33	5.31	3.56	2.42	
	OVARC1000069	74.66	74.66	101.53	75.95	84.36	86.42	
55	OVARC1000071	4.4	4.4	4.77	6.47	5.35	4.04	

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	OVARC1000075	55.43	55.43	125.63	120.89	150.97	117.03		
	OVARC1000083	9.58	9.58	9.24	13.12	12.7	10.64	*	+
	OVARC1000085	106.6	90.9	156.14	214.2	177.05	273.14	*	+
5	OVARC1000086	3.98	6.82	9.23	11.98	11.3	14.09	*	+
	OVARC1000087	1.51	2.83	1.79	4.03	3.57	3.35	*	+
	OVARC1000090	1.48	4.1	6.14	10.88	9.58	8.79	*	+
	OVARC1000091	4.88	8.33	8.01	7.99	7.76	6.82		
	OVARC1000092	2.83	6.81	4.18	4.68	6.25	4.85		
10	OVARC1000105	9.73	14.86	17.21	26.29	25.62	22.88	*	+
	OVARC1000106	26.02	23.03	46.38	66.36	50.1	53.01	*	+
	OVARC1000109	9.12	13.08	18.04	16.72	12.91	17.46		
	OVARC1000113	4.12	6.25	6.53	6.83	8.19	7.65		
15	OVARC1000114	2.14	3.44	5.77	5.94	5.86	4.98		
	OVARC1000133	2.53	4.96	6.36	4.05	4.97	2.95		
	OVARC1000137	6.14	10.05	13.51	13.3	18.59	14.39		
	OVARC1000139	14.75	20.77	83.44	71.14	98.1	69.29		
	OVARC1000145	0.72	6.64	2.89	1.78	2.42	2		
20	OVARC1000148	5.09	4.98	7.88	4.91	5.32	7.91		
	OVARC1000151	1.41	2.11	2.4	3.58	4.08	3.58	**	+
	OVARC1000157	10.99	14.16	17.51	21.21	25.06	22.76	*	+
	OVARC1000162	1.22	4.4	2.5	2.93	2.49	2.59		
	OVARC1000168	1.98	8.46	6.2	8.01	9.61	9.96		
25	OVARC1000169	32.03	45.07	49.48	70.63	69.6	89.08	*	+
	OVARC1000178	0.84	5.08	2.53	3.37	3.18	2.78		
	OVARC1000182	0.8	3.3	1.42	2.02	1.95	1.78		
	OVARC1000186	2.51	3.72	3.23	5.95	3.27	4.77		
	OVARC1000188	1.04	2.67	2.33	2.48	2.87	1.9		
30	OVARC1000191	1.01	3.8	2.63	3.12	2.85	2.54		
	OVARC1000198	2.09	3.59	4.32	5.62	5.12	5.06	*	+
	OVARC1000208	6.49	10.37	22.5	17.79	24.54	22.02		
	OVARC1000209	7.99	13.69	22.32	23.42	27.81	29.16		
	OVARC1000212	2.47	5.63	3.59	4.76	5.03	4.88		
35	OVARC1000216	1.72	4.96	4.36	15.43	11.3	12.54	**	+
	OVARC1000240	2.98	3.53	8.13	5.39	5.46	4.87		
	OVARC1000241	1.29	2.47	3.18	2.65	3.17	1.4		
	OVARC1000249	4.14	5.43	8.17	5.46	5	6.13		
40	OVARC1000254	33.15	39.39	100.99	100.41	131.42	100.89		
	OVARC1000255	0.85	4.83	2.51	2.98	2.45	1.95		
	OVARC1000267	2.37	6.41	6.71	6.66	7.16	7.31		
	OVARC1000275	79.02	93.7	161.08	199.43	240.76	175.96	*	+
	OVARC1000287	226.67	224.66	236.08	433.91	512.76	470.31	**	+
45	OVARC1000288	3.2	4.25	7.38	6.23	5.32	4.47		
	OVARC1000298	8.96	10.09	19.62	13.37	7.19	9.6		
	OVARC1000302	1.12	2.14	2.13	2.47	1.85	2		
	OVARC1000304	1.09	2.68	3.23	5.02	3.41	6		
	OVARC1000307	2.95	6.19	4.74	7.59	4.7	6.29		
50	OVARC1000309	1.18	7.16	3.22	3.24	2.85	2.4		
	OVARC1000312	2.83	11.64	6.03	4.17	5.4	2.46		
	OVARC1000313	10.48	19.25	14.81	9.39	17.54	22.17		
	OVARC1000321	31.6	24.05	47.79	30.5	31.37	15.43		
	OVARC1000326	1.52	2.3	3.9	3.84	3.17	2.79		
55	OVARC1000327	1.52	3.28	4.24	3.13	1.49	2.46		

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	OVARC1000331	2.22	4.72	2.41	4.33	4.45	4.58		
	OVARC1000335	2.3	5.84	4.02	2.72	5.16	4.75		
5	OVARC1000347	1.83	8.18	6.24	7.35	9.24	8.44		
	OVARC1000348	1.61	10.62	3.73	2.84	4.59	3.05		
	OVARC1000363	3.7	9.61	6.51	7.31	11.52	6.83		
	OVARC1000377	1.07	2.09	2.43	2.28	2.51	2.45		
	OVARC1000382	3.34	3.39	4.33	5.07	2.52	1.03		
10	OVARC1000384	4.2	5.42	8.35	5.32	4.4	6.04		
	OVARC1000401	0.62	3.63	2.09	3.35	4.08	3.64		
	OVARC1000406	18.98	23.3	49.12	57.09	74.48	54.63	*	+
	OVARC1000407	1.99	6.28	3.99	4.11	6.42	3.16		
	OVARC1000408	27.5	38.45	70.39	74.84	111.17	71.25		
15	OVARC1000410	6.83	12.72	10.41	4.78	6.65	5.01		
	OVARC1000411	0.91	1.5	2.6	3.49	3	2.22		
	OVARC1000414	1.31	2.22	3.7	4.5	3.78	3.71		
	OVARC1000420	1.44	2.76	3.29	3.3	2.59	2.1		
	OVARC1000421	1.42	2.65	3.33	3.96	4.21	4.99	*	+
20	OVARC1000427	25.78	27.02	130.06	156.9	215.67	142.19		
	OVARC1000431	10.51	17.6	19.12	33.66	31.78	25.78	*	+
	OVARC1000437	3.14	6.37	7.31	5.97	7.63	6.36		
	OVARC1000439	5.81	10.95	13.82	21.81	23.01	21.52	**	+
	OVARC1000440	2.56	3.74	5.01	7.47	9.31	7.08	*	+
25	OVARC1000442	2.34	2.38	6.81	6.66	9.5	8.12		
	OVARC1000443	2.09	2.2	2.88	3.29	3.41	2.62		
	OVARC1000461	1.11	2.84	2.2	2.55	1.12	2.14		
	OVARC1000465	3.27	5.01	3.51	3.94	4.62	3.95		
	OVARC1000466	1.94	5.47	5.9	6.54	10.13	6.76		
30	OVARC1000467	1.01	5.08	2.41	3.65	2.98	3.78		
	OVARC1000470	1.13	5.81	3.03	3.18	4.02	3.78		
	OVARC1000473	1.81	1.95	2.65	2.44	4.16	1.39		
	OVARC1000479	5.67	5.88	9.88	10.35	14.26	6.88		
	OVARC1000484	3.99	5.74	6.54	8.66	9.93	6.87		
35	OVARC1000486	3.17	4.71	4.49	5.74	4.93	4.28		
	OVARC1000496	0.93	3.55	0.66	0.31	1.07	0.62		
	OVARC1000520	0.84	5.89	1.18	1.32	2.27	2		
	OVARC1000522	4.1	7.19	12	13.85	14.03	10.34		
	OVARC1000526	1.96	7.04	3.75	5.93	5.48	4.69		
40	OVARC1000529	2.38	2.57	4.44	3.66	4.16	3.08		
	OVARC1000533	3.3	4.66	7.95	8.89	12.29	7.83		
	OVARC1000543	0.84	2.44	2.06	2.57	3.08	2.72		
	OVARC1000550	0.75	3.68	2.32	2.82	4.04	2.34		
	OVARC1000553	2.1	5.63	7.02	7.72	7.69	6.95		
45	OVARC1000556	5.77	15.21	11.77	8.95	13.91	8.96		
	OVARC1000557	0.83	5.12	1.4	1.61	2.29	1.88		
	OVARC1000561	3.48	7.38	9.26	13	17.66	15.09	*	+
	OVARC1000564	8.89	9.02	10.44	17.84	11.31	16.69	*	+
	OVARC1000573	1.87	3.68	4.86	5.75	5.32	3.83		
50	OVARC1000576	24.12	29.23	124.94	83.09	93.83	98.58		
	OVARC1000578	2.43	4.6	5.53	8.64	4.46	3.93		
	OVARC1000581	0.34	3.28	1.15	1.75	1.27	1.23		
	OVARC1000586	22.54	28.9	41.17	34.58	43.39	40.93		
55	OVARC1000588	0.74	5.23	2.03	2.75	3.72	2.05		

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	OVARC1000605	1.98	2.62	2.88	4.47	4.23	3.87	**	+
	OVARC1000622	3.86	4.59	11.57	12.7	11.13	11.6		
	OVARC1000636	1.64	3.79	4.58	4.19	4.03	5.09		
5	OVARC1000640	1.97	4.72	3.93	4.21	3.67	3.09		
	OVARC1000649	9.69	14.8	53.54	53.32	64.51	52.67		
	OVARC1000661	1.14	9.33	2.99	5.34	5.24	5.24		
	OVARC1000677	8.53	10.16	14.87	11.77	10.98	15.47		
10	OVARC1000678	1.21	4.49	2.71	3.28	4.17	3.26		
	OVARC1000679	2.86	3.25	4.09	5.29	5.16	6.25	*	+
	OVARC1000681	1.47	1.55	3.2	2.41	2.22	1.71		
	OVARC1000682	10.09	11.33	50.91	33.79	47.49	44.31		
	OVARC1000689	3.81	7.1	19.94	20.18	22.12	21.83		
15	OVARC1000700	1.8	10.37	3.18	4.98	4.37	5.14		
	OVARC1000703	1.74	7.18	5.35	6.4	6.64	7.77		
	OVARC1000722	10.59	11.92	47.93	43.41	60.06	39.34		
	OVARC1000726	1.44	3.48	4.62	4.88	5.89	3.58		
	OVARC1000727	1.93	2.09	4.13	3.78	3.79	3.89		
20	OVARC1000730	5.95	5.86	9.01	4.07	4.16	5.62		
	OVARC1000741	4.85	6.13	8.74	15.19	10.58	13.71	*	+
	OVARC1000746	0.89	3.61	2.43	2.06	2.9	2.84		
	OVARC1000764	1.76	4.93	4.77	5.35	7.01	5.44		
	OVARC1000769	1.13	4.3	3.6	3.76	4.42	5.2		
25	OVARC1000771	2.42	6.28	2.3	4.02	4.81	3.71		
	OVARC1000773	19.09	24.7	31.93	44.69	56.24	46.24	*	+
	OVARC1000775	11.67	8.94	16.44	12.16	8.7	4.26		
	OVARC1000778	2.37	3.89	5.69	4.59	6.23	4.92		
	OVARC1000779	0.8	2.02	1.85	2.23	2.45	1.46		
30	OVARC1000781	1.67	5.05	4.16	6.37	3.45	5.07		
	OVARC1000787	1.64	4.79	4.22	2.97	5.44	3.25		
	OVARC1000789	7.62	14.23	16.39	24.95	29.69	25.94	**	+
	OVARC1000800	2.91	10.72	5.72	6.41	10.65	6.2		
	OVARC1000802	1.55	8.77	2.97	2.99	5.34	2.76		
35	OVARC1000810	3.37	3.54	8.29	6.66	7.99	7.21		
	OVARC1000811	2.41	2.73	7.5	4.88	3.67	4.95		
	OVARC1000814	3.44	4.55	9.03	7.92	11.3	9.05		
	OVARC1000816	7.64	10.41	12.41	10.99	10.58	14.11		
	OVARC1000817	1.18	3.38	1.27	1.71	2.14	1.55		
40	OVARC1000834	2.46	8.3	3.39	4.84	5.81	4.01		
	OVARC1000846	2.23	10.02	5.35	7.38	9.66	7.72		
	OVARC1000850	1.74	8.37	3.38	3.39	2.51	3.1		
	OVARC1000853	23.21	24.23	43.4	30.67	37.81	18.39		
	OVARC1000862	2.28	2.66	4.91	3.05	1.61	1.49		
45	OVARC1000873	2.56	2.98	4.14	4.4	3.79	3.85		
	OVARC1000875	1.47	3.07	1.79	2.35	3.09	1.87		
	OVARC1000876	3.71	5.67	4.46	5.11	6.06	5.45		
	OVARC1000883	6.06	9.53	9.18	12.43	15.42	13.05	*	+
	OVARC1000885	2.84	9.95	3.38	3.74	5.66	4.11		
50	OVARC1000886	4.31	8.19	4.29	3.74	5.15	4.39		
	OVARC1000890	17.47	18.3	91.22	70.97	78.71	51.68		
	OVARC1000891	1.28	1.44	3.03	2.85	2.19	3.22		
	OVARC1000897	0.48	1.74	1.29	1.21	1.33	0.5		
55	OVARC1000912	2.06	3.22	4.33	5.21	6.1	5.86	*	+

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	OVARC1000914	1.48	6.18	1.61	3.68	3.02	2.18	
	OVARC1000915	1.71	6.64	4.14	4.87	3.54	4.76	
	OVARC1000916	1.91	5.19	2.56	4.05	4.32	3.88	
5	OVARC1000924	1.45	5.5	3.09	3.28	3.85	3.48	
	OVARC1000928	6.05	5.46	8.78	4.22	5.83	5.35	
	OVARC1000936	1.37	1.39	2.17	2.04	3.25	2.49	
	OVARC1000937	1.69	3.01	1.94	4.17	3.26	3.24	
	OVARC1000945	1.55	3.67	3.62	3.83	3.22	2.28	
10	OVARC1000948	1.57	3.85	2.66	3.15	3.68	1.99	
	OVARC1000956	1.41	5.08	4.36	7.56	7.26	5.51	
	OVARC1000959	1.8	4.87	3.39	4.88	3.02	3.9	
	OVARC1000960	2.64	7.53	9.55	11.64	13.89	12.86	* +
	OVARC1000964	19.89	17.19	103.98	118.41	165.46	96.14	
15	OVARC1000971	0.42	1.58	1.4	2.53	2.27	2.28	* +
	OVARC1000975	5.93	8.3	36.1	31.27	51.54	30.22	
	OVARC1000976	0.65	2.12	1.27	2.17	1.46	1.5	
	OVARC1000981	4.06	7.18	4.94	7.97	12.1	8.53	
20	OVARC1000982	2.83	5.41	2.23	3.13	3.02	3.54	
	OVARC1000984	1.78	5.43	3.32	3.01	3.08	2.16	
	OVARC1000995	2.94	6.59	4.5	5.98	6.19	6.72	
	OVARC1000996	1.68	1.87	4.29	3.58	4.15	4.56	
	OVARC1000999	6.02	5.65	15.29	15.61	13.18	13.29	
25	OVARC1001000	1.96	4.5	6.2	6.26	7.09	6.86	
	OVARC1001004	0.51	3.4	1.45	2.05	3.3	1.47	
	OVARC1001010	1.35	3.99	1.66	3.04	1.4	1.54	
	OVARC1001011	1.46	5.57	1.13	2.39	3.27	2.45	
	OVARC1001030	96.19	101.41	143.98	119.24	154.26	133	
30	OVARC1001032	1.42	5.34	1.89	1.83	2.82	1.92	
	OVARC1001034	4.44	5.58	6.51	3.29	5.21	3.77	
	OVARC1001038	3.62	5.03	7.4	10.3	10.88	8.61	* +
	OVARC1001040	2.63	3.77	6.93	5.25	6.51	4.25	
	OVARC1001041	4.54	8.03	12.87	8.57	12.25	9.4	
35	OVARC1001044	1.05	2.92	1.83	1.96	2.43	1.84	
	OVARC1001049	3.78	8.78	10.67	10.65	11.87	10.26	
	OVARC1001051	40.95	55.97	80.66	66.89	109.71	87.49	
	OVARC1001054	1.22	4.06	3.22	2.86	4.19	1.93	
	OVARC1001055	2.13	3.38	3.82	4.32	5.61	5.22	* +
40	OVARC1001062	5.8	6.15	12.54	8.04	9.94	9.57	
	OVARC1001065	8.85	13.63	51.33	51.41	60.3	56.97	
	OVARC1001068	2.82	5.62	4.76	4.72	4.02	5.52	
	OVARC1001072	0.73	4.18	4.41	3.2	3.71	3.07	
	OVARC1001073	0.92	5.7	2.65	2.91	2.54	1.79	
45	OVARC1001074	0.81	4.66	3.31	1.87	2.95	2.04	
	OVARC1001078	2	5.12	2.79	3.57	3.08	2.83	
	OVARC1001085	2.41	2.83	3.66	5.54	5.02	6.36	** +
	OVARC1001086	1.97	3.17	2.85	3.98	2.83	4.13	
50	OVARC1001091	16.24	19.32	92.73	76.48	96.74	77.99	
	OVARC1001092	4.62	5.35	7.22	9.69	7.84	6.05	
	OVARC1001104	1.05	4.37	2.66	3.16	2.58	2.03	
	OVARC1001107	11.59	15.6	40.28	31.21	49.49	42.22	
	OVARC1001113	1.04	5.81	1.59	2.46	3.05	2.39	
55	OVARC1001117	2.71	6.63	4.31	4.67	5.74	2.67	

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	OVARC1001118	2.38	3.69	7.08	7.36	6.91	8.28	
	OVARC1001125	2.02	2.9	3	5.92	4.97	5.9	** +
	OVARC1001129	2.61	4.58	3.19	8.46	9.43	11	** +
5	OVARC1001132	1.7	6.48	2.66	3.69	4.26	4.66	
	OVARC1001138	9.52	15.82	23.8	48.95	45.16	44.97	** +
	OVARC1001141	1.68	4.97	3.48	3.77	3.68	3.84	
	OVARC1001154	18.31	29.49	68.39	60.43	83.49	65.64	
	OVARC1001161	2.49	5.55	6.15	7.03	6.69	5.89	
10	OVARC1001162	2.2	3.13	5.34	5.09	4.86	5.26	
	OVARC1001163	0.69	3.59	2.77	2.2	3.98	2.54	
	OVARC1001167	3.03	4.57	7.69	10.19	12.95	9.3	* +
	OVARC1001169	0.74	4.87	2.68	2.47	1.91	2.06	
	OVARC1001170	7.81	15.04	17.59	14.61	19.45	14.99	
15	OVARC1001171	15.57	17.71	24.31	16.12	23.34	22.51	
	OVARC1001173	2.09	5.08	5.1	4.32	6.75	5.49	
	OVARC1001176	22.57	21.48	89.96	76.74	102.3	70.7	
	OVARC1001180	3.01	4.58	12.7	11.81	10.77	9.56	
20	OVARC1001188	2.66	3.7	3.95	3.62	3.44	4.16	
	OVARC1001200	1.52	4.56	3.62	3.47	2.9	2.96	
	OVARC1001202	3.75	6.65	6.53	9.26	7.79	10.23	* +
	OVARC1001206	1.52	5.52	1.15	1.59	1.13	1.9	
	OVARC1001209	4.89	8.92	27.46	24.69	30.38	24.27	
25	OVARC1001219	1.81	6.36	4.71	5.33	3.95	3.62	
	OVARC1001222	2.5	8.36	5.01	3.2	4.34	5.63	
	OVARC1001232	2.91	4.18	7.74	6.75	6.02	5.65	
	OVARC1001240	2.05	3.27	6.84	5.55	5.06	5.4	
	OVARC1001243	0.94	2.59	1.76	3.64	2.64	1.86	
30	OVARC1001244	9.07	12.05	18	21.61	18.57	26.62	
	OVARC1001246	30.48	50.95	48.51	80.54	100.83	101.88	** +
	OVARC1001247	3.64	9.86	7.7	6.57	7.02	4.49	
	OVARC1001260	1.05	9.07	1.85	2.62	2.65	1.85	
	OVARC1001261	4.23	10.5	6.99	3.46	2.08	2.94	
35	OVARC1001268	24.4	19.69	52.37	32.58	35.32	14.16	
	OVARC1001270	14.46	15.1	20.83	9.69	9.8	8.65	* -
	OVARC1001271	2.62	3.62	3.88	3.95	7.02	4.26	
	OVARC1001282	0.88	3.02	3.09	1.37	1.59	2	
	OVARC1001296	3.02	8.06	2.3	3.04	4.11	5.41	
40	OVARC1001306	1.48	8.27	2.4	2.04	2.29	3.82	
	OVARC1001314	0.49	8.47	1.57	1.06	1.79	1.32	
	OVARC1001316	2.77	7.17	4.81	5.48	8.11	5.36	
	OVARC1001329	6.12	6.18	21.11	17.09	19.29	16.22	
	OVARC1001330	0.2	1.89	1.38	1.22	1.35	1.42	
45	OVARC1001336	1.92	3.7	3.59	5.67	4.09	4.02	
	OVARC1001338	0.26	2.87	0.86	2.49	1.71	1.07	
	OVARC1001339	12.07	18.29	22.73	33.65	32.72	37.29	** +
	OVARC1001340	0.72	4.83	1.23	1.33	2.44	1.3	
50	OVARC1001341	4.35	9.25	6.77	7.94	11.38	9.69	
	OVARC1001342	90.37	98.53	136.12	129.68	163.22	127.78	
	OVARC1001344	2.1	2.51	6.27	6.52	6.89	6.2	
	OVARC1001357	5.61	8.93	16.02	15.52	11.34	11.69	
	OVARC1001359	8.96	12.4	16.15	21.66	13.84	10.6	
55	OVARC1001360	0.44	2.52	0.99	1.97	2.6	1.62	

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	OVARC1001369	1.56	5.66	1.89	3.41	1.88	3.1		
	OVARC1001372	0.96	4.23	3.33	1.52	2.77	1.95		
	OVARC1001376	1.82	5.1	3.62	5.79	5.79	4.18		
5	OVARC1001381	4.51	6.44	9.94	10.95	12.91	11.21		
	OVARC1001391	0.5	1.62	1.44	1.88	1.27	1.26		
	OVARC1001392	2.12	4.69	6.14	11.96	12.7	7.79	*	+
	OVARC1001399	0.98	3.59	2.16	1.77	2.54	1.1		
10	OVARC1001417	1.01	3.07	1.76	2.39	3.61	2.81		
	OVARC1001419	2.47	5.4	3.06	4.39	4.03	3.16		
	OVARC1001425	2.29	5.58	5.15	8.76	8.5	8.07	*	+
	OVARC1001436	1.37	5.85	2.54	2.9	3.57	3.18		
	OVARC1001442	0.64	4.84	1.39	2.27	1.52	0.69		
15	OVARC1001451	3.09	2	3.89	5.18	5.98	4.75	*	+
	OVARC1001452	1.35	2.41	2.87	2.96	4.69	3.13		
	OVARC1001453	1.21	2.84	1.88	2.3	1.82	1.57		
	OVARC1001476	10.67	14.38	16.52	17.22	12.9	13.09		
	OVARC1001480	0.93	4.73	1.5	3.1	2.98	2.21		
20	OVARC1001489	0.97	6.89	2.51	3.01	2.83	2.09		
	OVARC1001493	2.09	6.59	3.75	7.38	8.78	10.48	*	+
	OVARC1001496	4.65	9.58	8.63	10.74	7.37	11.03		
	OVARC1001499	1.24	1.18	2.6	3.47	2.68	2.84		
	OVARC1001506	2.9	2.7	5.31	5.33	6.73	5.48		
25	OVARC1001509	1.73	3.89	3.69	4.07	4.59	3.07		
	OVARC1001510	0.16	3.69	1.42	1.94	1.73	0.86		
	OVARC1001516	2.57	5.78	3.85	6.04	4.97	4.39		
	OVARC1001525	0.53	4.76	2.12	1.94	2.01	1.81		
	OVARC1001542	8.8	12.86	13.01	15.91	13.63	17.23		
30	OVARC1001544	2.14	6.6	6.72	7.54	8.33	6.22		
	OVARC1001546	4.08	4.32	4.6	6.12	5.31	7.23	*	+
	OVARC1001547	1.29	2.53	1.68	2.44	1.85	2.22		
	OVARC1001555	10.39	16.51	68.77	48.66	65.39	56.39		
	OVARC1001560	3.35	4.91	5.52	5.36	4.93	5.34		
35	OVARC1001569	1.63	4.75	4.79	5.92	5.19	5.1		
	OVARC1001570	3.96	7.9	6.93	7.72	10.7	8.55		
	OVARC1001577	1.68	5.89	5.41	8.61	6.9	10.2		
	OVARC1001578	0.25	3.47	-0.19	-0.47	0.24	0.15		
	OVARC1001596	12.13	11.65	14.23	13.51	14.82	27.15		
40	OVARC1001600	1.13	2.9	1.48	2.81	2.67	3.67		
	OVARC1001607	6.22	7.72	10.91	13.42	14.01	13.45	*	+
	OVARC1001610	1.81	5.25	2.84	4.25	2.66	2.7		
	OVARC1001611	0.13	5.11	1.24	1.48	2.89	1.79		
45	OVARC1001615	0.58	5.42	1.93	1.54	2.56	1.74		
	OVARC1001636	1.09	3.75	1.05	2.39	2.05	2.15		
	OVARC1001668	3.77	6.75	10.04	10.5	11.4	10.48		
	OVARC1001702	1.18	2.21	2.42	3.86	2.07	2.25		
	OVARC1001703	2.82	3.18	2.97	2.64	4.71	4.65		
50	OVARC1001710	3.58	7.03	8.67	8.01	6.28	9.55		
	OVARC1001711	1.96	7.3	3.36	5.01	4.15	5.4		
	OVARC1001713	9.17	11.54	44.65	36.47	51.48	43.79		
	OVARC1001725	1.01	5.45	6.11	2.56	3.77	4.01		
	OVARC1001726	1.64	4.48	3.23	4.97	5.6	5.18		
55	OVARC1001727	1.4	2.41	1.52	1.43	2.35	1.14		

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	OVARC1001731	120.62	110.86	255.43	140.73	139.03	74.2		
	OVARC1001735	1.29	3.44	3.54	3.75	3.25	2.89		
	OVARC1001741	3.3	4.73	15.28	13.09	12.93	13.17		
5	OVARC1001745	2.72	5.39	6.83	9.17	10.23	8.89	*	+
	OVARC1001759	3.31	9.01	6.31	7.61	7.61	11.95		
	OVARC1001762	3.96	7.78	6.38	10.3	11.01	13.4	*	+
	OVARC1001766	5.33	7.8	11.99	15.56	16.86	15.33	*	+
10	OVARC1001767	0.94	3.76	1.18	1.97	1.96	2.41		
	OVARC1001768	3.31	3.86	3.76	5.35	4.59	3.54		
	OVARC1001770	3.04	6.58	9.98	11.46	9.08	9.46		
	OVARC1001776	2.11	4.7	3.5	4.72	3.64	2.92		
	OVARC1001791	1.13	4.77	3.54	3.07	3.12	3.42		
15	OVARC1001795	0.89	6.19	1.24	2.31	2.87	2.11		
	OVARC1001798	2.81	12.11	7.57	9.72	11.93	9.04		
	OVARC1001802	1.73	11.64	4.9	5.6	5.93	4.01		
	OVARC1001805	1.92	6.96	2.58	3.62	4.59	3.51		
	OVARC1001807	1.9	2.53	4.18	3.06	3.12	2.46		
20	OVARC1001809	12.38	14.06	76.32	55.87	81.41	52.83		
	OVARC1001812	1.44	3.39	3.15	3.23	4.63	3.71		
	OVARC1001813	1.61	4.29	2.33	2.93	3.98	2.51		
	OVARC1001820	1.67	7.15	3.21	3.47	3.76	3.22		
	OVARC1001828	0.78	6.85	2.36	1.91	3.23	2.2		
25	OVARC1001833	1.07	8.12	2.02	2.4	2.1	1.92		
	OVARC1001839	1.56	8.43	2.98	2.91	3.59	1.15		
	OVARC1001846	1.91	1.38	2.9	2.15	2.11	1.8		
	OVARC1001849	1.21	2.52	2.42	5.79	3.69	4.03	*	+
30	OVARC1001861	1.46	3.56	2.73	2.78	2.5	2.09		
	OVARC1001873	3.09	3.78	4.63	5.47	4.42	4.73		
	OVARC1001879	1.44	6.08	3.48	2.35	2.93	2.22		
	OVARC1001880	0.91	7.84	2.94	3.63	5.78	3.8		
	OVARC1001883	0.99	7.61	3.12	2.61	3.42	2.52		
35	OVARC1001900	1.11	7.07	4.03	2.57	3.61	2.89		
	OVARC1001901	0.54	1.84	1.21	2.42	1.37	2.43		
	OVARC1001911	0.59	1.57	1.66	1.51	1.39	1.55		
	OVARC1001916	1.86	3.13	3.35	4.16	4.61	3.51		
	OVARC1001928	1.45	3.53	1.55	1.58	1.62	1.72		
40	OVARC1001937	5.12	11.69	8.13	17.41	11.63	15.16		
	OVARC1001940	1.1	4.51	3.13	3.72	3.14	2.78		
	OVARC1001942	3.85	7.4	8.03	11.47	13.91	12.77	*	+
	OVARC1001943	7.16	10.07	11.08	9.62	13.85	11.87		
	OVARC1001949	1.69	3.34	4.15	5.35	4.01	5.55		
45	OVARC1001950	1.53	2.41	3.79	6.3	4.35	3.98		
	OVARC1001952	11.3	11.38	53.57	52.33	78.84	38.05		
	OVARC1001954	1.12	2.99	2.2	3.09	2.67	2.05		
	OVARC1001963	1	4.91	2.89	4.5	3.39	3.21		
	OVARC1001983	3.62	14.16	14.25	20.96	19.21	21.67		
50	OVARC1001987	3.12	6.54	5.94	6.08	8.39	8.02		
	OVARC1001989	1.41	5.2	4.96	4.54	5.59	5.26		
	OVARC1001991	1.74	3.27	4.08	4.57	3.86	3.27		
	OVARC1002005	4.14	3.55	7.66	10.01	9.06	8.2	*	+
	OVARC1002044	3.73	3.94	6.17	6.57	8.32	6.99	*	+
55	OVARC1002046	10.28	16.21	20.07	29.4	37.78	37.02	**	+

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	OVARC1002050	1.7	5.6	2.43	3.96	3.82	2.53	
	OVARC1002058	4.23	6.11	4.02	4.69	5.55	5.43	
	OVARC1002066	11.47	13.5	25.49	26.02	28.69	22.63	
5	OVARC1002082	3.6	8.55	8.81	9.6	8.89	6.49	
	OVARC1002091	3.17	5.67	8.37	9.49	5.49	7.64	
	OVARC1002092	1.38	2.72	2.2	4	3.97	1.88	
	OVARC1002093	1.79	3.1	4.51	5.01	4.44	3.88	
	OVARC1002094	1.55	6.24	4.17	36.42	27.25	28.35	** +
10	OVARC1002107	1.42	4.63	2.69	4.86	5.48	3.6	
	OVARC1002112	6.17	11.59	8.5	13.47	17.48	11.92	
	OVARC1002126	2.66	6.35	6.68	7.95	6.44	8.79	
	OVARC1002127	0.73	5.04	1.86	1.92	2.61	1.52	
15	OVARC1002138	1.4	1.79	1.86	3.16	4.82	2.75	* +
	OVARC1002143	0.73	1.51	1.55	1.29	3.03	2.09	
	OVARC1002156	2.42	3.87	4.19	4.43	3.9	3.65	
	OVARC1002158	0.88	2.63	1.6	2.36	1.57	1.51	
	OVARC1002165	4.85	6.3	9.83	10.73	14.03	10.87	
20	OVARC1002176	0.86	5.08	3.59	2.01	3.46	2.64	
	OVARC1002178	0.83	5.35	3.12	3.8	5.02	4.25	
	OVARC1002182	1.29	2.89	3.77	2.45	4.64	3.12	
	OVARC1002185	11.45	13.19	62.79	43.91	53.43	55.56	
	PLACE1000004	1.42	3.23	2.35	3.87	4.25	4.05	* +
25	PLACE1000005	1.18	3.06	3.3	5.27	5.31	4.83	* +
	PLACE1000006	2.01	8.33	3.23	4.2	5.44	4.67	
	PLACE1000007	0.97	5.13	2.89	3.03	2.47	2.56	
	PLACE1000014	2.9	8.06	6.26	6.67	8.18	6.55	
30	PLACE1000031	0.88	4.81	0.45	2.61	2.71	2.79	
	PLACE1000033	1.23	2.15	2.75	2.42	3.17	2.56	
	PLACE1000040	3.08	4.43	6.18	7.11	5.54	7.37	
	PLACE1000048	1.83	3.24	2.14	3.32	3.96	3.74	
	PLACE1000050	2.12	5.36	9.1	9	6.55	8.25	
	PLACE1000061	138.29	147.36	249.77	165.55	233.98	230.37	
35	PLACE1000066	14.23	15	19.46	15.86	15.62	18.52	
	PLACE1000075	3.03	6.24	9.08	4.98	6.93	7.11	
	PLACE1000078	2.1	5.75	5	6.07	6.93	5.19	
	PLACE1000081	1.08	1.88	1.52	1.13	1.89	1.27	
40	PLACE1000086	4.97	6.55	11.25	8.1	9.16	7.75	
	PLACE1000094	0.7	4.18	1.72	1	3.44	2.96	
	PLACE1000101	4.67	8.44	7.7	11.69	10.38	13.65	* +
	PLACE1000121	0.87	6.29	2.02	1.95	2.85	2.39	
	PLACE1000133	6.65	11.93	17.66	15.19	17.59	21.71	
45	PLACE1000142	1.79	6.03	5.66	2.64	4.77	4.24	
	PLACE1000146	1.95	4.51	2.89	3.71	5.02	2.82	
	PLACE1000163	4.52	5.99	10.71	16.27	10.95	13.78	
	PLACE1000172	1.12	2.63	1.48	1.81	3.21	2.29	
	PLACE1000181	1.06	3	2.98	2.63	3.75	2.86	
50	PLACE1000184	1.17	3.08	1.48	1.87	3.28	2.27	
	PLACE1000185	2.99	6.52	8.47	9.53	9.99	12.03	
	PLACE1000198	0.78	4.09	2.49	2.19	2.17	1.93	
	PLACE1000213	3.3	5.87	7.36	4.35	5.38	8.09	
	PLACE1000214	1.37	4.29	4.54	5.22	6.72	4.22	
55	PLACE1000220	9.61	7.84	16.78	7.48	5.77	4.1	

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	PLACE1000231	2.48	4.1	4.92	4.57	4.65	3.91		
	PLACE1000236	0.66	3.33	2.43	2.8	3.63	2.37		
	PLACE1000245	2.92	5.88	6.34	9.34	11.24	10.55	*	+
5	PLACE1000246	5.15	8.27	9.95	3.29	2.55	2.86	*	-
	PLACE1000258	5.4	12.61	13.52	14.88	16.7	14.95		
	PLACE1000288	1.68	7.22	2.96	2.83	4.02	2.48		
	PLACE1000292	3.72	9.02	8.85	10.23	20.58	9.21		
10	PLACE1000302	0.56	1.01	1.39	1.07	0.92	0.62		
	PLACE1000304	1.13	3.26	3.17	3.75	2.32	3.05		
	PLACE1000308	2.54	4.35	4.17	4.42	3.87	1.34		
	PLACE1000309	2.29	4.02	4	6.72	5.23	7.88	*	+
	PLACE1000312	1.33	3.44	2.48	2.74	3.99	2.5		
15	PLACE1000330	0.46	5.76	3.02	1.32	1.93	1.35		
	PLACE1000332	1.02	8.82	2.01	3.01	3.78	1.68		
	PLACE1000347	2.3	9.48	3.89	2.59	5.81	3.22		
	PLACE1000351	1.2	1.5	2.87	2.2	2.4	2		
	PLACE1000374	2.01	3.03	7.02	8.89	6.55	6.85		
20	PLACE1000380	2.39	4.27	3.95	4.9	2.12	2.38		
	PLACE1000383	1.03	2.62	1.9	2.53	3.64	2.4		
	PLACE1000397	0.63	4.06	1.89	2.82	3.34	3.47		
	PLACE1000401	1.22	6.39	2.24	2.23	3.05	2.36		
	PLACE1000406	1.08	8.76	3.4	3.72	4.08	3.64		
25	PLACE1000412	1.61	6.38	1.56	1.62	3.45	1.46		
	PLACE1000420	2.59	3.51	4.6	8.95	7.28	5.6	*	+
	PLACE1000421	0.99	1.3	2.32	2.97	2	1.7		
	PLACE1000423	16.6	23.29	32.85	10.67	8.02	8.09	*	-
	PLACE1000424	1.36	3.09	2.12	3.35	2.65	1.97		
30	PLACE1000430	0.77	4.36	1.95	3.51	2.94	3.77		
	PLACE1000433	1.06	5.9	1.65	1.89	2.6	1.8		
	PLACE1000435	1.39	7.21	4.77	6.22	6.29	4.22		
	PLACE1000437	6.06	10.65	10.14	17.29	20.07	18.79	**	+
	PLACE1000442	3.75	3.85	6.27	7.81	5.7	6.7		
35	PLACE1000444	2.14	3.94	8.96	11.14	11.55	9.8		
	PLACE1000453	5.57	11.03	14.16	10.42	7.4	2.99		
	PLACE1000456	1.25	2.21	1.97	1.33	2.18	1.07		
	PLACE1000465	2.09	5.63	6.62	12.97	11.8	10.69	**	+
40	PLACE1000481	2.32	8.1	3.73	6.89	6.64	6.45		
	PLACE1000492	1.15	4.45	2.95	3.27	3.06	2.81		
	PLACE1000508	1.36	4.64	4	3.91	4.24	3.71		
	PLACE1000512	4.91	4.29	6.39	8.12	7.8	4.6		
	PLACE1000540	5.18	3.93	7.84	5.44	6.9	5.57		
45	PLACE1000541	13.59	15.07	48.84	60.62	81.24	41.96		
	PLACE1000546	0.86	3.61	2.82	4.72	4.63	2.5		
	PLACE1000547	2.16	4.61	3.83	6.31	5.64	5.92	*	+
	PLACE1000560	2.08	5.97	2.1	1.62	2.8	1.72		
	PLACE1000562	2.8	6.23	6.04	8.86	11.26	8.61	*	+
50	PLACE1000564	1.54	6.4	3.07	3.16	4.41	3.43		
	PLACE1000583	3.75	3.28	6.32	6.78	11.53	6.8		
	PLACE1000587	8.52	9.32	12.99	13.64	14.69	9.43		
	PLACE1000588	1.92	4.36	3.99	8.79	8.15	4.48		
	PLACE1000596	1.99	5.34	4.39	7.8	6.74	4.51		
55	PLACE1000599	2.39	5.51	7.05	7.92	7.79	6.46		

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	PLACE1000605	5.12	11.43	7.06	14.2	15.1	12.67	*	+
	PLACE1000610	2.01	6.08	3.54	5.26	4.48	2.94		
	PLACE1000611	13.18	19.13	24.68	16.45	20.37	22.79		
5	PLACE1000626	3.19	4.04	8.04	5.71	9.93	8.12		
	PLACE1000633	1.32	2.12	3.95	4.8	6.06	3.59		
	PLACE1000636	1.15	2.54	1.43	2.72	4.25	2.94		
	PLACE1000653	5.07	8.56	9.29	11.07	11.87	14.08	*	+
10	PLACE1000656	4.2	12.9	25.22	16.66	16.71	12.92		
	PLACE1000663	2	6.43	3.59	2.39	6.61	4.03		
	PLACE1000706	2	6.3	5.04	5.37	7.27	6.26		
	PLACE1000712	3.9	9.52	10.82	10.49	10.07	9.11		
	PLACE1000716	0.98	2.75	3.44	2.44	3.2	2.82		
15	PLACE1000740	2.74	5.28	6.24	8.83	8.13	9.69	*	+
	PLACE1000748	3.35	3.51	6.81	3.12	5.02	4.23		
	PLACE1000749	3.49	6.35	5.94	4.61	4.65	6.02		
	PLACE1000751	2.71	5.34	4.07	7.81	8.32	8.36	**	+
	PLACE1000755	1.39	6.14	1.93	2.55	5.1	2.96		
20	PLACE1000769	2.29	6.8	3.45	3.33	4.58	2.6		
	PLACE1000778	0.87	1.48	1.99	2.05	2.94	2.38		
	PLACE1000785	9.56	12.21	27.18	28	24.34	29.54		
	PLACE1000786	2.68	4.22	3.63	3.09	3.77	3.7		
	PLACE1000793	4.05	7.21	6.7	6.06	7.6	9.1		
25	PLACE1000795	2.15	5.5	3.99	4.44	5.29	4.31		
	PLACE1000798	0.88	8.44	3.24	3.13	3.8	3.72		
	PLACE1000812	2.13	5.08	4.46	5.06	5.16	6.03		
	PLACE1000823	1.71	5.2	4.89	5.67	7.28	4.84		
	PLACE1000825	1.6	2.86	2.02	3.77	3.96	3.76	*	+
30	PLACE1000838	16	15.77	23.73	13.88	15.6	15.65		
	PLACE1000841	1.22	3.78	3.31	3.97	10.65	3.77		
	PLACE1000843	2.14	6.2	5.68	5.79	7.7	5.38		
	PLACE1000849	2.79	8.82	6.72	7.24	6.78	10.02		
	PLACE1000856	2.01	5.3	3.59	3.42	4.79	4.19		
35	PLACE1000863	5.2	7.58	9.56	8.97	12.34	11.53		
	PLACE1000876	3.65	7.6	6.02	6.7	9.95	9.06		
	PLACE1000899	1.36	2.24	3.12	4.12	5.14	4.22	*	+
	PLACE1000907	4.82	5.53	9.59	6.77	8.44	5.83		
	PLACE1000909	1.18	3.31	2.45	3.65	3.88	3.44		
40	PLACE1000912	0.42	4.55	1.77	1.76	2.72	1.46		
	PLACE1000914	1.05	4.41	3.5	3	6.09	4.22		
	PLACE1000918	0.54	4.49	1.61	1.82	3.13	1.98		
	PLACE1000927	10.48	12.41	16.9	20.91	23.21	25.47	*	+
45	PLACE1000931	0.69	3.44	2.12	2.44	3.94	3.3		
	PLACE1000944	2.55	2.24	4.78	3.84	3.32	2.09		
	PLACE1000948	0.52	2.31	2.96	2.21	2.72	1.72		
	PLACE1000958	0.12	2.2	1.73	1.11	1.77	2.27		
	PLACE1000972	1.01	3.43	2.89	4.49	5.33	3.75		
50	PLACE1000977	2.33	5.67	4.42	2.71	5.33	5.25		
	PLACE1000979	1.63	8.01	3.93	4.24	5.92	4.57		
	PLACE1000986	3.37	16.51	6.63	6.97	8.75	7.69		
	PLACE1000987	1.76	10.13	4.79	4.17	4.74	5.11		
	PLACE1001000	4.85	4.62	7.76	6.02	4.25	3.02		
55	PLACE1001007	7	6.94	14.66	5.39	3.76	3.47		

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	PLACE1001010	0.61	2.04	2.45	2.56	2.73	2.84		
	PLACE1001015	0.88	2.55	1.84	2.36	1.72	2.42		
	PLACE1001016	1.79	4.54	4.29	6.37	9	6.57	*	+
5	PLACE1001022	0.68	6.5	2.45	1.9	2.39	1.29		
	PLACE1001024	1.05	8.89	1.83	1.34	2.49	2.35		
	PLACE1001036	2.63	10.55	5.42	3.62	5.49	5.43		
	PLACE1001038	50.16	49.81	118.83	82.67	64.83	52.8		
10	PLACE1001048	1.07	1.82	0.92	2.39	2.09	1.21		
	PLACE1001054	9.95	10.74	63.88	62.96	79.44	66.71		
	PLACE1001062	1.45	4.19	3.71	3.12	4.17	3.05		
	PLACE1001063	1.35	3.74	2.2	4.06	3.65	2.74		
	PLACE1001076	0.46	6.48	1	1.86	2.18	1.62		
15	PLACE1001081	1.53	7.95	3.33	3.65	5.24	4.8		
	PLACE1001088	1.32	5.24	1.22	1.42	2.81	1.37		
	PLACE1001092	2.31	2.47	4.68	5.8	4.18	3.9		
	PLACE1001098	0.93	2.62	4.53	5.49	4.05	3.17		
	PLACE1001100	1.31	2.58	2.48	4.27	4.17	3.37	*	+
20	PLACE1001104	1.95	4.09	4.54	3.39	3.42	4.47		
	PLACE1001114	1.56	6.54	4.33	5.17	3.78	3.27		
	PLACE1001118	2.52	5.77	6.12	6.21	6.14	5.1		
	PLACE1001123	2.86	5.3	7.53	7.08	8.51	7.63		
25	PLACE1001136	1.58	4.39	5.13	5.29	5.95	5.85		
	PLACE1001144	6.27	5.67	13.43	10.34	11	10.08		
	PLACE1001147	2.11	2.98	6.03	6.13	5.15	4.83		
	PLACE1001148	1.72	1.31	1.89	1.76	2.39	2.31		
	PLACE1001159	0.86	2.37	2.05	2.27	3.73	1.43		
30	PLACE1001168	8.87	14.52	15.09	25.46	23.18	30.79	*	+
	PLACE1001171	0.69	3.89	1.23	2.53	1.42	1.53		
	PLACE1001183	0.24	3.61	1.81	1.57	2.78	1.38		
	PLACE1001185	3.13	7.43	3.76	5	6.4	5.64		
	PLACE1001201	1.77	2.8	3.29	6.32	6.94	6.32	**	+
35	PLACE1001229	7.51	8.56	12.64	15.24	11.45	10.42		
	PLACE1001231	1.83	2.73	3.07	4.09	5.1	2.3		
	PLACE1001238	1.52	4.35	3.74	3.65	4.52	4.57		
	PLACE1001241	1.63	5.58	2.92	5.73	8.13	7.04		
	PLACE1001242	22.28	29.54	30.28	46.43	48.89	62.65	*	+
40	PLACE1001247	2.43	7.02	4.07	5.03	5.91	4.52		
	PLACE1001250	1.01	5.36	3.61	4.68	4.39	4.81		
	PLACE1001257	2.99	3.06	7.06	7.89	9.21	7.69		
	PLACE1001272	3.19	4.27	5.68	7.13	6.43	5.14		
	PLACE1001279	0.96	3.12	2.74	3.08	3.81	3.29		
45	PLACE1001280	1.08	4.75	2.68	4.98	4.45	2.86		
	PLACE1001294	1.91	7.23	6.91	4.88	5.57	6.18		
	PLACE1001295	4.16	9.94	7.53	8.55	11.85	8.43		
	PLACE1001300	2.46	7.9	4.31	4.65	14.73	4.95		
50	PLACE1001304	3	8.27	10.47	8.57	10.81	10.64		
	PLACE1001311	3.95	3.34	5.67	6.85	9.14	7.6	*	+
	PLACE1001323	2.17	2.95	5.12	5.66	8.43	5.5		
	PLACE1001325	0.88	1.95	3.71	2.84	3.56	3.27		
	PLACE1001340	5.18	6.99	9.8	8.69	12.02	10.48		
55	PLACE1001344	1.52	3.49	1.77	2.34	2.06	1.75		
	PLACE1001351	3.23	6.39	8.39	6.4	8.62	6.1		

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	PLACE1001366	1	4.49	4.02	4.19	4.6	3.72		
	PLACE1001377	3.02	4.97	5.1	7.91	7.28	5.83	*	+
	PLACE1001383	2.31	4.13	3.53	2.62	5.5	5.72		
5	PLACE1001384	1.81	3.23	2.89	2.05	3.43	3.15		
	PLACE1001387	1.65	3.64	3.7	3.03	4.83	3		
	PLACE1001395	3.72	6.64	6.54	7.01	7.61	7.73		
	PLACE1001399	3.71	6.58	9.31	7.37	8.61	9.22		
10	PLACE1001401	0.83	5.25	2.33	1.55	1.76	0.87		
	PLACE1001407	11.65	21.8	24.47	22.63	18.09	26.24		
	PLACE1001412	1.6	4.98	4.53	4.08	4.42	3.83		
	PLACE1001414	2.3	3.02	5.86	7.57	5.13	6.83		
	PLACE1001416	2.99	4.71	3.29	5.62	4.04	7.08		
15	PLACE1001433	33.62	33.05	51.64	49.1	58.33	55.88		
	PLACE1001440	1.95	3.99	3.96	3.6	3.53	2.1		
	PLACE1001456	1.64	5.5	4.26	4.15	4.87	4.49		
	PLACE1001464	32.76	28.05	47.41	53.22	68.42	61.32	*	+
	PLACE1001468	0.85	5.04	1.17	1.56	2.55	2.27		
20	PLACE1001484	1.31	4.85	2.96	4.25	5.8	3.04		
	PLACE1001500	0.92	2.22	2.14	2.72	3.34	3.26	*	+
	PLACE1001502	1.36	3.6	3.9	3.54	5.9	4.54		
	PLACE1001503	1.7	4.58	6.72	7.47	8.2	8.05		
	PLACE1001505	6.34	14.13	16.16	39.97	27.14	46.65	*	+
25	PLACE1001513	4.09	10.82	8.17	5.87	8.53	14.61		
	PLACE1001516	0.61	4.33	1.33	1.71	3.49	1.99		
	PLACE1001517	5.56	8.58	14.77	14.14	14.96	14.28		
	PLACE1001523	12.83	14.09	20.42	22.79	19.74	32.9		
30	PLACE1001526	5.12	4.89	8.42	9.51	9.11	6.89		
	PLACE1001534	2.12	5.12	3.58	3.62	5.55	3.99		
	PLACE1001536	0.61	2.5	1.52	2.11	3.2	1.9		
	PLACE1001545	17.97	23.9	38.46	33.78	45.13	66.08		
	PLACE1001551	2.55	6.26	6.15	4.72	6.59	6.71		
35	PLACE1001564	1.37	4.87	2.88	4.01	3.57	3.7		
	PLACE1001570	2.62	5.95	4.18	2.19	3.82	4.32		
	PLACE1001571	2.04	4.51	6.07	5.69	6.27	5.81		
	PLACE1001595	4.73	4.64	10.04	11.6	8.27	5.28		
	PLACE1001602	7.23	8.39	18.65	20.38	18.68	19.71		
40	PLACE1001603	2.01	3.83	5.37	6.86	5.86	4.56		
	PLACE1001608	3.44	7.22	5.9	5.82	7.73	8.7		
	PLACE1001610	3.77	8.4	8.22	9.26	9.49	9.85		
	PLACE1001611	1.94	7.34	3.65	2.28	3.85	1.88		
	PLACE1001629	0.78	6.77	2.24	3.62	3.36	3.52		
45	PLACE1001632	1.66	8.26	4.04	4.3	4.14	4.37		
	PLACE1001634	7.4	9.92	39.12	23.85	32.41	18.38		
	PLACE1001637	0.84	2.16	1.25	1.41	2.4	1.1		
	PLACE1001640	1.33	3.27	4.66	2.68	4.85	4.49		
	PLACE1001655	0.83	2.93	2.06	2.82	2.14	2.02		
50	PLACE1001672	1.84	7.04	4.01	3.3	4.41	4.09		
	PLACE1001676	1.38	8.49	3.54	4.63	4.77	3.85		
	PLACE1001683	12.79	23.62	24.61	25.33	30.22	27.13		
	PLACE1001691	3.41	12.29	6.72	9.03	8.96	9.83		
	PLACE1001692	1.47	2.96	5.25	5.87	5.6	5.13		
55	PLACE1001705	3.02	3.75	9.88	10.06	9.21	8.32		

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	PLACE1001716	1.68	3	2.61	2.24	3.79	3.58		
	PLACE1001720	1.49	2.62	2.21	1.56	2.45	1.71		
	PLACE1001728	1.43	6.19	4.24	1.96	2.04	2.51		
5	PLACE1001729	2.12	8.13	4.44	3.8	4.52	4.36		
	PLACE1001739	2.61	9.55	4.04	4.95	7.24	6.16		
	PLACE1001740	0.92	5.36	2.09	1.92	2.1	1.69		
	PLACE1001745	1.15	0.98	3.22	1.87	2.48	2.31		
10	PLACE1001746	1.04	2.25	2.55	4.64	3.4	2.82		
	PLACE1001748	4.74	7.01	8.18	8.19	6.58	5.96		
	PLACE1001753	2.06	3.54	3.29	7.44	5.57	5.82	*	+
	PLACE1001756	5.6	11.31	38.07	31.78	44.99	35.99		
	PLACE1001760	6.54	12.23	12.85	16.36	16.96	16.66	*	+
15	PLACE1001767	11.26	14.98	59.72	45.37	61.46	45.39		
	PLACE1001771	1.96	6.64	4.03	4.32	5.22	4.54		
	PLACE1001775	2.23	2.81	6.72	5.1	3.11	4.79		
	PLACE1001777	83.34	145.9	190.82	142.92	71.27	59.69		
	PLACE1001781	1.9	3.86	4.91	8.72	3.39	2.3		
20	PLACE1001783	0.76	3.21	2.06	4.84	2.09	1.54		
	PLACE1001786	1.77	6.61	2.72	3.7	3.32	2.6		
	PLACE1001788	5.16	9.07	7.14	10.52	8.74	9.32		
	PLACE1001795	1.92	4.4	4.82	5.42	4.61	5.42		
	PLACE1001799	0.69	3.62	2.11	1.86	2.83	1.97		
25	PLACE1001810	0.89	1.52	1.76	2.73	3.91	1.73		
	PLACE1001817	5.53	6.12	10.88	10.56	9.4	6.38		
	PLACE1001821	4.68	6.07	7.11	8.37	9.92	4.99		
	PLACE1001836	0.91	3.12	2.38	2.69	4.12	2.63		
30	PLACE1001844	1.55	5.1	3.48	4.42	4.36	4.09		
	PLACE1001845	3.62	8.38	7.39	7.88	7.55	9.93		
	PLACE1001858	2.56	6.58	3.52	5.26	7.48	6.05		
	PLACE1001869	3.13	7.15	4.85	6.09	6.46	5.66		
	PLACE1001890	11.74	11.92	21.45	173.44	255.31	125.13	*	+
35	PLACE1001897	9.19	13.85	16.44	22.22	23.13	12.95		
	PLACE1001902	10.13	12.6	21.53	22.74	27.67	12.77		
	PLACE1001904	1.38	3.72	1.51	2.45	2.53	2.35		
	PLACE1001907	3.36	6.76	5.71	7.67	5.67	5.59		
	PLACE1001910	83.6	82.16	135.34	301.29	325.42	244.59	**	+
40	PLACE1001912	1.53	6.6	3.36	5.54	5.48	4.85		
	PLACE1001918	17.31	22.95	30.16	31.14	40.44	40.02	*	+
	PLACE1001920	2.07	3.51	5.43	11.97	13.8	11.4	**	+
	PLACE1001928	3.06	2.96	4.67	5.29	9.7	5.31		
	PLACE1001930	1.17	3.92	2.2	2.9	4.73	3.22		
45	PLACE1001949	1.16	3.67	1.78	3.84	4.24	3.18		
	PLACE1001959	1.36	4.7	3.16	2.63	3.17	2.26		
	PLACE1001969	2.09	7.83	7.21	6.56	10.73	6.57		
	PLACE1001974	7.39	11.98	11.87	11.43	16.09	16.06		
	PLACE1001981	0.77	4.38	3.22	1.77	3.88	2.36		
50	PLACE1001983	3.81	4.12	5.32	5.92	6.16	5.72	*	+
	PLACE1001989	2.34	4.15	5.02	4.37	5.91	3.72		
	PLACE1002004	3.07	4.06	8.05	9.22	9.69	7.18		
	PLACE1002008	8.4	11.76	17	23.36	22.19	22.42	*	+
	PLACE1002015	26.96	30.92	67.62	105.75	88.42	94.15	*	+
55	PLACE1002044	3.79	8.07	5.86	4.64	6.39	6.4		

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	PLACE1002046	1.78	5.68	1.9	4.3	5.79	4.97		
	PLACE1002052	1.09	4.98	2.26	1.38	2.41	2.32		
	PLACE1002066	4.79	6.3	8.29	10.24	10.77	9.93	*	+
5	PLACE1002072	2.55	3.91	4.86	6	5.48	6	*	+
	PLACE1002073	0.51	2.83	2.29	2.35	4.06	2.91		
	PLACE1002080	1.81	6.49	6.13	4.76	6.82	5.72		
	PLACE1002081	1.66	6.13	4.06	3.74	4.86	4.3		
10	PLACE1002090	7.74	16.55	13.87	12.53	14.4	19.41		
	PLACE1002095	2.97	6.22	8.45	10.01	10.18	11.32	*	+
	PLACE1002102	4.26	8.56	8.81	9.47	9.56	10.67		
	PLACE1002109	2.57	5.08	3.81	4.66	6.17	6.32		
	PLACE1002115	1.75	3.57	2.48	2.78	4.26	2.59		
15	PLACE1002119	15.65	15.3	35.78	37.28	32.59	38.23		
	PLACE1002140	5.25	8.45	14.05	19.93	17.14	17.19	*	+
	PLACE1002150	1.54	8.26	4.25	3.23	5.36	4.12		
	PLACE1002153	1.6	5.75	2.58	3.47	5.76	4.48		
	PLACE1002157	0.87	2.96	1.72	1.76	3.28	3.73		
20	PLACE1002163	2.13	4.67	4.55	6.21	8.81	6.03		
	PLACE1002168	2.39	4.04	4.42	4.68	6.28	3.22		
	PLACE1002170	2.73	3.53	7.35	4.89	5.33	3.74		
	PLACE1002171	3.09	6.11	10.02	18.44	14.63	13.93	*	+
	PLACE1002180	3.16	6.23	6.77	4.63	8.54	8.39		
25	PLACE1002184	9.2	15.58	18.42	124.63	250.27	333.14	*	+
	PLACE1002200	1.35	5.67	2.38	2.97	2.89	2.26		
	PLACE1002205	3.3	6.47	18.07	17.08	18.38	14.61		
	PLACE1002213	2.2	4.16	4.93	5.52	8.03	6.03		
	PLACE1002219	1.05	1.91	2.23	3.33	3.53	1.96		
30	PLACE1002227	0.68	2.65	1.7	1.5	3.03	1.67		
	PLACE1002253	0.32	2.67	1.28	1.47	0.76	0.43		
	PLACE1002256	1.16	4.78	3.31	3.54	3.01	4.79		
	PLACE1002259	1.46	5.69	4.48	3.22	2.98	2.31		
	PLACE1002285	1.16	10.74	2.29	1.55	2.38	1.24		
35	PLACE1002301	9.42	17.5	14.68	12.7	10.48	11.7		
	PLACE1002310	4.28	10.16	9.86	8.82	7.87	9.94		
	PLACE1002311	1.84	2.94	3.87	2.96	2.87	2.03		
	PLACE1002319	2.31	2.64	2.94	3.21	3.23	3.92	*	+
40	PLACE1002329	0.56	2.54	2.5	4.07	3.58	3.07		
	PLACE1002333	1.34	3.1	1.96	1.22	2.44	2		
	PLACE1002342	4.19	9.04	9.44	5.06	8.52	8.17		
	PLACE1002343	0.49	6.98	2.94	2.08	1.9	2.52		
	PLACE1002355	1.31	9.39	2.36	3.33	4.35	2.63		
45	PLACE1002358	1.15	7.94	3.3	2.6	2.65	2.13		
	PLACE1002359	1.91	2.17	3.47	4.7	3.91	3.42		
	PLACE1002374	29.69	28.18	54.19	53.9	34.73	36.14		
	PLACE1002376	3.58	5.91	7.86	6.23	6.82	6.56		
	PLACE1002379	6.24	7.66	6.63	10.13	9.68	10.9	**	+
50	PLACE1002386	0.86	5.32	1.35	1.87	2.05	1.51		
	PLACE1002395	3.69	9.97	17.13	16.43	20.62	16.16		
	PLACE1002399	2.38	11.09	3.42	5.31	10.38	7.39		
	PLACE1002407	1.09	5.22	2.31	2.3	4.01	3.66		
	PLACE1002433	1.63	2.17	2.97	2.96	4.35	3.66		
55	PLACE1002437	0.79	1.4	1.47	1.41	3.28	1.35		

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	PLACE1002438	0.74	2.38	1.96	1.8	2.43	3.38		
	PLACE1002446	4.64	8.42	5.95	10.27	8.88	11.99	*	+
	PLACE1002447	1.26	6.06	2.05	3.92	3.14	4.32		
5	PLACE1002450	1.19	5.92	3.24	4.32	4.21	5.05		
	PLACE1002462	0.81	4.02	2.94	3.51	2.99	3.13		
	PLACE1002465	0.96	4.69	2.2	2.69	4.31	2.24		
	PLACE1002474	1.61	2.26	3.23	3.85	4.41	3.6	*	+
	PLACE1002477	11.11	14.51	32.39	44.06	41.42	26.68		
10	PLACE1002493	3.39	4.1	10.1	14.39	16.66	9.49		
	PLACE1002497	0.68	2.81	0.67	1.45	0.93	0.99		
	PLACE1002499	2.12	4.73	3	5.98	6.44	5.28	*	+
	PLACE1002500	2.61	6.52	7.36	7.58	10.45	7.25		
	PLACE1002514	0.3	4.49	1.84	1.74	2.47	1.75		
15	PLACE1002518	2.86	7.65	6.9	5.62	7.55	4.67		
	PLACE1002529	1.14	1.56	2.21	3.19	3.4	1.44		
	PLACE1002532	1.31	1.82	3.18	5.75	4.94	5.59	**	+
	PLACE1002536	3.59	3.75	3.44	5.84	6.07	3.85		
20	PLACE1002537	1.63	4.06	2.7	2.69	4.07	3.08		
	PLACE1002539	1.86	5.68	2.75	4.53	5.29	4.78		
	PLACE1002547	6.09	8.06	7.3	12.32	11.02	11.26	**	+
	PLACE1002571	2.84	6.85	5.19	6.84	8.65	6.23		
	PLACE1002578	3.57	8.34	8.35	11.11	12.19	8.11		
25	PLACE1002583	1.33	1.61	2.32	3.18	4.02	2.46		
	PLACE1002591	0.82	1.62	2.34	3.25	4.43	1.92		
	PLACE1002598	6.56	10.95	12.39	11.93	9.04	7.74		
	PLACE1002604	1.73	3.57	2.69	3.75	5.38	3.51		
	PLACE1002612	2.89	8.47	5.95	11.25	10.88	8.06		
30	PLACE1002625	1.25	4.79	3.18	2.7	3.25	1.82		
	PLACE1002638	2.94	8.01	6.66	7.78	6.81	7.29		
	PLACE1002655	1.39	6.51	5.57	7.19	7.62	6.46		
	PLACE1002665	4.57	3.88	5.4	7.47	12.16	10.75	*	+
	PLACE1002685	0.58	1.12	1.3	0.67	2.43	0.98		
35	PLACE1002692	7.42	8.56	16.7	19.27	22.67	16.29		
	PLACE1002714	1.8	3	2.11	2.43	3.14	2.24		
	PLACE1002721	2.94	4.37	3.88	5.88	7.1	4.28		
	PLACE1002722	0.92	5.42	1.97	1.37	3.28	1.85		
	PLACE1002726	1.6	6.24	3.66	4.6	5.7	5.26		
40	PLACE1002756	1.57	4.5	7.04	5.92	9.63	7.78		
	PLACE1002768	1.05	3.72	2.16	2.1	2.34	1.71		
	PLACE1002772	0.54	2.15	1.32	2.49	2.86	2.3		
	PLACE1002775	4.33	4.71	9.15	7.05	7.08	8.67		
	PLACE1002780	185.63	218.72	325.36	272.21	244.38	305.38		
45	PLACE1002782	0.4	3.76	1.1	1.62	1.69	1.14		
	PLACE1002794	1.5	6.71	3.27	2.26	4.59	4.36		
	PLACE1002795	1.92	6.45	0.81	2.37	3.63	2.77		
	PLACE1002811	0.6	1.57	1.34	1.9	1.46	1.16		
50	PLACE1002815	6.39	7	10.49	7.24	3.16	9.21		
	PLACE1002816	8.5	9.72	9.05	7.22	8.2	7.97	*	-
	PLACE1002822	0.58	2.51	2.05	2.2	2.87	1.94		
	PLACE1002833	9.98	15.11	16.78	15.42	15.99	16.56		
	PLACE1002834	3.2	8.08	6.57	6.23	6.79	8.41		
55	PLACE1002835	0.62	4.14	1.72	0.85	1.83	1.79		

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	PLACE1002839	1.13	5.75	2.72	2.89	4.72	2.81	
	PLACE1002851	1.52	1.87	1.41	1.98	2.15	2.7	
	PLACE1002853	4.18	6.23	9.15	6.26	5.6	7	
5	PLACE1002881	3.42	5.2	11.04	8.35	11.57	10.26	
	PLACE1002901	9.66	12.66	20.09	24.14	25.51	30.67	* +
	PLACE1002904	0.89	7.35	1.41	1.98	1.95	3.09	
	PLACE1002905	1.36	5.46	3.26	4.04	4.46	3.4	
10	PLACE1002908	1.6	5.19	3.18	3.84	5.27	3.81	
	PLACE1002911	3.91	6.96	6.9	4.66	7.89	6.75	
	PLACE1002941	1.57	2.2	2.48	3.94	2.02	2.31	
	PLACE1002950	9.59	9.15	14.74	5.31	8.02	14.51	
	PLACE1002955	47.83	40.69	72.7	82.17	62.5	84.64	
15	PLACE1002958	19.36	26.92	35.27	35.6	35.35	59.02	
	PLACE1002962	1.03	4.03	2.2	1.41	2.63	1.67	
	PLACE1002967	1.34	4.83	3.19	4.37	3.52	2.81	
	PLACE1002968	1.2	5.14	2.7	2.55	3.05	1.81	
	PLACE1002976	8.94	12.08	24.23	24.5	36.89	30.05	
20	PLACE1002991	2.68	3.05	6.66	3.49	4.56	3.6	
	PLACE1002993	2.72	3.86	5.52	8.21	6.92	5.56	
	PLACE1002996	2.02	3.03	3.43	5.54	3.52	3.01	
	PLACE1003010	1.91	3.69	4.27	4.31	3.86	3.32	
	PLACE1003025	2.85	7.01	6.1	8.57	11.37	10.11	* +
25	PLACE1003027	5.02	13.08	9.31	8.55	12.45	12.76	
	PLACE1003044	1.95	8.24	2.61	3.64	4.16	2.74	
	PLACE1003045	1.41	7.75	1.77	1.88	2.64	1.01	
	PLACE1003052	2.19	3.16	5.74	4.44	3.6	1.99	
30	PLACE1003083	1.59	3.04	3.23	3.06	1.61	2.25	
	PLACE1003085	3.91	6.19	5.6	9.46	5.89	3.33	
	PLACE1003092	3.94	4.87	6.25	7	5.6	6.17	
	PLACE1003097	0.37	3.06	1.44	2.12	1.88	1.63	
	PLACE1003100	1.65	7.1	4.2	3.88	4.74	4.29	
35	PLACE1003108	1.26	10.37	2.91	3.32	4.44	2.39	
	PLACE1003115	11.39	18.3	58.59	73.64	99.24	69.1	* +
	PLACE1003120	3.1	3.08	9.71	11.34	8.32	10.19	
	PLACE1003135	0.72	2.04	1.09	1.56	2.89	1.08	
	PLACE1003136	3.95	5.82	6.05	9.03	6.55	7.34	
40	PLACE1003141	2.04	2.97	2.1	1.97	2.49	1.8	
	PLACE1003145	1.21	4.17	2.52	6.24	6.88	7.67	* +
	PLACE1003147	2.87	7.85	5.71	5.02	5.25	6.28	
	PLACE1003153	0.54	7.63	2.14	1.66	3.2	1.82	
	PLACE1003163	6.09	13.55	8.19	8.39	14.09	12.26	
45	PLACE1003172	23.21	21.74	44.19	47.78	43.17	39.52	
	PLACE1003174	2.31	2.49	3.75	4.3	3.55	1.68	
	PLACE1003176	0.47	2	1.89	2.88	1.27	1.46	
	PLACE1003181	1.72	4.19	2.72	2.5	2.76	2.36	
	PLACE1003184	0.76	3.92	1.53	1.91	1.49	2.06	
50	PLACE1003190	2.39	9.81	8.67	10.73	7.98	10.34	
	PLACE1003200	0.29	4.48	1.84	0.72	1.92	1.16	
	PLACE1003205	3.94	7.07	9.68	6.82	10.38	7.2	
	PLACE1003209	1.43	2.18	2.62	2.28	1.82	2.89	
	PLACE1003214	0.83	1.3	2	2.15	2.44	1.81	
55	PLACE1003229	2.08	2.78	2.9	2.78	3.35	3.48	

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	PLACE1003238	0.46	2.34	1.24	1.35	2	0.75	
	PLACE1003249	1.87	5.04	4.7	7.33	7.56	5.89	
	PLACE1003256	3.47	7.69	7.94	8.82	7.68	6.08	
5	PLACE1003258	1.03	3.81	3.48	2.42	2.19	0.87	
	PLACE1003279	3.09	7.19	9.02	11.15	13.56	11.58	* +
	PLACE1003294	0.95	1.54	1.59	1.57	1.25	2.64	
	PLACE1003296	1.49	2.6	2.45	2.59	3.11	2.4	
10	PLACE1003297	7.52	10.15	31.88	23.01	23.49	19.3	
	PLACE1003302	3.92	5.16	6.99	5.8	4.72	5.47	
	PLACE1003334	1.51	4.41	1.91	2.4	3.59	3.09	
	PLACE1003337	13.69	16.3	29.83	28.53	34.27	25.76	
	PLACE1003342	1.05	4.07	1.89	2.15	2.35	1.97	
15	PLACE1003343	1.07	4.98	1.61	2.02	2.75	2.12	
	PLACE1003344	6.25	5.33	12.83	11.18	11.35	11.98	
	PLACE1003353	19.67	16.04	40.09	37.78	42.55	40.26	
	PLACE1003361	1.82	3.64	3.72	5.85	5.31	4.6	* +
	PLACE1003366	1.45	4.35	3.63	3.22	3.33	2.97	
20	PLACE1003369	2.75	4.51	3.49	3.29	3.25	4.62	
	PLACE1003372	2.08	5.73	2.68	5.45	4.72	3.39	
	PLACE1003373	2.85	7.37	6.62	8.8	11.81	9.89	
	PLACE1003375	1.42	4.91	1.92	2.59	2.95	3.21	
	PLACE1003378	0.94	0.94	0.98	0.7	1.66	1.08	
25	PLACE1003383	0.87	1.55	2.33	1.59	3.15	1.57	
	PLACE1003394	10.55	12.49	24.08	11.75	22.99	17.27	
	PLACE1003401	0.79	3.91	1.34	1.03	2.13	1.04	
	PLACE1003405	1.5	3.97	2.22	2.54	2.46	2.04	
	PLACE1003407	2.39	6.06	5.16	3.96	6.3	4.02	
30	PLACE1003420	3.26	7.69	6.19	6.8	10.92	8.7	
	PLACE1003428	0.63	3.3	2.62	2.07	2.94	1.96	
	PLACE1003432	6.14	5.81	8.2	6.64	7.05	5.42	
	PLACE1003438	0.45	2.66	0.93	2.41	2.34	1.99	
	PLACE1003452	1.87	5.02	5.08	4.53	3.43	3.84	
35	PLACE1003454	2.49	5.59	7.34	7.31	6.95	5.61	
	PLACE1003455	2.58	4.26	2.35	2.97	3.01	3.17	
	PLACE1003456	3.22	7.74	8.62	6.9	7.2	7.79	
	PLACE1003460	6.39	13.35	14.87	13.02	16.76	12.86	
40	PLACE1003478	1.15	1.71	0.86	2.33	2.07	1.24	
	PLACE1003484	12.06	12.21	45.33	28.12	31.5	34.2	
	PLACE1003493	1.61	4.72	4.9	3.84	5.96	5.08	
	PLACE1003503	85.45	87.35	107.79	115.17	111.85	172.81	
	PLACE1003505	1.99	6.77	4.78	7.44	6.63	8.87	
45	PLACE1003516	0.86	6.78	2.7	2.8	3.95	2.39	
	PLACE1003519	17.58	26.29	50.41	45.77	36.97	58.75	
	PLACE1003520	14.18	25.48	35.96	25.73	31.4	32.19	
	PLACE1003521	2.71	3.64	4.93	5.97	4.71	7.4	
	PLACE1003525	8.45	11.81	45.05	33.94	43.71	36.88	
50	PLACE1003528	39.18	44.68	136.4	106.04	122.76	127.22	
	PLACE1003529	1.46	4.26	3.29	2.4	3.94	3.83	
	PLACE1003537	4.41	9.05	11.05	11.36	13.77	13.3	
	PLACE1003549	1.1	5.02	4.59	5.61	6.01	5.93	
	PLACE1003553	1.6	5.89	3.88	4.02	4.17	4.23	
55	PLACE1003566	5.93	9.8	17.51	13.03	19.09	14.58	

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	PLACE1003568	3.01	2.71	5.76	5.69	4.43	4.04	
	PLACE1003573	0.98	2.43	1.19	2.16	1.87	1.48	
5	PLACE1003575	2.16	3.09	3.44	3.34	3.5	4.15	
	PLACE1003583	0.97	3.45	3.34	2.29	4.16	2.23	
	PLACE1003584	1.23	4.46	4.01	3.56	3.8	2.65	
	PLACE1003592	4.4	8.48	9.48	7.11	10.48	9.53	
	PLACE1003593	0.84	5.55	2.4	2.23	3.02	1.55	
10	PLACE1003594	4.24	6.76	6.01	5.78	6.68	7.36	
	PLACE1003596	13.77	11.31	22.53	15.68	17.69	8.25	
	PLACE1003598	2.83	3.63	5.02	4.89	3.7	2.95	
	PLACE1003602	1.8	4.24	6.36	4.37	3.54	2.68	
	PLACE1003605	17.43	21.72	45.86	94.65	95.6	91.55	** +
15	PLACE1003611	2.34	5.18	6.07	5.65	7.14	6	
	PLACE1003618	0.67	7.39	2.09	1.58	2.4	1.32	
	PLACE1003625	1.78	10.41	2.75	3.33	5.48	2.8	
	PLACE1003626	8.77	15.99	17.14	10.87	14.46	13.19	
20	PLACE1003630	1.8	2.57	5.8	7.05	4.67	5.86	
	PLACE1003635	2.15	1.83	3.19	2.96	2.82	2.44	
	PLACE1003638	1.3	2.58	3	5.21	4.19	3.13	
	PLACE1003644	4.01	5.7	7.25	7.81	9.13	8.76	* +
	PLACE1003654	2.56	6.14	4.04	3.54	6.96	6.4	
25	PLACE1003656	2.69	7.79	6.12	6.54	5.63	4.77	
	PLACE1003660	0.26	9.54	3.5	3.08	4.92	4.11	
	PLACE1003669	2.43	9.05	3.67	2.59	4.26	3.08	
	PLACE1003670	5.37	5.7	9.44	11.01	8.26	8.76	
	PLACE1003671	1.66	1.22	3.57	3.11	2.57	1.57	
30	PLACE1003697	7.27	7.99	9.8	8.23	6.06	6.42	
	PLACE1003704	3.12	3.97	5.17	5.96	7.25	5.97	* +
	PLACE1003709	0.89	2.63	0.8	1.19	1.24	2.44	
	PLACE1003711	0.74	5.48	1.35	1.87	1.8	1.39	
	PLACE1003723	1.07	6.99	4.7	4.2	5.31	4.16	
35	PLACE1003724	3.31	10.74	9.1	9.11	11.79	10.49	
	PLACE1003737	2.14	2.21	4.72	3.35	3.1	3.29	
	PLACE1003738	1.06	1.94	3.13	3.96	3.92	3.41	
	PLACE1003742	2.25	3.58	5.71	6.81	6.18	2.85	
	PLACE1003744	6.13	8.86	14.6	16.21	17.96	19.13	* +
40	PLACE1003758	0.85	4.55	0.96	2	1.46	1.16	
	PLACE1003760	13.44	18.68	27.23	31.82	20.52	22.79	
	PLACE1003762	1.45	4.97	3.7	3.77	3.78	3.49	
	PLACE1003765	1.18	5.23	3.45	2.01	3.1	2.11	
45	PLACE1003768	0.36	1.14	1.36	1.45	2.75	1.07	
	PLACE1003771	1.28	1.94	2.07	1.84	3.13	1.43	
	PLACE1003772	34.15	38.19	97.86	62.42	64.06	52.43	
	PLACE1003783	1.48	3.02	2.22	18.65	19.53	16.61	** +
	PLACE1003784	0.69	3.92	0.87	2.09	2.19	2.68	
50	PLACE1003788	0.4	4.92	1.06	1.85	1.71	0.32	
	PLACE1003795	1.01	4.1	3.57	4.73	4.38	3.54	
	PLACE1003827	13.83	20.46	20.72	22.48	30.84	25.92	
	PLACE1003833	0.98	1.49	3.9	3.65	4.33	3.31	
	PLACE1003839	22.55	19.18	52.95	50.39	56.11	43.86	
55	PLACE1003845	6.09	6.88	11.72	24.98	19.99	10.6	
	PLACE1003850	3.16	4.84	7.19	5.45	5.95	6.39	

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	PLACE1003852	0.25	3.36	1.09	0.99	1.58	1.05	
	PLACE1003858	1.34	4.42	1.99	2.04	1.85	2.92	
	PLACE1003861	0.95	4.51	1.63	2.98	2.78	1.73	
5	PLACE1003864	0.94	5.5	2.74	2.88	3.86	2.69	
	PLACE1003870	3.84	3.4	13.2	10.71	16.12	12.03	
	PLACE1003885	1.33	1.42	1.59	3.07	3.76	2.38	* +
	PLACE1003886	4.56	6.01	5.75	9.27	6.87	4.3	
10	PLACE1003888	0.75	3.79	1.96	2.87	3.42	2.68	
	PLACE1003892	4.93	6.91	20.79	17.21	22.33	14.87	
	PLACE1003900	2.27	5.92	7.17	6.34	9.75	6.6	
	PLACE1003902	1.91	7.39	5.25	5.43	8.07	6.29	
	PLACE1003903	0.42	5.07	2.94	2.55	3.5	2.59	
15	PLACE1003915	8.15	7.04	10.78	8.31	9.79	9.84	
	PLACE1003918	1.88	2.45	4.75	3.47	6.26	3.75	
	PLACE1003923	2.06	3.73	5.63	2.7	5.54	3.32	
	PLACE1003932	3.99	5.16	5.47	4.06	7.58	5.09	
	PLACE1003936	1.02	3.82	2.81	3.63	2.42	2.78	
20	PLACE1003966	3.11	7.43	7.76	4.89	7.32	4.21	
	PLACE1003968	1.68	5.68	5.94	3.33	4.26	4.57	
	PLACE1004018	25.49	33.73	48.16	32.56	40.53	28.62	
	PLACE1004020	8.91	10.18	13.26	11.42	18.03	24.15	
	PLACE1004028	0.41	2.55	1.3	1.38	1.23	1.91	
25	PLACE1004034	3.56	4.53	5.22	8.42	9.03	13.04	* +
	PLACE1004042	17.25	20.19	68.35	79.51	93.32	79.44	* +
	PLACE1004078	1.14	4.1	3.3	4.95	6.51	4.45	
	PLACE1004103	5.54	10.93	13.98	13.77	15.09	14.14	
30	PLACE1004104	5.94	12.29	27.78	24.18	34.98	29.71	
	PLACE1004113	1.37	3.7	3.28	2.75	3.27	1.29	
	PLACE1004114	1.12	2.55	2.23	2.84	2.49	2.93	
	PLACE1004118	1.58	3.52	2.09	2.74	3.64	2.5	
	PLACE1004128	4.4	6.84	5.66	6.61	8.13	9.01	
35	PLACE1004130	2.25	4.83	8.35	6.86	9.26	6.73	
	PLACE1004149	3.59	7.3	9.86	10.23	13.29	10.12	
	PLACE1004156	3.61	7.91	10.12	11.66	17.62	13.31	
	PLACE1004160	5.45	9.54	14.36	13.1	19.65	14.53	
	PLACE1004161	2.2	4.86	3.54	4.85	5.73	7.48	
40	PLACE1004166	5.61	5.81	9.91	8.3	8.66	11.2	
	PLACE1004168	3.35	4.97	3.73	4.73	6.65	6.79	
	PLACE1004170	0.78	3.28	1.93	2.98	3.42	2.76	
	PLACE1004178	0.83	5.23	2.37	2.4	2.59	2.36	
	PLACE1004183	0.89	7.99	4.41	3.53	4.32	4.84	
45	PLACE1004197	0.64	5.14	1.55	1.73	3.54	1.65	
	PLACE1004199	1.66	4.52	4.09	3.78	5.88	4.35	
	PLACE1004203	1.8	3.57	4.17	2.43	3.62	2.83	
	PLACE1004242	3.8	5.64	11.04	8.55	8.14	8.64	
	PLACE1004249	31.4	56.31	117.88	127.93	152.54	151.22	* +
50	PLACE1004255	0.79	2.65	1.26	2.59	2.15	1.93	
	PLACE1004256	9.06	11.68	13.63	14.66	14.18	23.37	
	PLACE1004257	2.63	7.95	6.48	7.89	8.8	8.64	
	PLACE1004258	1.87	5.21	3.13	4.59	3.15	3.11	
	PLACE1004270	0.72	3.8	2.5	2.7	4.01	1.65	
55	PLACE1004272	1.34	3.68	3.73	3.86	5.38	6.15	

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	PLACE1004273	92.91	89.59	212.62	212.05	129.56	99.82	
	PLACE1004274	2.09	3.61	6.51	6.42	7.14	6.74	
	PLACE1004277	2.3	4.4	5.76	6.45	7.7	6.04	
5	PLACE1004279	0.54	3.39	2.23	3.16	2.64	2.02	
	PLACE1004282	2.43	8.25	6.62	4.22	5.56	4.49	
	PLACE1004284	4.59	11.31	7.84	7.38	8.16	7.15	
	PLACE1004289	1.28	7.85	2.46	3.06	3.63	2.1	
10	PLACE1004299	0.33	6.41	1.38	1.54	2.67	1.83	
	PLACE1004302	1.01	2.98	3.27	2.41	2.45	1.12	
	PLACE1004305	1.11	2.09	1.9	1.9	1.82	1.78	
	PLACE1004316	2.3	4.48	5.4	6.06	3.85	4.52	
	PLACE1004322	2.49	3.41	5.25	6.35	7.14	5.75	* +
15	PLACE1004325	2.43	6.38	3.84	3.85	3.66	4	
	PLACE1004332	1.21	7.18	2.8	3.72	3.46	3.01	
	PLACE1004336	2.87	9.6	5.36	6.88	9.21	6.71	
	PLACE1004346	0.47	7.22	2.58	1.87	2.54	1.69	
	PLACE1004358	1.3	2.41	2.41	2.46	2.09	2.03	
20	PLACE1004376	11.07	10.15	23.35	19.16	17.04	16.46	
	PLACE1004384	0.65	3.46	1.46	1.92	2.48	2.1	
	PLACE1004385	1.4	2.89	1.69	3.52	1.88	2.67	
	PLACE1004388	1.79	5.73	4.27	3.44	4.87	3.04	
	PLACE1004405	2.16	8.39	4.42	13.36	14.48	16.74	** +
25	PLACE1004407	5.05	13.12	13.37	11.2	16.24	11.85	
	PLACE1004424	0.37	5.78	0.85	1.7	1.81	1.58	
	PLACE1004425	1.14	1.94	3.57	3.28	3.27	3.44	
	PLACE1004427	1.96	3.31	4.56	4.67	4.22	3.24	
30	PLACE1004428	0.88	2.05	2.17	2.66	2.08	2.62	
	PLACE1004433	5.7	8.3	10.82	12.94	15.67	12.05	* +
	PLACE1004435	0.72	4.17	1.43	1.95	1.9	2.15	
	PLACE1004437	4.05	7.68	14.2	11.07	13.01	12.37	
	PLACE1004441	7.82	11.68	34.06	30.75	43.19	26.41	
35	PLACE1004446	1.5	4.36	0.9	1.03	1.35	1.39	
	PLACE1004450	0.33	1.46	1.34	2.57	1.71	0.7	
	PLACE1004451	0.51	1.45	2.14	1.89	2.69	0.88	
	PLACE1004456	8.22	9.7	10.97	16.68	10.4	4.18	
	PLACE1004458	3.39	4.81	3.66	7.77	7.05	8.24	** +
40	PLACE1004460	0.84	4.58	2.1	2.91	2.69	1.75	
	PLACE1004467	5.31	6.81	10.65	7.67	10.14	10.48	
	PLACE1004471	2.65	5.93	6.64	6.79	7.34	6.14	
	PLACE1004473	1.16	4.66	3.5	3.18	3.23	3.21	
	PLACE1004475	14.03	16.41	32.49	31.09	32.51	18.17	
45	PLACE1004482	8.37	6.7	10.79	10.04	9.76	9.15	
	PLACE1004491	0.39	2.51	1.49	1.19	2.68	1.3	
	PLACE1004492	61.52	74.8	127.94	129.92	127.64	123.82	
	PLACE1004506	10.71	14.35	14.4	8.45	11.13	10.03	
	PLACE1004507	2.9	7.37	5.09	7.15	6.87	6.18	
50	PLACE1004510	2.51	6.23	6.33	6.59	7.8	8.16	
	PLACE1004516	0.98	7.36	2.12	2.79	3.78	2.22	
	PLACE1004518	1.64	1.78	3.03	2.41	3.88	2.83	
	PLACE1004519	0.17	0.82	0.62	1.43	2.79	1.51	* +
	PLACE1004520	6.08	8.09	10.06	7.44	9.11	2.52	
55	PLACE1004530	33.19	43.86	68.13	41.86	27.72	38.09	

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	PLACE1004545	1.13	3.83	2.12	3.03	3.31	3.65	
	PLACE1004547	5	7.61	7.82	8.66	11.2	10.28	
	PLACE1004548	1.69	6.73	4.43	5.93	8.48	6.5	
5	PLACE1004550	2.27	6.24	6.67	5.92	6.78	6.15	
	PLACE1004551	0.8	2.16	1.62	2.14	2.21	1.95	
	PLACE1004559	2.9	2.89	5.11	4.45	6.75	4.82	
	PLACE1004562	8.67	11.27	16.07	13.01	14.38	13.34	
	PLACE1004564	1.84	5.19	4.36	4.64	5.98	4.49	
10	PLACE1004604	1.69	4.21	9.88	2.49	4.34	1.97	
	PLACE1004611	2.73	5.87	4.89	3.86	4.17	3.99	
	PLACE1004629	9.42	15.75	19.92	23.93	30.49	29.01	* +
	PLACE1004630	16.66	20.82	35.1	16.76	23.04	19.17	
15	PLACE1004637	5.03	8.82	10.34	6.61	9.17	8.29	
	PLACE1004645	36.5	39.28	92.04	85.16	87.94	74.59	
	PLACE1004646	1.07	2.91	2.87	3.68	2.19	2.28	
	PLACE1004648	0.8	3.42	2.52	2.53	3.15	1.22	
	PLACE1004655	45.95	58.09	130.94	112.14	126.25	99.01	
20	PLACE1004658	2.4	7.34	6.31	6.64	8.37	6	
	PLACE1004664	1.26	4.83	1.3	3.02	2.65	1.89	
	PLACE1004672	2.32	6.79	8.02	6.3	7.51	7.14	
	PLACE1004674	9.4	11.97	14.7	8.3	9.75	15.25	
	PLACE1004681	1.97	3.84	5.62	5.05	5.69	4.39	
25	PLACE1004686	2.74	4.33	7.46	9.22	10.77	8.59	* +
	PLACE1004690	10.64	13.43	19.62	21.75	19.21	31.72	
	PLACE1004691	1.14	6.71	3.71	2.92	4.13	2.75	
	PLACE1004693	1.34	7.54	4.89	3.91	4.59	5.97	
30	PLACE1004701	13.01	18.45	24.24	25.21	24.46	25.1	
	PLACE1004705	1.29	3.33	2.27	1.8	1.96	1.47	
	PLACE1004708	37.69	46.37	80.19	41.34	39.66	50.98	
	PLACE1004716	6.37	8.81	11.08	4.22	12.55	14.26	
	PLACE1004722	1.31	3.05	2.6	2.26	3.28	2.51	
	PLACE1004736	5.25	7.71	7.6	9.16	8.89	11.63	
35	PLACE1004737	5.42	12.71	16.14	8.15	11.23	13.78	
	PLACE1004740	4.88	9.06	8.22	7.37	7.93	8.2	
	PLACE1004743	1.31	4.04	3.1	1.97	4	3.55	
	PLACE1004751	0.98	2.89	2.88	2.75	3.74	3.06	
	PLACE1004757	3.45	4.34	10.53	8.4	9.6	7.22	
40	PLACE1004761	6.41	7.32	12.59	9.99	10.44	9.72	
	PLACE1004773	1.05	2.34	1.7	1.94	2.31	2.72	
	PLACE1004775	0.35	3.26	1.37	1.29	2.14	1.07	
	PLACE1004777	2.1	7.57	2.97	3.68	4.25	4.4	
45	PLACE1004793	0.83	4.58	1.37	1.9	2.06	1.25	
	PLACE1004796	6.65	8.7	13.08	7.79	8.57	7.88	
	PLACE1004804	0.99	4.46	3.25	2.44	2.38	3.22	
	PLACE1004813	4.55	7.11	9.84	6.45	5.19	5.45	
	PLACE1004814	7.16	11.76	17.62	15.83	11.39	10.1	
50	PLACE1004815	0.7	2.81	2.43	3.12	2.61	3.44	
	PLACE1004816	1.16	2.63	2.04	2.36	2.26	1.84	
	PLACE1004824	3.25	7.37	5.27	8.1	9.13	8.85	
	PLACE1004827	1.4	10.89	3.17	2.57	3.05	1.3	
	PLACE1004836	1.72	12.95	4.26	6.25	7.99	4.49	
55	PLACE1004838	1.35	8.81	2.2	2.49	2.34	1.68	

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	PLACE1004840	1.59	2.06	2.21	1.85	2.08	1.37	
	PLACE1004842	0.86	1.98	1.89	1.98	1.78	2.33	
	PLACE1004850	0.81	2.35	1.63	1.83	2.76	2.36	
5	PLACE1004868	0.81	2.97	2.04	1.62	2.23	2	
	PLACE1004885	1.5	7.09	3.51	3.4	6.03	4.77	
	PLACE1004886	1.87	8.53	2.76	3.33	5.12	4.93	
	PLACE1004887	18.14	34.01	58.51	36.9	38.66	30.33	
10	PLACE1004896	8.39	14.15	15.4	9.39	11.14	14.03	
	PLACE1004900	1.75	2.7	6.69	5.66	5.74	4.44	
	PLACE1004902	5.42	6.25	9.27	6.39	4.2	3.6	
	PLACE1004904	1.7	4.66	2.52	6.49	4.78	3.03	
	PLACE1004911	0.69	2.5	1.12	5.95	4.82	6.09	** +
15	PLACE1004913	3.63	5.72	7.38	4.49	5.45	4.79	
	PLACE1004918	1.3	6.69	2.05	2.39	3.24	2.64	
	PLACE1004930	2.74	8.84	5.93	10.63	16.57	14.71	* +
	PLACE1004934	1.14	4.3	3.34	2.97	2.03	2.5	
	PLACE1004937	2.1	4.03	4.91	2.74	3.59	2.36	
20	PLACE1004949	4.32	4.98	7.67	8.53	8.48	6.04	
	PLACE1004969	0.74	1.74	1.99	1.39	2.34	1.4	
	PLACE1004970	0.45	2.18	1.2	1.43	1.31	1.01	
	PLACE1004972	1.63	6.56	2.69	5.66	3.17	4.76	
	PLACE1004974	1.27	5.21	4.2	5.6	5.7	5.62	
25	PLACE1004975	0.59	2.84	1.11	1.94	1.98	1.24	
	PLACE1004979	1.58	4.06	4.26	4.91	5.69	4.75	
	PLACE1004982	5.66	6.45	9.74	10.03	10.67	5.65	
	PLACE1004985	1.4	1.47	1.46	2.5	2.17	1.2	
	PLACE1005003	2.85	4.22	6	6.05	6.37	5.78	
30	PLACE1005004	0.47	3.36	0.92	1.5	0.73	0.85	
	PLACE1005005	3.35	6.9	5.32	6.67	9.65	7.17	
	PLACE1005011	6.03	11.12	35.8	37.66	56.97	36.62	
	PLACE1005026	0.79	4.18	2.29	2.44	2.49	2.16	
	PLACE1005027	2.46	6.72	6.69	5.36	6.92	5.68	
35	PLACE1005031	1.21	1.47	3.69	5.72	7.1	4.6	* +
	PLACE1005036	2.27	3.6	6.83	9.08	8.91	7.53	* +
	PLACE1005041	2.5	2.84	2.84	5.05	4.41	3.25	* +
	PLACE1005046	2.23	4.11	4.56	6.04	3.92	4.33	
40	PLACE1005047	0.23	3.19	2.6	1.43	1.23	2.1	
	PLACE1005052	4.24	8.53	6.36	8.08	8.15	8.1	
	PLACE1005055	2.54	7.45	4.66	7.2	6.45	5.62	
	PLACE1005066	4.33	8.26	7.58	12.9	14.14	16.49	** +
	PLACE1005077	1.17	0.68	1.2	2.1	2.43	1.54	* +
45	PLACE1005085	1.41	1.97	3.06	3.34	4.14	3.45	
	PLACE1005086	1.93	3.77	5.17	5.62	7.78	4.79	
	PLACE1005088	24.66	32.47	46.03	43.45	31.47	27.46	
	PLACE1005089	1.57	4.78	3.15	2.52	3.67	3.14	
	PLACE1005101	3.37	8.11	5.46	6.11	8.96	6.39	
50	PLACE1005102	2.56	7.14	5.01	4.11	5.51	3.8	
	PLACE1005108	2	6.08	5.87	6.58	6.19	5.09	
	PLACE1005110	1.34	1.89	3.08	1.75	2.75	2.15	
	PLACE1005111	1.31	1.34	1.23	1.45	2.17	1.54	
	PLACE1005123	26.23	26.21	47.58	34.26	49.34	34.98	
55	PLACE1005124	3.2	4.66	4.18	4.2	6.91	5.44	

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	PLACE1005128	9.54	8.89	18.22	16.37	16.36	16.13	
	PLACE1005130	2.65	6.57	5.54	2.84	4.98	3.58	
	PLACE1005141	6.3	9.92	11.25	16.15	20.75	18.95	** +
5	PLACE1005146	1.3	2.71	3.03	2.17	2.53	2.29	
	PLACE1005152	1.85	3.9	4.56	4.13	4.23	4.79	
	PLACE1005157	2.66	5.19	5.3	4.38	4.09	7.01	
	PLACE1005162	2.79	3.72	9.31	6.57	7.45	7.1	
10	PLACE1005170	17.34	18.92	29.76	21.38	18.18	23.73	
	PLACE1005176	0.57	5.6	1.7	2.33	2.47	1.94	
	PLACE1005181	0.53	5.14	0.96	0.89	1.36	0.37	
	PLACE1005184	4.06	9.09	10.4	8.97	12.82	11.26	
	PLACE1005186	3.5	3.41	8.56	8.05	5.79	5.73	
15	PLACE1005187	2.85	4	4.13	6.1	4.99	4.25	
	PLACE1005189	6.12	7.71	5.34	10.84	10.65	12.22	** +
	PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61	
	PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1	
	PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95	
20	PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12	
	PLACE1005223	1.43	6.21	5	4.38	5.66	3.27	
	PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65	
	PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88	
	PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41	
25	PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75	
	PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88	
	PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51	
	PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76	
	PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95	
30	PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64	
	PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91	
	PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06	
	PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25	
35	PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84	
	PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79	
	PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8	
	PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26	
	PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43	
40	PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33	
	PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42	
	PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15	
	PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52	
	PLACE1005366	2.04	6.93	3	2.99	3.71	4.23	
45	PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37	
	PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41	
	PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03	
	PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2	
	PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97	
50	PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	* +
	PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45	
	PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75	
	PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28	
	PLACE1005467	3.09	11.87	7	5.57	11.63	7.28	
55	PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28	

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	PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46	
	PLACE1005477	1.58	2.26	2.51	3	2.93	2.74	
	PLACE1005480	0.77	2.01	1.86	1.93	1.4	0.53	
5	PLACE1005481	0.44	4.81	2.3	2.77	3.62	2.44	
	PLACE1005494	0.27	6.66	1.68	1.21	1.73	1.06	
	PLACE1005495	3.86	12.83	8.31	6.85	9.25	7.62	
	PLACE1005497	2.27	7.72	3.95	4.24	5.68	5.91	
10	PLACE1005499	5.71	5.86	11.07	10.82	7.9	6.49	
	PLACE1005502	1.59	2.87	3.43	4.07	3.45	1.49	
	PLACE1005513	1.77	4.14	3.35	1.86	2.85	1.98	
	PLACE1005515	2.89	4.76	4.22	4.58	5.29	3.78	
	PLACE1005519	1.04	4.53	3.29	2.85	2.85	2.83	
15	PLACE1005526	0.58	5.55	1.38	1.3	1.59	0.71	
	PLACE1005528	2.08	7.71	5.57	5.94	7.12	5.33	
	PLACE1005530	2.16	7.09	4.32	5.17	8.23	4.67	
	PLACE1005536	1.74	1	2.74	3.12	2.43	2.88	
20	PLACE1005539	10.1	11.64	23.77	8.65	8.66	5.22	
	PLACE1005543	1.7	3.57	5.62	3.54	4.32	2.57	
	PLACE1005544	0.86	3.26	3.15	2.49	2.68	2.27	
	PLACE1005550	4.32	7.61	7.85	10.16	7.25	6.86	
	PLACE1005554	1.15	5.47	2.67	2.17	2.17	1.17	
	PLACE1005557	1.76	7.21	4.95	8.22	7.64	7.7	
25	PLACE1005563	0.51	4	1.89	1.45	2.07	1.06	
	PLACE1005569	0.6	0.5	1.56	1.59	1.81	1.09	
	PLACE1005574	1.07	1.88	2.49	2.48	4.43	2.22	
	PLACE1005584	1.3	2.68	3.91	3.91	5.58	3.03	
30	PLACE1005590	4.28	5.14	8.4	9.87	10.73	8.02	
	PLACE1005595	3.08	4.03	2.89	3.65	3.81	3.89	
	PLACE1005601	2	5.66	4.22	3.77	4	4.02	
	PLACE1005603	1.08	4.9	1.04	2.49	0.95	1.94	
	PLACE1005604	1.2	6.71	2.42	3.6	4.2	3.46	
35	PLACE1005611	2.22	2.3	3.98	5.15	5.65	2.89	
	PLACE1005622	0.65	1.71	1.98	2.94	3.88	1.26	
	PLACE1005623	1.42	3.08	3.27	3.71	3.65	1.61	
	PLACE1005630	3.31	5.81	7.75	87.83	72.15	89.12	** +
	PLACE1005639	0.75	4.36	1.28	1.66	2.02	1.18	
40	PLACE1005646	2.13	5.41	4.31	5.4	5.08	2.55	
	PLACE1005647	2.77	9.69	6.72	7.34	9.11	6.25	
	PLACE1005648	3	8.11	9.21	8.34	10.59	8.22	
	PLACE1005653	1.99	1.43	2.74	2.74	2.13	2.67	
	PLACE1005656	0.92	2.48	2.24	1.68	2.78	1.58	
45	PLACE1005659	0.87	2.64	1.01	1.62	1.84	1.32	
	PLACE1005660	3.91	8.03	5.77	8.87	8.88	8.34	
	PLACE1005664	2.69	6.57	6.14	3.39	4.27	3.19	
	PLACE1005666	0.89	5.91	3.55	4.63	4.93	3.97	
	PLACE1005669	4.46	10.41	11.39	11.64	13.9	14.6	
50	PLACE1005682	1.94	5.27	4.49	6.2	5.2	5.47	
	PLACE1005698	0.6	2.7	2.92	2.01	2.67	2.38	
	PLACE1005708	25.32	34.08	53.46	53.89	59.98	53.76	
	PLACE1005725	3.25	3.75	6.41	5.64	5.82	7.29	
	PLACE1005727	2.97	4.54	4.15	3.9	3.49	4	
55	PLACE1005730	0.77	4.29	3.26	1.1	1.54	1.28	

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	PLACE1005736	5.37	7.55	5.73	9.25	12.55	10.19	*	+
	PLACE1005739	0.81	4.96	1.38	2.46	3.17	1.74		
	PLACE1005745	8.03	7.11	11.52	11.98	6.97	11.44		
5	PLACE1005752	1.31	3.15	2.96	2.55	2.24	1.25		
	PLACE1005755	0.8	2.79	3.02	1.72	3.28	2.27		
	PLACE1005756	10.79	12.06	17.2	18.22	19.3	21.47	*	+
	PLACE1005760	10.22	15.24	68.06	49.69	68.81	53.09		
10	PLACE1005763	1.47	7.04	3.58	3.79	4.63	3.02		
	PLACE1005768	1.25	5.63	3.69	4.58	5.13	4.19		
	PLACE1005771	5.71	13.63	13.7	11.28	17.49	17.27		
	PLACE1005783	1.82	2.44	3.64	3.05	3.71	3.47		
	PLACE1005799	4.79	5.25	8.37	6.12	8.78	8.62		
15	PLACE1005802	1.07	3.78	3.64	2.7	3.64	1.96		
	PLACE1005803	3.06	6.15	4.78	5.6	4.94	7.36		
	PLACE1005804	0.92	8.41	1.33	2	1.91	2.44		
	PLACE1005813	17.23	18.71	78.06	70.01	94.17	74.89		
	PLACE1005815	1.43	5.6	4.38	3.8	5.01	4.1		
20	PLACE1005828	2.11	3.62	4.42	5.34	6.24	3.56		
	PLACE1005833	119.17	92.82	182.22	122	114.37	107.96		
	PLACE1005834	2.04	4.33	3.95	3.55	3.56	2.56		
	PLACE1005835	22.7	19.1	51.52	72.32	60.34	68.56	*	+
	PLACE1005836	2.39	4.21	4.97	2.61	3.83	2.55		
25	PLACE1005845	0.97	5.42	2.66	2.67	3.05	3.65		
	PLACE1005850	1.82	3.91	3.04	2.84	2.85	2.15		
	PLACE1005851	1.03	3.44	1.46	1.2	2.01	1.11		
	PLACE1005856	0.92	4.01	2.42	2.24	3.37	3.37		
	PLACE1005875	1.78	3.89	4.77	3.3	3.48	3.17		
30	PLACE1005876	1.33	3.99	4.76	6.87	6.34	6.9	*	+
	PLACE1005878	1.3	2.67	2.08	3.54	4.46	2.79		
	PLACE1005880	2.36	4.09	4.31	4.16	3.07	3.45		
	PLACE1005884	1.6	4.87	1.89	2.48	2.21	2.73		
	PLACE1005890	1.9	9.57	3.7	2.26	3.09	1.88		
35	PLACE1005898	3.29	10.87	5.34	7.36	8.12	6.36		
	PLACE1005913	1.46	9.31	8.05	4.99	6.47	4.33		
	PLACE1005921	0.99	1.92	2.03	1.49	2.22	0.79		
	PLACE1005923	0.74	1.61	1.17	1.47	2.42	1.43		
40	PLACE1005925	0.83	2.67	3.18	2.19	2.14	1.68		
	PLACE1005927	1.26	2.49	1.93	1.95	2.56	2.3		
	PLACE1005932	2.04	5.66	2.44	2.53	2.32	2.52		
	PLACE1005934	0.88	7.91	3.16	3.9	5.61	4.19		
	PLACE1005936	1.31	8.96	3.02	2.02	2.84	2.3		
45	PLACE1005939	54.61	68.58	111.22	157.61	194.58	212.18	**	+
	PLACE1005951	2.36	3.39	4.98	5.56	4.48	2.35		
	PLACE1005953	1.5	1.64	2.64	2.59	2.43	3.03		
	PLACE1005955	1.64	2.01	3.8	4.07	3.43	2.55		
	PLACE1005966	0.76	3.42	1.69	1.75	2	2.19		
50	PLACE1005968	1.52	4.96	3.2	4.71	5.15	6.12		
	PLACE1005975	2.58	7.11	5.42	6.18	7.01	6.49		
	PLACE1005990	0.7	7.7	1.54	2.1	1.87	0.88		
	PLACE1005997	88.15	118.52	196.48	189.6	226.97	172.1		
	PLACE1006002	3.38	3.97	8.87	8.4	7.71	9.18		
55	PLACE1006003	1.55	3.02	4.83	5.09	4.44	5.33		

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	PLACE1006011	1.85	3.63	3.46	4.48	2.68	1.91	
	PLACE1006017	0.84	2.74	2.81	3.4	3.4	3.58	
	PLACE1006037	2.99	7.05	2.48	6.14	3.64	4.29	
5	PLACE1006040	2.2	7.87	3.97	6.64	6.9	7.77	
	PLACE1006063	0.94	4.64	2.59	2.11	3.15	2.25	
	PLACE1006071	3.06	6.52	4.97	5.36	4.03	4.47	
	PLACE1006073	2.74	3.53	6.43	7.19	6.81	6.93	
10	PLACE1006074	1.4	2.22	3.34	2.62	3.23	1.69	
	PLACE1006076	1.36	2.51	2.98	3.15	2.47	2.75	
	PLACE1006079	1.38	4.32	1.78	2.1	1.1	1.11	
	PLACE1006093	0.49	3.76	1	3.56	3.85	1.83	
	PLACE1006116	2.99	6.44	4.04	5.28	5.01	4.91	
15	PLACE1006119	3.15	6.81	7.07	9.22	10.4	8.03	
	PLACE1006129	2.12	5.6	3.98	6.59	7.62	5.65	
	PLACE1006139	3.44	2.98	6.03	7.77	8.85	5.58	
	PLACE1006143	0.5	1.48	1.87	3.18	4.13	3.17	* +
	PLACE1006157	1.55	2.54	4.82	2.96	3.9	2.44	
20	PLACE1006159	0.69	3.61	0.94	2.68	1.98	1.04	
	PLACE1006164	0.35	3.18	1.37	1.73	1.85	1.21	
	PLACE1006167	2.18	6.5	3.37	3.95	4.52	3.13	
	PLACE1006170	2.79	6.09	6.09	4.34	5.31	3.68	
	PLACE1006181	2.75	7.34	2.84	5.8	5.51	5.22	
25	PLACE1006187	0.76	1.3	2.15	2.01	2.41	1.48	
	PLACE1006195	0.11	1.24	1.73	1.93	1.93	0.87	
	PLACE1006196	1.8	4.01	4.15	4.32	5.77	2.19	
	PLACE1006197	2.12	5.6	5.24	4	3.47	3.39	
30	PLACE1006198	0.27	3.68	1.21	0.84	1.63	0.5	
	PLACE1006205	0.89	5.59	0.99	2.43	2.18	1.28	
	PLACE1006208	7.28	13.32	13.46	14.09	14.99	12.5	
	PLACE1006211	2.6	8.05	7.92	6.07	9.08	9.35	
	PLACE1006219	6.77	5.77	8.94	14.88	22.25	15.35	* +
35	PLACE1006223	1.55	1.46	3.19	1.39	3	1.64	
	PLACE1006225	0.56	2.27	1.3	1.04	2.3	0.99	
	PLACE1006236	1.53	3.2	2.92	3.06	5.01	2.29	
	PLACE1006239	0.67	3.62	1.97	2.61	3.66	3.41	
	PLACE1006245	3.86	7.13	5.45	4.43	7.44	3.28	
40	PLACE1006246	1.66	6.56	6.19	5.59	7.66	6.33	
	PLACE1006248	1.58	4.47	5.6	2.77	3.1	2.82	
	PLACE1006262	0.93	2.24	1.49	2.08	1.61	1.4	
	PLACE1006269	2.28	4.71	3.42	2.06	2.47	2.33	
	PLACE1006275	1.6	3.57	3.37	4.12	3.68	3.53	
45	PLACE1006277	1.01	2.42	1.4	1.79	3.01	0.88	
	PLACE1006288	9.32	13.59	22.49	26.85	18.4	25.21	
	PLACE1006290	1.79	6.81	5.99	8.87	7.56	9.13	
	PLACE1006298	1.93	5.52	2.47	3.87	5.08	4.55	
	PLACE1006311	0.65	3.38	1.75	225.97	161.43	251.12	** +
50	PLACE1006318	3.52	4.03	4.17	4.04	3.17	4.01	
	PLACE1006325	5.43	6.73	6.31	8.09	8.38	8.08	** +
	PLACE1006331	1.87	3.36	3.21	4.44	3.59	2.56	
	PLACE1006335	1.76	3.64	2.55	4.45	2.98	2.92	
	PLACE1006357	0.27	4.51	1.59	1.7	1.49	1.2	
55	PLACE1006360	1.1	5.11	1.79	2.46	2.74	2.62	

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	PLACE1006364	4.51	8.06	7.29	7.37	9.19	5.75		
	PLACE1006365	1.68	4.65	1.97	1.8	2.12	0.97		
	PLACE1006368	1.53	3.11	2.57	3.01	3.04	4.27		
5	PLACE1006371	1.38	3.2	1.46	1.68	3.01	1.67		
	PLACE1006373	2.21	5.21	5.75	7.83	8.02	7.56	*	+
	PLACE1006382	0.9	4.67	2.81	3.3	1.92	2.95		
	PLACE1006385	1.59	6.33	1.86	2.68	2.59	2.71		
	PLACE1006391	1.19	5	1.95	1.96	2.79	1.63		
10	PLACE1006412	1.88	5.53	5.92	7.07	9.93	5.27		
	PLACE1006414	0.63	3.42	0.95	1.22	1.87	1.6		
	PLACE1006419	7.79	9.8	11.93	5.19	7.29	5.32	*	-
	PLACE1006438	0.99	6.07	3.42	3.29	4.56	5.14		
15	PLACE1006443	2.05	5.01	5.12	5.01	5.31	6.44		
	PLACE1006445	0.84	5.76	3.65	3.53	3.27	3.55		
	PLACE1006447	1.34	5.81	3.28	2.95	3.26	3.96		
	PLACE1006466	0.75	4.38	1.35	1.49	1.66	1.08		
	PLACE1006469	0.67	4.66	2.31	1.65	2.26	1.67		
20	PLACE1006470	2.47	3.71	3.74	5.25	7.02	4.35		
	PLACE1006472	24.4	23.44	52.17	26.23	28.52	9.36		
	PLACE1006476	2.52	4.31	8.67	6.21	7.23	5.93		
	PLACE1006482	1.64	3.35	4.43	4.25	4.67	4.98		
	PLACE1006488	14.12	19.42	32.69	40.76	34.77	41.4	*	+
25	PLACE1006492	2.03	6.41	4.38	4.04	4.98	3.02		
	PLACE1006506	1.78	6.67	4.04	4.41	5.71	4.17		
	PLACE1006515	1.65	5.7	3.08	3.19	2.84	4.08		
	PLACE1006516	1.1	7.32	7.05	4.89	5.69	7.28		
	PLACE1006520	1.02	2.74	2.12	1.19	3	1.54		
30	PLACE1006521	2.4	3.54	6.38	6.49	6.86	5.08		
	PLACE1006529	5.96	7.35	6.96	10.56	8.2	7.93		
	PLACE1006531	1.01	4.31	3.33	1.84	2.05	2.43		
	PLACE1006534	1.68	6.04	2.59	3.01	3.86	3.19		
	PLACE1006540	2.68	9.7	7.77	8.71	11.21	4.46		
35	PLACE1006549	0.6	9.45	2.09	1.6	2.28	1.65		
	PLACE1006550	1.76	8.82	4.07	2.77	2.94	4.14		
	PLACE1006552	1.3	2.48	2.14	1.97	1.3	0.81		
	PLACE1006557	2.38	4.01	3.79	2.84	2.51	2.45		
	PLACE1006563	2.49	3.44	5.7	4.23	4.15	4.3		
40	PLACE1006579	1.53	7.5	4.82	4.88	5.38	5.78		
	PLACE1006594	236.53	241.11	397.64	122.37	278.58	324.29		
	PLACE1006598	0.72	8.53	2.4	1.53	1.58	2.07		
	PLACE1006607	1.47	7.69	4.18	3.45	5.86	4.29		
45	PLACE1006610	9.46	13.73	38.26	27.65	32.76	22.64		
	PLACE1006615	6.22	9.09	18.78	20.25	15.74	15.86		
	PLACE1006617	0.91	1.54	2.66	1.87	2.49	2.09		
	PLACE1006618	5.42	8.01	9.24	5.33	8.59	5.76		
	PLACE1006626	1.53	4.11	1.3	2.47	2.78	1.16		
50	PLACE1006629	0.99	5.05	1.36	2.22	2.56	1.76		
	PLACE1006637	1.29	6.54	3.97	3.77	4.23	4.87		
	PLACE1006640	0.59	5.14	1.17	0.85	2.54	0.94		
	PLACE1006644	1.66	4.46	2.12	2.79	2.49	2.39		
	PLACE1006657	1.28	2.09	2.31	4.55	3.09	2.19		
55	PLACE1006673	2.29	4.73	10.34	11.06	10.89	6.45		

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	PLACE1006678	2.54	2.98	1.44	1.37	1.96	1.39		
	PLACE1006682	3.5	5.93	2.58	15.44	20.96	23.99	**	+
	PLACE1006684	1.12	4.8	1.81	1.64	2.54	1.65		
5	PLACE1006698	1.54	5.86	4.52	2.15	3.57	1.9		
	PLACE1006704	1.81	5.41	2.71	2.93	2.92	2.97		
	PLACE1006708	1.69	5.07	3.49	3.46	4.11	3.7		
	PLACE1006711	14.21	16.18	29.77	24.34	26.25	22.42		
10	PLACE1006714	2.27	3.26	4.74	4.57	5.23	3.53		
	PLACE1006716	1.51	2.75	3.7	6	7.05	3.99		
	PLACE1006731	1.65	3.77	2.83	2.71	4	3.09		
	PLACE1006754	0.43	3.94	1.73	1.8	1.81	0.99		
	PLACE1006760	7.56	10.98	10.08	8.58	8.89	11.31		
15	PLACE1006779	1.44	4.12	2.88	3.19	3.79	2.97		
	PLACE1006782	0.44	5.17	2.42	2.95	1.57	1.15		
	PLACE1006783	9.34	11.46	18.65	157.98	223.05	66.46	*	+
	PLACE1006786	3.31	4.08	6.07	5.9	6.24	3.34		
	PLACE1006792	1.61	3.31	5.38	5.66	3.33	4.18		
20	PLACE1006795	0.89	2.43	0.74	0.81	1.27	1.01		
	PLACE1006800	1.62	4.94	2.53	4.7	4.56	3.93		
	PLACE1006805	3.94	7.79	5.5	10.83	9.8	8.79	*	+
	PLACE1006809	3.55	5.7	5.94	9.58	10.61	8.97	**	+
	PLACE1006815	1.7	7.57	4.1	5.12	5.23	5.8		
25	PLACE1006819	0.33	0.88	0.95	0.89	1.76	0.63		
	PLACE1006820	2.35	2.01	4.91	4.84	6.72	4.18		
	PLACE1006826	2.28	6.22	4.84	7.68	7.62	5.58		
	PLACE1006829	3.76	5.51	6.54	9.49	8.66	8.69	*	+
30	PLACE1006853	1.2	4.21	1.97	2.25	2.93	2.88		
	PLACE1006860	1	4.29	1.62	1.61	2.1	1		
	PLACE1006867	5.65	9.36	11.34	7.04	8.33	7.63		
	PLACE1006875	1.15	6.19	5.66	4.84	4.53	4.63		
	PLACE1006878	1.59	2.84	3.09	2.99	3.22	2.39		
35	PLACE1006883	3.21	5.08	6.78	6.83	7.38	6.19		
	PLACE1006898	1.67	4.23	3.67	3.54	4.77	4.59		
	PLACE1006901	2.59	4.75	4.03	3.71	3.28	4.14		
	PLACE1006904	0.91	3.59	2.7	3.26	2.92	2.04		
40	PLACE1006917	3.63	7.13	6.1	5.8	7.21	7.03		
	PLACE1006932	0.54	5.85	1.29	0.92	1.34	1.19		
	PLACE1006935	1.3	5.46	2.54	1.59	4.03	1.6		
	PLACE1006956	0.92	2.55	3.4	2.55	2.41	2.09		
	PLACE1006958	0.78	2.41	1.35	1.76	4.2	3.39		
	PLACE1006959	4.97	8.48	9.98	11.46	9.58	13.62		
45	PLACE1006961	8.03	9.85	14.42	13.73	11.57	14.2		
	PLACE1006962	2.97	7.44	6.56	5.04	7.26	6.22		
	PLACE1006966	2.02	6.94	3.46	3.15	3.89	2.89		
	PLACE1006979	0.95	4.44	2.03	1.46	2.64	1.77		
	PLACE1006989	2.19	5.05	3.02	3.27	3.9	5.06		
50	PLACE1007001	4.98	6.79	10.71	4.03	7.43	7.38		
	PLACE1007014	1.37	3.03	3.45	1.79	2.18	2.2		
	PLACE1007021	0.74	3.03	2.11	0.75	2.2	1.73		
	PLACE1007026	2.1	9.23	3.93	4.15	4.27	5.42		
55	PLACE1007028	4.12	8.5	10.56	7.89	8.34	9.35		
	PLACE1007038	237.33	267.91	446.14	406.27	622.67	671.17		

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	PLACE1007040	1.55	3.14	2.85	1.57	3.31	2.45
	PLACE1007045	1.08	3.74	2.85	2.9	5.03	2.74
	PLACE1007048	147.06	149.67	259.53	121.61	211.26	109.43
5	PLACE1007053	4.9	6.69	10	3.59	4.91	4.71
	PLACE1007068	7.56	10.33	62.76	39.52	45.9	36.69
	PLACE1007070	5.97	10.85	10.28	8.65	9.6	14.3
	PLACE1007076	8.22	14.4	14.19	16.53	23.62	24.67 * +
10	PLACE1007077	2.65	6.45	4.01	5.2	5.28	5.43
	PLACE1007081	0.36	4.47	1.94	1.92	1.92	1.37
	PLACE1007082	1.23	4.66	4.95	4.32	4.5	3.99
	PLACE1007092	2.49	4.12	7.26	4.77	5.22	4.34
	PLACE1007096	0.72	2.19	0.74	1.35	1.63	0.97
15	PLACE1007097	0.54	2.49	1.35	1.61	1.28	1.04
	PLACE1007099	1.58	4.66	2.56	2.77	3.64	3.72
	PLACE1007105	1.18	6.51	3.44	2.65	4.13	2.21
	PLACE1007108	3.55	13.02	7.41	5.03	6.87	5.75
20	PLACE1007111	1.33	9.51	1.52	1.74	2.37	1.52
	PLACE1007112	1.23	7.26	1.79	2.09	3.12	2.36
	PLACE1007130	0.54	2.02	1.92	0.87	1.47	0.33
	PLACE1007132	1.46	3.32	4.63	3.58	3.38	2.88
	PLACE1007140	0.61	2.58	2.41	1.98	1.98	1.32
25	PLACE1007143	2.79	6.32	4.62	4.9	5.34	5.33
	PLACE1007169	2.21	8.59	3.46	5.44	8.46	7.99
	PLACE1007178	0.82	8.66	2.48	3.28	6.28	4.1
	PLACE1007190	3.31	10.9	6.7	10.51	13.57	11.14
	PLACE1007201	0.81	5.82	1.41	1.72	3.04	2.51
30	PLACE1007202	37.76	34.95	76.28	58.23	34.42	37.86
	PLACE1007226	2.01	2.39	2.73	1.89	3.14	2.29
	PLACE1007238	1.64	3.07	1.83	2.39	2.73	2.2
	PLACE1007239	1.81	3.68	2.99	1.76	2.72	2.44
	PLACE1007242	0.61	5.18	1.87	1.54	1.14	1.67
35	PLACE1007243	2.21	7.36	2.29	2.24	3.27	3.31
	PLACE1007247	0.36	6.17	1.71	1.11	1.36	1.34
	PLACE1007257	1.67	5.33	3.34	3.3	5.27	4.25
	PLACE1007274	1.46	2.18	4.43	4.38	4.03	4.06
40	PLACE1007276	0.93	2.02	1.1	2.13	2.1	1.74
	PLACE1007282	2.51	4.2	5.72	4.28	3.62	4.66
	PLACE1007286	2.97	4.8	7.85	10.14	12.47	8.79 * +
	PLACE1007296	10.55	19.45	24.46	31.43	17.57	27.05
	PLACE1007301	0.65	5.17	1.55	1.19	1.54	1.11
45	PLACE1007314	3.11	6.61	8.64	7.98	8.96	10.24
	PLACE1007317	1.19	3.34	1.27	1.88	1.62	1.79
	PLACE1007329	0.89	0.73	1.78	2.38	2.35	2.09 * +
	PLACE1007338	3.96	6.47	9.58	11.59	8.93	2.32
	PLACE1007342	0.71	1.8	1.3	1.1	1.1	0.7
50	PLACE1007345	1.72	4.57	2.54	2.72	3.6	3.29
	PLACE1007346	1.43	4.61	3.89	5.77	4.53	4.1
	PLACE1007359	0.74	4.55	2.16	2.59	2.44	3.53
	PLACE1007367	4.53	8.63	15.16	12.49	13.49	11.75
	PLACE1007375	0.36	3.24	2.02	1.75	2.56	1.59
55	PLACE1007377	1.49	2.01	3.18	3.29	3.96	2.36
	PLACE1007386	1.55	1.75	1.47	2.37	1.68	1.36

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	PLACE1007392	1.57	2.99	2.49	2.79	4.48	3.51	
	PLACE1007402	2.41	5.66	3.08	1.52	2.91	1.8	
	PLACE1007409	1.05	4.57	1.04	2.51	2.68	2.02	
5	PLACE1007416	3.45	6.97	6.5	7.05	9.14	6.52	
	PLACE1007420	12.12	12.66	20.8	25.26	23.9	22.88	* +
	PLACE1007431	1.87	7.4	5.51	7.17	5.28	5.91	
	PLACE1007450	0.79	1.22	2.65	3	2.99	2.39	
10	PLACE1007452	0.42	2.36	1.76	2.09	2.98	1.45	
	PLACE1007454	23.74	28.02	76.56	59.97	75.95	46.61	
	PLACE1007460	0.75	3.52	2.35	2.34	1.93	2.58	
	PLACE1007478	0.41	3.07	1.33	1.35	2.18	1.92	
	PLACE1007484	0.6	4.8	2.57	2.56	1.45	1.69	
15	PLACE1007488	0.4	6.24	1.64	1.74	2.61	1.46	
	PLACE1007507	2.91	6.36	4.49	5.31	8.29	8.11	
	PLACE1007511	0.53	1.29	1.06	1.06	1.29	0.42	
	PLACE1007513	10.57	10.43	24.05	12.24	16.88	16.9	
20	PLACE1007524	1.55	3.33	3.53	3.96	4.72	2.96	
	PLACE1007525	1.24	2.95	3.14	2.38	2.85	2.24	
	PLACE1007537	8.6	9.68	49.88	43.78	63.66	40.1	
	PLACE1007544	1.55	6.45	4.97	3.2	3.92	4.61	
	PLACE1007547	1.36	5.03	4.15	2.37	2.84	2.4	
25	PLACE1007557	1.12	3.16	3.14	3.07	3.9	3.41	
	PLACE1007560	9.38	8.86	12.57	11.03	9.62	17.59	
	PLACE1007565	0.37	2.27	1	1	1.16	0.91	
	PLACE1007580	1.06	3.71	3.06	10.8	11.15	13.74	** +
30	PLACE1007583	0.76	3.88	1.78	2.51	2.37	1.09	
	PLACE1007591	0.79	4.62	1.7	2.2	2.53	2.07	
	PLACE1007598	1.13	6.98	3.86	2.71	3.46	4.71	
	PLACE1007610	0.41	5.63	1.28	1.33	3.18	1.5	
	PLACE1007618	1.57	1.91	2.01	1.75	2.2	2.41	
35	PLACE1007621	1.78	2.83	3.64	3.33	3.57	4.38	
	PLACE1007626	23.99	25.61	32.78	30.53	30.94	13.53	
	PLACE1007632	2.03	3.26	2.52	2.65	3.81	4.63	
	PLACE1007635	1.61	4.62	6.42	2.8	4.19	3.37	
	PLACE1007645	10.59	11.55	15.06	9.99	11.58	11.95	
40	PLACE1007649	1.7	5.88	3.47	2.78	4.95	3.13	
	PLACE1007659	1.33	5.85	3.61	4.88	6.22	4.9	
	PLACE1007669	2.01	2.1	3.74	2.97	4.63	4.4	
	PLACE1007677	1.25	2.29	2.81	2.68	3.07	2.91	
	PLACE1007688	3.4	5.69	5.43	1.98	4.53	4.98	
45	PLACE1007690	1.4	4.03	2.12	3.74	3.37	4.61	
	PLACE1007697	0.69	7.13	1.37	1.84	2.56	1.8	
	PLACE1007702	2.03	7.08	5.7	4.03	3.91	4.08	
	PLACE1007705	1.38	3.93	1.59	1.74	4.45	2.75	
	PLACE1007706	3.11	6.08	4.69	5.25	8.84	7.49	
50	PLACE1007725	3.41	4.69	6.65	5.1	3.29	5.39	
	PLACE1007729	0.98	2.65	1.8	2.7	3.11	1.99	
	PLACE1007730	1.25	4.29	3.07	3.66	3.75	4.32	
	PLACE1007737	1.43	4.79	3.39	3.79	4.7	4.17	
	PLACE1007743	1.38	4.26	2.29	2.3	2.83	2.03	
55	PLACE1007746	6.56	9.02	10.42	9.65	13.29	12.97	
	PLACE1007753	0.53	4.48	1.71	1.35	2.86	1.94	

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	PLACE1007769	1.31	4.31	3.5	3.27	4.51	4.58	
	PLACE1007780	5.77	4.63	7.11	6.51	3.75	2.17	
	PLACE1007791	1.82	3.29	3.38	3.16	3.69	2.87	
5	PLACE1007807	0.67	2.79	1.72	2.33	1.76	1.29	
	PLACE1007810	0.39	4.45	2.63	4.11	4.08	3.27	
	PLACE1007814	3.57	5.98	5.04	4.2	4.62	6.3	
	PLACE1007828	2.01	7.64	3.34	2.69	4.64	3.44	
10	PLACE1007829	1.32	6.9	2.88	2.87	4.87	3.06	
	PLACE1007841	1.64	7.26	1.87	2.25	3.14	3.39	
	PLACE1007842	1.1	3.32	2.44	2.09	3.96	1.39	
	PLACE1007843	1.2	1.92	1.43	2.13	1.48	1.86	
	PLACE1007845	1.76	3	4.11	3.45	3.42	2.36	
15	PLACE1007846	0.99	3.26	1.64	2.02	2.73	1.5	
	PLACE1007848	1.09	3.51	2.23	2.39	2.62	2.25	
	PLACE1007852	2.26	7.88	3.82	2.94	4.61	3.24	
	PLACE1007858	3.65	11.57	5.81	61.71	80.46	57.09	** +
	PLACE1007866	19.42	25.98	40.48	43	80.39	56.73	
20	PLACE1007871	8.1	7.9	15.45	16.17	12.35	11.08	
	PLACE1007877	1.09	2.09	1.45	1.4	2.39	1.53	
	PLACE1007878	5.98	9.75	14.61	13.65	7.49	8.9	
	PLACE1007881	0.43	2.66	1.34	1.59	1.94	1.93	
	PLACE1007885	4.35	7.85	6.76	5.57	6.53	7.01	
25	PLACE1007897	0.27	6.51	1.85	1.72	1.53	1.41	
	PLACE1007908	3.14	12.29	5.73	5.96	7.9	8.24	
	PLACE1007922	6.08	11.75	8.75	5.24	7.15	4.54	
	PLACE1007946	1.07	2.03	1.86	2.71	2.28	1.94	
30	PLACE1007950	6.98	7.6	18.21	16.17	19.34	12.63	
	PLACE1007954	-0.03	2.45	1.15	2.46	1.57	1.51	
	PLACE1007955	0.92	4.01	2.17	2.05	2.52	3.05	
	PLACE1007956	0.6	3.61	2.91	2.35	2.1	2.22	
	PLACE1007958	0.75	6.31	1.34	0.79	1.21	0.8	
35	PLACE1007965	0.64	5.88	3.25	3.38	2.91	2.17	
	PLACE1007969	1.09	6.37	3.06	2.35	3.29	2.21	
	PLACE1007971	2.73	4.17	5.21	6.1	4.41	5.92	
	PLACE1007990	1.95	2.33	2.31	3.22	3.09	1.88	
	PLACE1008000	0.32	2.16	1.98	1.85	1.27	0.66	
40	PLACE1008002	0.99	3.38	1.7	1.81	2.04	0.51	
	PLACE1008037	0.57	4.19	1.7	4.59	2.86	2.02	
	PLACE1008044	1.42	5.81	2.46	4.18	4.93	4.16	
	PLACE1008045	0.4	4.07	1.54	1.75	2	1.65	
	PLACE1008080	2.05	6.08	3.22	4.23	4.03	4.78	
45	PLACE1008092	1.56	1.56	1.48	1.48	2.98	1.86	
	PLACE1008095	0.59	2.14	1.48	2.38	2.73	1.23	
	PLACE1008105	0.95	1.76	1.71	2.24	2.71	0.74	
	PLACE1008107	0.27	2.33	0.7	1.72	1.44	1.68	
50	PLACE1008111	1.73	5.01	2.12	4.57	5.4	4.04	
	PLACE1008113	5.88	9.24	12.48	16.57	20.29	19.24	* +
	PLACE1008122	1.22	5.54	2.55	1.61	1.57	1.5	
	PLACE1008129	1.5	5.64	2.8	2.43	5.36	2.91	
	PLACE1008132	5.51	4.47	8.34	6.61	11.2	7.63	
55	PLACE1008137	0.96	1.82	1.02	2.12	3.88	0.8	
	PLACE1008174	0.77	3.16	2.43	5.12	4.39	2.46	

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	PLACE1008177	1.62	4.87	3.09	3.79	3.26	3.77		
	PLACE1008181	1.76	3.87	1.6	2.06	2.43	1.43		
	PLACE1008195	2.66	6.08	2.97	4.34	4.14	3.9		
5	PLACE1008198	1.06	5.56	2.52	2.55	3.31	1.54		
	PLACE1008201	1.22	4.45	3.58	5.92	7.69	5.64	*	+
	PLACE1008209	2.35	2.29	4.46	2.51	5.31	4.44		
	PLACE1008226	1.8	2.35	5.25	4.72	5.68	7.08		
10	PLACE1008227	0.77	2.67	3.02	2.38	4.6	3.54		
	PLACE1008231	1.26	3.85	1.85	1.05	1.83	0.78		
	PLACE1008238	1.22	3.21	2.9	2.47	2	1.72		
	PLACE1008244	1.01	4.69	1.56	1.68	3.2	1.56		
	PLACE1008249	0.8	4.94	2.55	1.22	2.17	2.01		
15	PLACE1008266	11.31	18.61	43.04	60.04	82.48	59.04	*	+
	PLACE1008273	1.47	3.95	3.81	3.53	3.8	4.47		
	PLACE1008275	1.59	3.67	2.17	2.62	2.57	2.34		
	PLACE1008280	0.85	2.6	1.84	2.42	2.48	2.36		
	PLACE1008282	4.71	8.19	6.89	7.27	9.02	6.38		
20	PLACE1008297	2.32	4.7	3.36	2.89	3.42	3.21		
	PLACE1008303	1.65	6.68	1.24	4.12	3.83	2.65		
	PLACE1008309	0.43	6.52	0.82	1.77	1.5	1.29		
	PLACE1008315	5.3	5.93	8.61	4.92	4.79	9.83		
	PLACE1008329	0.47	2.23	2.06	2.32	2.8	2.49		
25	PLACE1008330	0.72	4.06	3.16	2.48	3.36	2.96		
	PLACE1008331	0.84	5.01	2.1	4.5	2.17	2.91		
	PLACE1008351	4.34	8.66	7.41	7.91	7.31	7.1		
	PLACE1008356	1.56	8.23	1.93	2.86	4.16	3.35		
30	PLACE1008359	1.57	4.11	2.89	2	2.97	2.94		
	PLACE1008368	2.27	6.38	7.43	5.72	7.33	6.95		
	PLACE1008369	0.57	2.46	1.45	1.12	1.59	1.68		
	PLACE1008392	0.8	3.09	2.54	2.44	3.22	3.24		
	PLACE1008394	2.08	4.84	3.75	3.98	5.03	4.76		
35	PLACE1008398	5.32	9.36	11.44	11.36	11.3	12.33		
	PLACE1008401	1.19	7.06	3.21	2.82	3.43	3.33		
	PLACE1008402	3.21	6.45	7.2	7.23	10.15	9.26		
	PLACE1008405	10.3	10.95	18.42	17.17	18.82	20.4		
40	PLACE1008409	1.88	5.19	5.69	4.97	5.41	5.65		
	PLACE1008420	1.4	1.87	1.96	2.67	2.69	2.27	*	+
	PLACE1008424	0.88	2.69	2.54	1.69	2.34	1.71		
	PLACE1008426	0.98	2.58	1.58	1.7	2.66	2.32		
	PLACE1008429	0.92	3.17	2.14	1.91	3.4	1.84		
	PLACE1008430	1.63	4.85	3.04	2.93	3.52	3		
45	PLACE1008437	0.87	3.64	3.01	2.83	1.82	1.57		
	PLACE1008453	1.16	4.8	1.02	1.64	2.06	1.17		
	PLACE1008454	2.14	6.46	9.23	5.46	9.02	5.92		
	PLACE1008455	2.06	4.33	7.2	5.26	6.68	4.87		
50	PLACE1008457	0.51	2.6	2.01	2.28	2.43	2.47		
	PLACE1008465	0.49	2.41	1.72	1.56	2.13	0.48		
	PLACE1008469	2.42	4.36	5.32	5.16	4.75	7.1		
	PLACE1008488	0.81	5.48	1.97	2.44	2.03	1.8		
	PLACE1008519	1.48	10.85	6.17	4.41	4.99	4.51		
55	PLACE1008524	1.04	11.09	1.72	2	3.22	2.02		
	PLACE1008531	0.64	8.37	1.92	1.33	2.05	1.72		

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	PLACE1008532	2.12	3	5.51	5.66	4.72	4.19	
	PLACE1008533	2.01	4	4.07	5.53	5.18	3.77	
	PLACE1008542	1.61	2.36	0.96	2.05	2.1	1.72	
5	PLACE1008549	0.96	3.06	0.67	1.45	2.1	1.53	
	PLACE1008560	1.18	4.23	2.28	2.29	3.93	3.47	
	PLACE1008567	0.87	7.26	1.85	2.33	3.67	2.38	
	PLACE1008568	2.37	10.67	5.49	2.97	7.47	4.21	
	PLACE1008569	3.94	10.32	6.74	6.1	8.6	7.6	
10	PLACE1008584	0.88	1.4	1.58	2.86	3.38	1.31	
	PLACE1008585	4.96	4.8	7.56	11.08	4.84	3.57	
	PLACE1008603	5.9	7.25	31	30.55	43.67	29.76	
	PLACE1008621	0.55	2.28	0.95	0.72	1.89	1.16	
15	PLACE1008625	0.64	4.01	0.9	1.18	1.41	2.03	
	PLACE1008626	0.55	6.06	0.9	1.03	0.83	0.95	
	PLACE1008627	0.46	8.32	1.86	1.87	3.34	2.7	
	PLACE1008629	3.22	9.18	5.84	5.44	6.75	4.41	
	PLACE1008630	1.68	3.39	4.23	4.21	3.01	3.51	
20	PLACE1008643	1.31	0.93	1.98	1.72	2.34	1.94	
	PLACE1008650	0.25	3.05	1.62	2.23	1.63	1.24	
	PLACE1008657	1.17	2.39	2.51	2.34	4.04	2.91	
	PLACE1008664	0.91	5.93	2.37	2.91	2.51	1.13	
	PLACE1008693	0.97	4.93	3.09	2.53	3.81	2.2	
25	PLACE1008696	0.88	3.84	2.21	2.26	2.11	1.47	
	PLACE1008715	1.05	4.71	2.11	1.34	2.65	2.65	
	PLACE1008716	2.48	3.94	4.19	5.75	6.9	7.07	* +
	PLACE1008722	3.85	4.34	7.37	7.64	7.19	3.45	
30	PLACE1008738	5.17	9.13	12.7	9.49	5.83	4.8	
	PLACE1008742	6.57	6.87	14.66	14.94	15.06	12.41	
	PLACE1008744	3.52	6.98	5.61	5.83	4.55	2.74	
	PLACE1008748	0.63	4.39	2.75	2.44	1.67	1.61	
	PLACE1008757	0.99	4.74	4.51	2.77	5.74	2.17	
35	PLACE1008766	2.66	6.75	3.77	3.51	6.47	4.06	
	PLACE1008785	1.39	1.68	2.6	3.26	3.8	3.89	* +
	PLACE1008790	1.57	1.8	2.29	3.5	5.39	2.96	
	PLACE1008798	1.71	3.82	4.45	6	5.93	3.32	
	PLACE1008807	1.34	3.95	1.61	2.54	2.62	1.8	
40	PLACE1008808	1.6	4.53	3.01	4.24	3.69	5.04	
	PLACE1008813	1.38	4.85	1.97	1.9	1.95	2.3	
	PLACE1008836	1.34	5.81	3.68	3.89	6.17	4.1	
	PLACE1008851	1.21	6.65	3.94	4.85	10.04	4.54	
45	PLACE1008854	0.56	0.48	1.14	1.16	1.41	1.6	
	PLACE1008864	1.98	1.92	2.96	2.73	2.65	2.49	
	PLACE1008867	1.2	6.57	6.22	6.43	5.71	4.82	
	PLACE1008876	11.7	16.5	27.29	26.74	20.94	23.24	
	PLACE1008887	1.37	4.31	1.44	3.26	2.07	3.28	
50	PLACE1008902	1.33	5.62	2.93	3.17	4.58	2.06	
	PLACE1008911	4.04	8.56	10.48	11.31	13.99	15.66	
	PLACE1008917	0.6	4.53	2.72	1.7	2.9	1.71	
	PLACE1008920	0.75	0.77	0.87	0.61	1.58	1.44	
	PLACE1008925	0.25	0.9	1.04	0.94	1.91	0.84	
55	PLACE1008930	4.12	7.32	9.83	5.11	10.36	7.17	
	PLACE1008934	0.9	3.42	2.9	2.89	2.28	1.7	

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	PLACE1008941	1.57	4.14	2.8	2.06	2.59	4.05	
	PLACE1008947	2.3	5.41	5.51	3.96	5.84	5.16	
	PLACE1008984	1.26	6.31	3.25	3.1	3.93	3.19	
5	PLACE1008985	0.94	2.75	2.74	2.84	2.43	2.7	
	PLACE1008994	0.27	1.72	0.65	-1.11	0.78	0.68	
	PLACE1009020	0.46	3.49	2.42	2.49	3.1	2.16	
	PLACE1009027	0.89	2.7	1.59	2.24	1.75	2.09	
	PLACE1009039	-0.06	3.31	3.42	2.39	1.59	1.49	
10	PLACE1009045	1.53	6.33	6.05	23.13	20.76	22.2	** +
	PLACE1009048	0.41	5.97	2.3	0.61	1.04	0.54	
	PLACE1009050	0.97	4.9	1.68	1.07	1.47	1.55	
	PLACE1009060	5.61	8.4	9.51	10.74	8.55	11.96	
15	PLACE1009067	1.14	2.8	2.03	1.6	2.34	3.4	
	PLACE1009071	1.44	4.05	3.9	3.79	7.24	9.82	
	PLACE1009090	1.27	6.46	2.35	3.11	4.73	2.86	
	PLACE1009091	5.58	10.22	38.11	38.77	49.35	36.29	
	PLACE1009094	0.26	5.68	1.88	1.67	5.04	1.71	
20	PLACE1009099	1	5.52	3.47	3.49	3.36	3.84	
	PLACE1009110	1.59	5.82	1.16	1.68	4.3	4.39	
	PLACE1009111	1.88	5.24	2.65	3.95	3.77	2.88	
	PLACE1009113	2.24	3.52	3.62	6.14	4.87	7.29	* +
	PLACE1009130	4.46	6.8	7.84	6.68	9.36	10.47	
25	PLACE1009150	0.88	3.54	1.95	3.23	3.3	3.01	
	PLACE1009155	1.11	5.06	2.98	4.46	4.43	3.87	
	PLACE1009158	1.06	5.77	1.95	1.77	2.35	2.88	
	PLACE1009166	0.76	4.8	1.53	1.59	2.16	1.3	
30	PLACE1009172	1.43	3.96	2.45	2.26	5.85	2.61	
	PLACE1009174	1.13	3.45	2.42	1.67	3.02	2.38	
	PLACE1009183	1.62	3.54	4.47	4.1	6.33	8.06	
	PLACE1009186	1.04	5.07	2.3	2.46	2.86	2.91	
	PLACE1009190	0.75	2.32	1.44	1.53	1.9	1.65	
35	PLACE1009196	0.81	4.01	2.73	2.24	2.38	1.99	
	PLACE1009200	1.01	4.44	2.94	2.84	4.39	2.91	
	PLACE1009217	2.55	4.91	3.43	4.46	7.29	7.23	
	PLACE1009230	1.9	5.55	6.63	5.63	9.16	9.46	
	PLACE1009236	4.97	7.07	12.6	8.21	10.79	7.13	
40	PLACE1009246	11.71	11.96	24.75	14.59	16.36	9.05	
	PLACE1009265	6.95	7.82	14.01	15.61	5.19	12.17	
	PLACE1009279	0.67	2.07	2.46	1.93	2.54	1.63	
	PLACE1009298	5.54	9.92	9.52	10.21	11.25	17.55	
	PLACE1009308	1.13	6.82	2.04	2.48	2.48	2.34	
45	PLACE1009319	2.04	9.25	3.15	2.92	3.54	2.5	
	PLACE1009328	1.04	5.78	1.81	2.98	3.39	2.17	
	PLACE1009335	1.38	6.55	4.72	2.24	3.21	3.01	
	PLACE1009338	2.56	4.14	5.1	3.24	4.3	1.57	
	PLACE1009344	0.73	2.45	1.08	1.31	1.55	0.84	
50	PLACE1009355	5.41	7.37	9.95	13.44	10.76	13.55	* +
	PLACE1009368	1.3	2.56	2.41	2.43	2.32	2.19	
	PLACE1009375	1.21	6.41	3.05	3.04	4.46	2.53	
	PLACE1009388	1.18	8.68	3.01	3.46	4.53	2.72	
	PLACE1009398	1.19	9.2	3.74	3.17	4.28	3.96	
55	PLACE1009404	2.78	9.18	4.51	5.33	6.73	6.94	

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	PLACE1009410	1.27	2.35	2.33	2.51	2.31	1.44		
	PLACE1009417	0.95	2.25	4.34	2.55	3.08	1.71		
	PLACE1009424	1.88	3.61	3.18	2.85	3.24	3.93		
5	PLACE1009434	0.84	3.94	2.91	1.29	1.82	2.19		
	PLACE1009443	1.21	7.2	2.55	2.42	3.43	3.17		
	PLACE1009444	1.33	7.71	4.05	2.51	3.17	3.79		
	PLACE1009459	0.23	7.99	1.55	1.71	1.83	0.86		
10	PLACE1009460	1.75	6.84	3.26	5.15	4.31	4.08		
	PLACE1009468	0.99	2.83	3.42	4.43	4.42	2.97		
	PLACE1009476	0.21	1.21	0.73	1.05	0.67	1.33		
	PLACE1009477	1.35	3.13	2.67	3.06	2.35	2.2		
	PLACE1009493	0.87	3.35	0.94	1	1.87	1.41		
15	PLACE1009502	0.76	4.64	2.13	1.19	1.89	1.66		
	PLACE1009524	1.32	4.22	1.63	0.94	2.14	1.6		
	PLACE1009527	0.95	4.51	2.11	1.64	2.55	1.28		
	PLACE1009531	20.82	28.24	41.52	46.25	43.25	49.96		
	PLACE1009535	1.1	1.56	2.68	2.42	2.15	1.11		
20	PLACE1009539	2.15	3.41	4.18	3.88	2.65	2.57		
	PLACE1009540	5.89	8	11.66	14.8	4.47	3.84		
	PLACE1009542	1.11	3.37	1.42	1.51	2.06	1.44		
	PLACE1009546	0.62	5.27	0.97	2.24	1.64	1.25		
	PLACE1009556	0.35	4.46	3.46	3.36	2.86	3.16		
25	PLACE1009569	0.05	3.93	2.46	3.34	2.7	3.11		
	PLACE1009571	1.67	4.27	2.52	3.04	2.85	2.67		
	PLACE1009573	3.81	2.97	6.73	6.92	8.12	6.49		
	PLACE1009576	1.92	2.51	4.3	2.73	3.66	2.08		
30	PLACE1009580	1.42	1.81	1.74	2.73	3.47	2.33	*	+
	PLACE1009581	0.89	4.25	2.03	2.91	4.38	2.74		
	PLACE1009587	0.96	4.91	2.29	2.43	3.2	1.99		
	PLACE1009593	2.71	6.73	4.37	4.94	6.85	5.03		
	PLACE1009595	1.81	5.44	2.66	2.67	5	2.79		
35	PLACE1009596	1.57	6.83	2.6	3.44	3.97	2.7		
	PLACE1009600	3.03	4.27	4.48	5.48	9.14	4.42		
	PLACE1009604	2.32	4.64	5.02	4.22	6.11	3.23		
	PLACE1009607	1.29	2.48	3.18	3.19	4.17	3.18		
	PLACE1009613	1.94	5.23	2.94	2.65	3.08	2.23		
40	PLACE1009621	1.66	6.72	3.32	8.21	8.67	8.06	*	+
	PLACE1009622	1.78	5.93	3.78	3.9	4.1	3.9		
	PLACE1009624	1.16	5.77	3.42	3.2	3.65	3.5		
	PLACE1009637	2	6.88	3.36	3.07	4.59	3.91		
	PLACE1009639	1.94	1.76	4.15	3.44	3.67	4.99		
45	PLACE1009654	20.88	17.13	34.95	14.94	24.53	20.64		
	PLACE1009659	2.77	6.78	7.45	6.38	8.38	6.55		
	PLACE1009665	1.04	4.21	1.93	1.19	2.72	1.93		
	PLACE1009669	7.73	9.64	14.54	9.85	16.89	8.82		
	PLACE1009670	1.76	5.36	2.54	2.77	4.47	4.01		
50	PLACE1009708	2.1	5.57	5.09	3.64	6.54	5.84		
	PLACE1009721	1.34	4.28	3.56	5.78	5.81	3.01		
	PLACE1009731	1.36	3.59	3	3.58	6.53	5		
	PLACE1009735	1.94	3.94	3.21	5.16	7.52	4.78		
	PLACE1009737	1.89	4.29	2.95	4.83	5.61	5.47	*	+
55	PLACE1009741	1.3	4.32	3.45	2.09	5.03	3.07		

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	PLACE1009752	1.34	5.64	2.65	2.3	3.33	1.68
	PLACE1009763	3.95	9.73	6.82	7.13	7.44	8.39
	PLACE1009766	1.46	6.98	3.32	3.07	5.19	3.75
5	PLACE1009772	0.48	5.19	0.6	1.01	2.46	0.89
	PLACE1009782	0.91	2.39	2.03	2.88	2.91	3.74
	PLACE1009794	2.58	4.45	5.11	3.54	3.66	5.03
	PLACE1009798	1.59	5.37	4	6.26	5.57	5.67
10	PLACE1009845	1.05	6.02	2.92	2.79	3.39	3.92
	PLACE1009849	0.96	6.61	2.35	1.79	3.41	2.59
	PLACE1009857	0.79	4.86	1.45	1.19	1.27	1.56
	PLACE1009861	1.43	4.67	3.87	4.1	3.47	3.11
	PLACE1009872	53.53	52.43	88.5	74.95	49.47	81.73
15	PLACE1009877	5.45	7.59	12.08	10.03	10.3	12.32
	PLACE1009879	0.82	3.28	1.59	1.55	2.99	1.34
	PLACE1009886	0.68	4.04	1.53	1.62	3.04	1.72
	PLACE1009888	1.03	7.4	3.23	5.34	5.84	7.94
	PLACE1009908	1.56	7.63	8.64	3.37	6.71	5.9
20	PLACE1009919	4.5	7.53	8.26	5.84	10.72	10.15
	PLACE1009921	0.96	3.94	3.32	1.63	4.28	2.47
	PLACE1009923	3.82	5.56	6.85	6.32	8.13	5.57
	PLACE1009924	3.01	2.49	4.53	4.43	4.31	1.04
	PLACE1009925	0.61	2.77	1.84	2.51	2.2	2.5
25	PLACE1009931	2.78	5.21	9	8.71	6.93	8.09
	PLACE1009935	0.74	3.71	2.1	1.19	1.08	1.5
	PLACE1009947	0.47	3.83	1.64	1.51	2.46	2.03
	PLACE1009961	0.43	4.08	1.39	1.69	2.18	1.9
	PLACE1009971	0.92	4.9	1.98	1.35	1.74	1.45
30	PLACE1009982	40.34	48.71	89.8	53.8	57.87	66.96
	PLACE1009992	0.94	1.9	2.59	1.47	2.52	0.68
	PLACE1009995	6.47	10.83	15.72	7.79	9.03	11.23
	PLACE1009997	0.55	3.7	3.03	2.76	3.2	2.64
35	PLACE1010002	1.4	4.14	2.82	2.89	3.04	3.46
	PLACE1010011	2.09	8.13	3.85	4.4	5.21	4.68
	PLACE1010013	0.18	12.85	1.74	0.92	1.81	0.68
	PLACE1010021	3.18	11.98	5.42	4.12	4.13	6.06
	PLACE1010023	2.15	8.45	5.16	5.62	6.52	6.14
40	PLACE1010031	4.6	4.35	7.23	6.79	4.91	1.82
	PLACE1010039	1.17	3.3	1.45	1.28	1.23	1.19
	PLACE1010045	1.1	2.83	3.66	2.52	3.55	2.64
	PLACE1010053	1.42	3.56	1.65	2.21	2.76	2.37
	PLACE1010060	1.63	6.1	4.13	4.11	4.6	4.05
45	PLACE1010069	0.41	7.96	2.32	1.48	2.91	1.3
	PLACE1010070	0.92	8.04	1.5	0.45	1.78	1.09
	PLACE1010074	5.25	11.67	11.8	12.32	9.51	11.22
	PLACE1010076	12.75	11.95	29.01	19.58	15.88	16.82
	PLACE1010078	2.96	2.42	4.36	4.64	4.39	3.85
50	PLACE1010081	2.74	4.1	3.7	6.85	7.81	4.59 * +
	PLACE1010083	0.69	2.53	1.51	1.22	1.86	2.26
	PLACE1010089	1.86	4.89	3.35	3.45	3.47	3.48
	PLACE1010096	2.17	7.73	2.91	3.43	4.19	3.2
	PLACE1010102	3.89	10.9	5.33	7.1	9.64	7.57
55	PLACE1010105	2.98	7.46	4.93	7.31	9.04	9.82

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	PLACE1010106	2.46	2.95	4.48	5.47	4.88	5.8	*	+
	PLACE1010130	0.53	1.79	1.17	2.27	2.55	1.23		
	PLACE1010132	2.49	4.65	5.3	5.07	4.39	4.19		
5	PLACE1010134	0.8	3.32	1.15	1.97	2.31	1.67		
	PLACE1010139	6.67	10.51	12.98	14.99	16.1	14.58		
	PLACE1010148	0.96	5.07	1.62	1.48	1.9	1.97		
	PLACE1010152	3.11	5.68	5.16	6.33	6.64	5.76		
	PLACE1010155	3.8	6.17	6.52	16.85	20.56	20.32	**	+
10	PLACE1010156	13.71	15.43	32.21	132.45	85.59	134.99	**	+
	PLACE1010161	1.9	2.81	5.05	3.29	2.92	1.97		
	PLACE1010181	0.73	2.22	1.51	2.58	1.99	2.53		
	PLACE1010194	0.64	3.35	1.03	2.26	2.14	1.64		
15	PLACE1010202	0.4	4.14	1.2	2.91	1.65	2.16		
	PLACE1010231	1.1	3.78	2.39	1.31	2.99	2.73		
	PLACE1010235	1.26	4.24	1.94	2.68	2.42	3.16		
	PLACE1010237	1.01	3.4	2.1	1.14	1.97	0.87		
	PLACE1010251	0.59	0.98	1.95	2.57	3.18	1.62		
20	PLACE1010261	0.97	2.63	2.07	2.69	1.69	1.55		
	PLACE1010270	0.76	2.7	1.3	1.39	2.33	1.42		
	PLACE1010273	0.97	3.27	0.46	1.48	2.25	1.5		
	PLACE1010274	6.28	9.23	9.66	10.49	12.18	14.28		
	PLACE1010277	6.03	10.14	12.68	14.6	16.06	15.84	*	+
25	PLACE1010293	1.8	5.68	3.55	3.65	3.37	3.96		
	PLACE1010297	5.17	11.37	21	24.84	32.59	22.06		
	PLACE1010300	4.18	4.78	8.22	8	9.95	6.87		
	PLACE1010310	16.52	14.75	49.45	70.74	71	77.01	*	+
	PLACE1010321	2.03	4.92	2.46	3.37	4.99	2.73		
30	PLACE1010324	0.88	3.49	1.56	1.12	1.54	1.2		
	PLACE1010329	0.73	4.64	1.95	2.56	3.37	1.96		
	PLACE1010330	3.78	9.09	7.29	2.42	10.45	7.67		
	PLACE1010335	6.43	11.15	7.43	13.15	17.89	19.1	*	+
	PLACE1010341	0.19	4.81	1.24	1.07	3.13	1.54		
35	PLACE1010342	0.77	0.9	0.75	0.48	2.12	0.8		
	PLACE1010346	1.47	1.73	3.61	2.96	4.47	1.71		
	PLACE1010362	1.31	2.69	2.22	2.18	3.49	3.31		
	PLACE1010364	0.78	2.56	1.65	1.19	2.32	1.49		
	PLACE1010368	1.66	5.44	3.51	3.41	3.87	4.48		
40	PLACE1010373	9.05	10.48	16.82	12.13	15.45	12.28		
	PLACE1010383	1.91	5.52	5.13	5.58	6.39	4.9		
	PLACE1010385	0.3	3.01	1.07	0.04	0.6	0.9		
	PLACE1010389	6.28	7.98	13.24	22.3	13.64	22.94	*	+
45	PLACE1010401	0.73	2.72	1.32	1.99	2.87	2.21		
	PLACE1010410	3.15	4.83	6.71	4.78	7.55	7.32		
	PLACE1010418	1.88	4.73	4.2	4.71	5.14	4.66		
	PLACE1010425	0.93	4.78	1.43	1.78	1.96	2.15		
	PLACE1010443	6.98	13.83	51.39	36.22	63.67	48.93		
50	PLACE1010445	0.95	5.02	0.68	2.69	3.81	2.44		
	PLACE1010481	1.19	2.06	2.46	1.75	2	1.85		
	PLACE1010482	28.99	29.39	53.06	31.75	19.63	40.44		
	PLACE1010491	3.36	6.4	5.38	4.96	5.98	3.26		
	PLACE1010492	4	4.75	5.95	5.57	8.15	7.77		
55	PLACE1010509	0.8	4.32	3.15	3.09	3.01	2.99		

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	PLACE1010518	3.33	6.72	6.58	7.3	8.25	8.24	
	PLACE1010522	2.3	5.96	4.35	1.87	3.52	2.64	
	PLACE1010529	1.8	6.5	3.84	5.43	8.44	7.2	
5	PLACE1010547	0.79	1.57	1.76	1.51	1.93	2.45	
	PLACE1010560	0.63	2.51	2.06	3.31	2.2	2.51	
	PLACE1010562	0.74	2.68	1.65	1.64	2.1	1.63	
	PLACE1010579	1.11	7.13	2.63	3.45	4.67	3.26	
10	PLACE1010580	1.35	9.12	3.79	3.27	2.49	4.52	
	PLACE1010599	3.56	6.07	7.94	8.32	9.26	8.13	
	PLACE1010606	1.17	4.42	1.64	3.39	4.17	3.51	
	PLACE1010616	1.84	3.72	5.49	4.09	8.09	6.81	
	PLACE1010622	2.1	3.43	3.91	5.07	4.74	4.69	*
15	PLACE1010624	1.43	3.35	3.98	4.21	6.17	5.22	+
	PLACE1010628	1.37	3.97	2.83	2.14	3.63	4.22	
	PLACE1010629	1.08	4.64	2.24	3.01	3.3	3.5	
	PLACE1010630	1.64	4.77	3.69	4.22	4.78	5.29	
	PLACE1010631	0.5	5.35	2.64	1.55	1.66	2.67	
20	PLACE1010651	14.24	15.75	24.44	37.62	40.09	52.12	*
	PLACE1010661	1.62	4.09	2.28	3.56	6.43	3.22	+
	PLACE1010662	1.32	2.48	1.6	2.98	2.3	1.61	
	PLACE1010668	12.87	15.91	27.82	37.63	30.53	28.75	
	PLACE1010702	1.46	2.34	4.24	3.59	3.6	3.2	
25	PLACE1010709	79.16	78.33	115.91	107.07	96.3	133.25	
	PLACE1010713	7	10.81	14.7	9.14	8.16	15.14	
	PLACE1010714	0.82	7.41	1.58	1.75	2.04	1.47	
	PLACE1010716	0.71	6.19	4.31	2.08	2.3	1.93	
	PLACE1010717	0.9	6.49	2.13	2.17	3.9	2.61	
30	PLACE1010720	14.03	17.05	53.79	46.72	50.7	41.49	
	PLACE1010739	0.9	1.2	1.11	1.73	1.21	1.93	
	PLACE1010743	1.09	2.3	1.99	2.63	2.05	2.21	
	PLACE1010752	0.87	2.92	1.85	1.76	2.05	1.53	
35	PLACE1010761	3.6	8.83	13.51	12.07	16.4	17.08	
	PLACE1010771	1.41	6.89	5.03	6.13	10.3	5.42	
	PLACE1010784	0.9	9.66	1.97	2.07	1.72	1.34	
	PLACE1010786	1.21	8.77	2.83	2.91	3.68	2.21	
	PLACE1010789	0.6	1.16	1.52	1.8	1.89	1.17	
40	PLACE1010800	2.18	2.86	3.25	3.95	3.24	2.93	
	PLACE1010802	2.97	4.63	5.31	5.72	4.27	3.3	
	PLACE1010811	0.89	2.19	1.96	1.83	1.75	2.18	
	PLACE1010813	8.89	13.3	55.85	48.82	72.26	46.7	
	PLACE1010827	1.54	6.43	3.94	4.3	5.52	4.81	
45	PLACE1010833	0.93	8.13	2.63	2.68	3.64	2.09	
	PLACE1010839	1.57	6.22	3.21	4.22	6.72	4.13	
	PLACE1010856	7.58	8.94	12.34	8.02	6.53	8.59	
	PLACE1010857	3.41	3.81	7.63	8.24	5.98	4.56	
	PLACE1010870	1.3	2.24	2.05	1.62	2.38	1.94	
50	PLACE1010877	1.67	4.66	2.69	2.77	3.92	2.62	
	PLACE1010882	0.49	4.8	0.99	1.74	1.27	0.51	
	PLACE1010891	1.1	7.73	1.12	1.85	1.73	0.95	
	PLACE1010896	1.19	5.29	3.18	3.98	3.05	3.47	
	PLACE1010900	7.41	13.29	27.9	23.88	20.99	18.85	
55	PLACE1010916	1.55	1.18	2.06	1.89	1.9	2.2	

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	PLACE1010917	-0.04	0.82	0.36	1.05	2.25	0.56	
	PLACE1010924	1.15	2.31	1.55	1.11	1.88	0.92	
5	PLACE1010925	2.76	5.36	2.17	4.92	6.32	4.16	
	PLACE1010926	1.8	5.73	4.31	5.37	4.35	4.45	
	PLACE1010942	1.7	6.25	5.63	5.53	7.88	7.69	
	PLACE1010943	7.38	10.43	17.12	24.62	29.5	31.96	** +
	PLACE1010944	4.33	7.39	9.3	13.11	11.44	15.58	* +
10	PLACE1010947	1.43	0.9	2.41	2.57	2.8	2.25	
	PLACE1010954	3.56	2.92	7.4	7.92	8.55	7.64	
	PLACE1010960	2.06	3.44	6.07	4.23	7.89	2.6	
	PLACE1010965	2.33	3.81	3.54	6.09	4.92	5.03	* +
	PLACE1010968	1.55	4.69	1.38	4.95	6.51	3.68	
15	PLACE1010978	3.63	6.12	7.05	9	8.94	6.45	
	PLACE1010982	2.23	5.77	5.6	4.74	5.66	4.88	
	PLACE1010990	0.88	5.4	2.04	3.11	3.03	2.19	
	PLACE1011017	5.6	3.78	22.57	25.64	35.47	20.97	
20	PLACE1011019	1.1	1.5	2.48	3.78	4.42	0.88	
	PLACE1011026	4.17	4.93	6.23	6	5.19	2.74	
	PLACE1011032	0.89	3.95	2.03	1.44	1.58	0.56	
	PLACE1011041	1.07	4.13	1.03	1.69	1.22	1.43	
	PLACE1011045	1.49	5.62	2.36	3.26	3.67	4.45	
25	PLACE1011046	0.83	5.25	1.79	2.57	3.17	1.87	
	PLACE1011054	2.33	5.33	6.64	5.26	7.29	5.05	
	PLACE1011056	5.78	5.43	16.22	14.56	19.78	15.67	
	PLACE1011057	2	2.18	3.5	3.29	5.68	3.9	
	PLACE1011059	0.93	1.37	1.56	1.74	2.96	1.79	
30	PLACE1011066	4.49	5.74	6.76	5.38	7.72	5.49	
	PLACE1011087	7.6	7.04	16.48	12.43	17.42	9.79	
	PLACE1011090	2.98	6.14	6.74	3.36	4.13	3.26	
	PLACE1011109	1.99	7.29	4.29	4.08	7.96	3.83	
	PLACE1011114	1.62	4.4	3.13	3.33	4.68	3.29	
35	PLACE1011116	4.89	5.94	6.66	7.43	6.81	8.98	
	PLACE1011122	0.93	2.52	1.84	2.1	1.61	1.64	
	PLACE1011133	0.83	2.22	3.03	3.48	3.52	2.77	
	PLACE1011134	12.47	15.29	66.86	44.95	68.68	51.65	
	PLACE1011143	0.68	4.53	1.48	1.84	2.62	1.41	
40	PLACE1011146	0.91	5.93	1.74	1.97	3.23	2.36	
	PLACE1011160	1.67	7.36	3.81	3.42	4.53	4.24	
	PLACE1011165	1.77	2.34	3.39	2.15	3.39	3.8	
	PLACE1011181	5.25	8.31	37.21	29.38	38.44	30.55	
45	PLACE1011185	2.47	4	3.57	4.66	5.15	4.8	* +
	PLACE1011186	13.16	12.8	16.45	21.18	25.69	28.83	* +
	PLACE1011203	1.08	4.64	2.19	1.75	2.94	1.96	
	PLACE1011214	9.02	16.55	59.24	46.39	62.58	47.89	
	PLACE1011219	1.41	4.91	3.6	3.26	4.96	2.9	
50	PLACE1011221	2.68	5.47	6.15	6.23	8.57	7.51	
	PLACE1011229	1.38	4.2	2.69	2.43	2.43	3.09	
	PLACE1011231	0.53	1.5	1.62	1.84	2.59	2.4	
	PLACE1011236	5.69	7.9	43.53	33.48	56.77	44.25	
	PLACE1011247	8.36	10.08	19.16	24.17	26.33	29.74	* +
55	PLACE1011263	0.57	6.43	4.23	2.62	4.11	5.09	
	PLACE1011273	0.72	3.62	1.17	2.01	1.64	1.72	

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	PLACE1011278	2.42	5	6.12	3.98	4.84	4.31
	PLACE1011289	2.73	5.84	7.57	6.34	6.13	6.08
	PLACE1011291	3.2	5.19	8.31	7.32	8.04	7.95
5	PLACE1011296	0.93	2.45	1.94	1.76	2.63	2.05
	PLACE1011310	1.72	2.64	3.36	4.51	2.77	4.48
	PLACE1011311	1.8	3.97	6.33	7.8	9.34	6.73
	PLACE1011321	1.29	4.77	3.5	3.3	2.63	3.33
10	PLACE1011325	0.63	4.2	1.84	2	2.74	1.59
	PLACE1011332	5.65	10.55	9.4	14.8	14.57	15.04 * +
	PLACE1011340	0.86	4.88	3.38	3.81	4.71	3.47
	PLACE1011353	5.39	5.53	8.39	10.06	8.58	4.43
	PLACE1011360	1.09	3.29	2.18	2.11	3.06	2.41
15	PLACE1011364	4.88	5.69	7.92	6.34	4.57	4.57
	PLACE1011365	0.92	3.36	2.95	3.01	3.6	2.06
	PLACE1011371	9.37	10.69	63.06	56.51	87.51	64.33
	PLACE1011375	1.62	9.37	3.35	2.61	2.74	1.62
	PLACE1011386	3.91	12.96	4.18	6.88	5.51	5.93
20	PLACE1011399	1.52	10.14	4.27	2.12	4.22	3.77
	PLACE1011406	1.25	2.05	1.81	5.03	3.26	2.38
	PLACE1011407	0.64	2.05	2.58	2.08	2.19	2.02
	PLACE1011419	2.83	3.2	6.02	6.23	4.18	3.72
	PLACE1011433	3.09	4.43	6.13	3.41	4.74	4.99
25	PLACE1011440	0.77	5.81	2.48	2.1	2.24	2.27
	PLACE1011452	1.06	8.86	2.43	2.87	2.71	2.68
	PLACE1011465	0.09	8.53	1.96	1.04	1.68	0.85
	PLACE1011472	1.52	7.67	3.98	0.97	2.87	1.59
30	PLACE1011477	11.18	12.29	54.35	31.86	55.86	45.67
	PLACE1011478	1.24	1.64	3.11	5.03	3.02	3.01
	PLACE1011492	2.24	3.54	5.01	5.45	6.74	5.27
	PLACE1011498	0.57	2.77	0.98	1.18	1.69	1.15
	PLACE1011501	0.49	4.67	1.8	4.87	5.63	7.5
35	PLACE1011503	0.44	5.37	0.79	0.5	0.82	0.35
	PLACE1011509	1.1	7.8	3.38	4.62	5.08	5.74
	PLACE1011514	5.86	11.61	11.98	13	17.7	13.17
	PLACE1011516	10.37	13.29	18.32	18.32	8.08	3.63
	PLACE1011520	0.34	0.95	1.34	1.3	1.73	1.01
40	PLACE1011538	52.87	99.27	185.04	129.45	86.87	63.9
	PLACE1011555	0.87	2.88	2.83	1.55	2.03	1.48
	PLACE1011561	3.2	4.53	1.98	6.81	5.31	3.08
	PLACE1011563	1.35	4.74	3.49	2.52	2.64	2.87
	PLACE1011567	1.04	4.94	3.36	2.75	4.19	2.77
45	PLACE1011569	0.32	4.35	2.77	2.38	2.46	2.28
	PLACE1011576	3.25	1.88	7.94	7.85	9.1	8.03
	PLACE1011586	3.24	2.5	6.22	4.43	4.35	2.94
	PLACE1011635	1.85	2.56	4.53	9.96	12.43	8.71 ** +
50	PLACE1011641	0.43	2.9	0.9	1.71	1.18	1.19
	PLACE1011642	5.05	6.96	10.37	12.13	10.86	10.09
	PLACE1011643	1.29	3.69	1.14	2.38	2.28	2.14
	PLACE1011646	8.68	12.8	30.53	39.05	54.16	37.76 * +
	PLACE1011649	1.35	5.7	3.88	4.5	4.61	5.46
55	PLACE1011650	1.15	1.45	2.54	2.47	3.24	3.75
	PLACE1011661	1.02	2.26	2.8	3.95	5.92	3.46

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	PLACE1011664	2.21	3.18	3.99	5.31	3.93	1.73		
	PLACE1011672	0.88	4.14	0.72	2.69	3.57	2.04		
	PLACE1011675	0.51	2.31	1.32	1.66	0.99	0.83		
5	PLACE1011682	2.04	4.56	2.23	2.22	4.03	2.12		
	PLACE1011708	1.1	5.89	3.8	5.5	8.12	4.66		
	PLACE1011719	1.07	4.58	1.66	3.55	3.88	3.03		
	PLACE1011725	1.23	1.19	2.72	3.73	5.19	4.3	*	+
10	PLACE1011729	0.86	1.03	1.8	2.38	3.26	1.22		
	PLACE1011741	2.36	3.67	3.64	4.16	2.52	4.23		
	PLACE1011749	1.58	3.89	4.09	3.49	4.85	3.27		
	PLACE1011757	20.92	30.53	55.88	56.6	55.88	49.59		
	PLACE1011762	0.4	4.34	2.69	3.91	2.14	2.3		
15	PLACE1011778	0.51	4.39	1.99	1.34	2.02	1.34		
	PLACE1011783	2.59	4.63	5.46	4.8	8.41	5.55		
	PLACE1011795	0.74	1.28	2.24	1.47	1.8	1.22		
	PLACE1011810	9.28	10.82	19.51	13.32	17.73	15.47		
	PLACE1011824	5.38	8.17	38.05	25.52	42.89	16.75		
20	PLACE1011825	10.61	16.39	22.6	17.63	18.92	16.07		
	PLACE1011835	24.64	32.67	47.67	32.09	26.75	37.23		
	PLACE1011836	18.11	18.97	31.43	33.14	47.23	13.95		
	PLACE1011847	2.67	6.74	6.42	5.34	7.18	5.84		
	PLACE1011855	0.9	6.06	3.53	3.23	4.47	3.49		
25	PLACE1011858	5.83	7.44	9.37	6.88	6.25	8.35		
	PLACE1011874	1.35	3.14	3.55	4.18	5.28	4.65		
	PLACE1011875	0.57	2.29	1.11	2.66	2.48	2.64		
	PLACE1011877	3.8	5.03	4.4	7.67	6.8	9.97	*	+
30	PLACE1011891	0.17	3.81	1.31	1.13	1.34	1.26		
	PLACE1011896	-0.1	5.22	1.45	-0.19	1.07	0.32		
	PLACE1011920	0.21	5.87	1.04	1.1	1.92	1.76		
	PLACE1011922	2.4	4.18	4.72	3.72	2.88	3.98		
	PLACE1011923	3.42	4.82	7.51	8.09	5.38	12.28		
	PLACE1011937	3.16	2.24	3.76	3.81	5.58	4.64		
35	PLACE1011939	14.93	17.81	26.01	41.75	45.05	47.88	**	+
	PLACE1011940	6.13	7.58	12.68	5.73	7	7.23		
	PLACE1011962	3.28	7.83	7.35	6.39	8.38	8.01		
	PLACE1011964	0.39	5.05	1.66	1.04	1.95	1.46		
40	PLACE1011978	1.55	4.65	3.35	4.48	5.91	5.14		
	PLACE1011980	2.1	4.62	6.07	3.95	4.91	5.35		
	PLACE1011981	5.77	7.28	38.2	27.22	35.24	34.99		
	PLACE1011982	0.83	3.1	2.23	1.82	2.59	1.57		
	PLACE1011995	0.81	3.4	3.73	2.51	3.59	2.86		
45	PLACE1012023	1.38	5.37	1.87	2.09	2.46	1.91		
	PLACE1012026	1.95	5.72	4.23	6.08	9.51	9.8		
	PLACE1012031	2.49	5.81	4.54	4.34	6.35	4.03		
	PLACE2000003	1.18	3.64	6.86	7.38	8.12	8.92		
	PLACE2000005	1.16	2.41	2.16	2.76	2.03	1.89		
50	PLACE2000006	2.52	4.13	15.6	11.34	16.58	13.4		
	PLACE2000007	0.96	4.85	4.24	3.94	5.13	3.33		
	PLACE2000011	1.72	3.27	3.34	4.3	5.06	3.62		
	PLACE2000014	4.04	5.93	23.94	27.19	30.87	30.97	*	+
	PLACE2000015	1.27	4.79	3.52	2.77	3.31	2.69		
55	PLACE2000017	0.48	4.78	2.15	2.65	2.56	2.45		

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	PLACE2000021	1.99	5.06	4.09	3.72	6.24	5.61
	PLACE2000022	1.8	2.8	4.31	3.35	4.64	2.71
5	PLACE2000030	9.37	11.08	71.38	55.43	60.32	35.97
	PLACE2000032	1.23	2.89	3.51	3.53	3.24	2.32
	PLACE2000033	3.29	6.3	12.11	12.49	14.25	9.37
	PLACE2000034	0.6	4.3	1.92	1.79	2.19	2.44
	PLACE2000039	2.75	8.06	3.92	6.27	8.01	4.81
10	PLACE2000043	7	11.08	22.94	19.27	26.58	17.38
	PLACE2000044	0.63	6.92	1.12	1.8	1.71	1.29
	PLACE2000047	0.84	5.25	5.15	5.4	6.46	7.32
	PLACE2000050	1.48	2.68	4.78	2.92	2.98	1.2
	PLACE2000061	0.47	2.07	1.17	0.95	1.34	0.25
15	PLACE2000062	1.99	2.83	4.12	4.89	4.4	3.09
	PLACE2000072	0.78	2.45	1.57	1.85	1.62	1.69
	PLACE2000073	0.89	5.86	2.86	2.8	2.61	3.07
	PLACE2000097	8.54	19.93	23.93	27.69	35.36	26.36
20	PLACE2000100	1.87	7.79	3.53	4.23	6.29	4.22
	PLACE2000103	1.03	7.44	2.25	3.51	5.17	4.38
	PLACE2000106	1.53	2.42	4.19	5.71	3.29	4.01
	PLACE2000111	2.05	3.17	4.37	4.07	6.6	4.75
	PLACE2000115	0.3	2.06	0.75	0.31	1.29	0.97
25	PLACE2000118	10.15	17.04	21.09	13.73	15.21	22.01
	PLACE2000124	10.14	17.83	62.13	53.2	98.37	62.96
	PLACE2000132	0.06	6.26	1.48	0.99	1.5	1.56
	PLACE2000136	0.55	7.94	0.91	1.47	1.37	1.02
	PLACE2000137	0.96	4.46	2.4	2.65	4.12	3.14
30	PLACE2000140	2.91	5.24	14.34	13.2	12.08	9.43
	PLACE2000147	1.49	1.52	2.83	1.06	0.97	1.12
	PLACE2000153	0.3	3.44	2.15	1.69	2.45	1.95
	PLACE2000164	0.66	2.78	1.13	2.66	1.62	1.62
	PLACE2000170	1.54	6.18	4.69	5.26	9.09	6.24
35	PLACE2000172	0.33	4.34	2.15	1.25	1.93	2.43
	PLACE2000173	0.92	4.97	3.37	3.33	3.71	2.74
	PLACE2000174	1.17	4.68	2.43	1.85	2.89	2.05
	PLACE2000176	1.22	1.57	2.58	3.28	2.27	1.42
	PLACE2000187	1.01	2.08	2.55	3.45	3.66	2.19
40	PLACE2000216	7.03	9.28	11.47	14.09	9.13	3.68
	PLACE2000219	0.69	4.02	2.72	3.55	3.58	2.3
	PLACE2000221	2.49	6.81	6.53	7.22	9.33	8.56
	PLACE2000223	0.72	3.2	1.71	1.16	1.05	0.48
	PLACE2000231	1.02	3.97	3.11	3.43	2.61	2.47
45	PLACE2000235	1.82	5.27	6.17	6.02	7.45	6.97
	PLACE2000246	1.93	2	6.06	4.58	5.09	3.93
	PLACE2000264	0.67	1.39	1.85	2.45	3.74	3 * +
	PLACE2000274	0.65	2.4	2.12	3.09	4.11	2.1
	PLACE2000287	0.81	4.44	1.49	2	2.59	1.34
50	PLACE2000296	1.01	4.56	1.55	2.5	3.16	1.69
	PLACE2000302	1.34	4.67	2.86	3.52	3.35	3.45
	PLACE2000305	3.09	6.65	5.42	6.3	7.15	5.02
	PLACE2000317	0.92	6.34	2.26	3.15	2.95	2.4
	PLACE2000324	1.19	1.25	3.09	4.2	5.84	3.3
55	PLACE2000334	3.52	5	6.6	7.33	8.12	5.88

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	PLACE2000335	1.47	4.35	4.24	5.68	6.25	4.76	
	PLACE2000340	0.64	3.47	1.63	1.58	1.52	1.65	
	PLACE2000341	4.21	7.87	28.81	18.94	32.45	19.16	
5	PLACE2000342	2.07	5.11	4.32	4.84	5.82	4.49	
	PLACE2000347	1.24	5.26	5.58	7.83	6.22	7.55	
	PLACE2000357	8.49	13.56	15.35	17.83	18.98	21.24	* +
	PLACE2000358	2.87	3.65	8.67	4.88	7.63	4.37	
10	PLACE2000359	1.27	1.79	4.45	3.28	6.65	3.61	
	PLACE2000366	1.93	3.14	3.22	3.99	5.6	4.17	
	PLACE2000371	4.29	5.2	6.08	5.95	9.06	7.32	
	PLACE2000373	1.91	4.8	5.98	5.69	6.29	4.19	
	PLACE2000374	1.86	5.17	2.78	1.62	2.79	1.49	
15	PLACE2000379	0.34	4.85	1.32	1.28	0.92	0.04	
	PLACE2000386	39.29	43.92	84.66	87.53	104.55	76.56	
	PLACE2000388	1.96	3.35	3.89	2.78	3.48	3.49	
	PLACE2000392	33.29	39.2	59.56	42.5	52.12	58.24	
	PLACE2000394	1.26	3.27	3.01	5.69	4.35	4.34	* +
20	PLACE2000398	0.73	3.88	2.36	2.03	3.59	1.35	
	PLACE2000399	3.7	6.82	7.01	7.15	7	6.79	
	PLACE2000402	2.15	6.88	3.84	2.86	3.68	3.9	
	PLACE2000404	5.2	9.96	10.67	10.03	11.04	6.47	
	PLACE2000411	3.21	7.2	5.21	5.27	5.73	6.68	
25	PLACE2000418	0.73	2.28	2.41	2.22	3.07	2.37	
	PLACE2000419	0.99	2.32	2.54	4.95	4.55	3.29	* +
	PLACE2000425	1.26	3.98	3.11	4.28	4.81	5.2	
	PLACE2000427	0.7	5.13	3.27	2.54	3.04	2.47	
30	PLACE2000433	0.77	7.05	2.6	2.33	3.09	2.46	
	PLACE2000435	0.48	5.19	1.49	1.69	1.63	1.5	
	PLACE2000438	1.61	4.74	3.66	2.33	2.81	3.15	
	PLACE2000450	3.01	4.38	5.67	6.51	7.39	5.63	
	PLACE2000455	0.24	2.62	1.24	1.65	2	1.82	
	PLACE2000458	0.38	3.3	1.81	1.06	2.7	1.24	
35	PLACE2000464	2.15	4.91	5.3	7.43	9.68	8.83	* +
	PLACE2000465	1.43	6.72	6	6.51	8.27	6.31	
	PLACE2000473	120.94	179.35	328.3	214.7	297.75	279.74	
	PLACE2000477	0.43	3.87	1.34	1.13	2.22	0.97	
40	PLACE3000004	2.22	4.63	6.39	5.27	7.51	5.2	
	PLACE3000009	19.91	19.71	105.63	77.3	140.99	92.95	
	PLACE3000020	10.03	9.03	49.6	36.74	46.52	23.82	
	PLACE3000029	6.59	9.63	24.88	14.88	18.47	20.04	
	PLACE3000038	0.52	2.37	2.47	1.44	2.4	2.05	
45	PLACE3000052	5.13	7.95	23.92	25.01	29.61	24.94	
	PLACE3000059	0.57	5	2.42	0.75	2.8	1.27	
	PLACE3000067	2.51	5.79	7.44	5.66	8.53	7.75	
	PLACE3000069	1.95	5.61	3.58	5.24	3.79	4.55	
	PLACE3000070	2.57	5.57	9.04	9.5	10.42	10.57	
50	PLACE3000103	3.85	7.84	11.87	6.6	8.32	4.37	
	PLACE3000119	1.59	2.74	3.15	3.24	3.67	2.95	
	PLACE3000121	7.58	8.44	38.1	30.63	42.28	32.64	
	PLACE3000124	1.53	4.54	5.95	6.35	7.75	7.18	
	PLACE3000135	0.69	5.46	1.1	0.76	0.9	0.59	
55	PLACE3000136	0.77	10.46	4.46	2.12	2.77	2.01	

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	PLACE3000142	0.7	9.94	1.75	1.53	2.76	1.13	
	PLACE3000145	8.69	17.55	55.33	42.85	49.12	39.96	
	PLACE3000147	15.7	12.92	39.97	64.96	54.76	30.34	
5	PLACE3000148	0.7	2.08	1.48	0.82	1.4	1.38	
	PLACE3000154	0.48	1.86	0.67	1.5	0.87	0.44	
	PLACE3000155	1.28	4.26	2.53	3.97	4.76	3.04	
	PLACE3000156	1.11	7.96	2.07	1.96	3.4	2.81	
10	PLACE3000157	0.92	8.37	1.75	2.06	3.02	2.72	
	PLACE3000158	1.73	8.82	5.05	3.81	5.63	4.77	
	PLACE3000160	8.11	15.22	19.5	33.66	34.71	33.78	** +
	PLACE3000169	2.15	2.65	6.87	4.3	5.11	5.12	
	PLACE3000181	1.06	2.14	3.94	3.22	2.62	3	
15	PLACE3000194	0.31	2.83	1.77	1.89	2.58	2.42	
	PLACE3000197	1.18	2.66	2.09	2.42	2.46	2.21	
	PLACE3000199	0.22	4.8	1.63	0.55	0.86	0.43	
	PLACE3000205	11.79	17.95	57.49	51.4	63.83	42.63	
20	PLACE3000207	3.37	6.91	7.13	6.7	8.92	6.23	
	PLACE3000208	2.26	4.96	2.66	5.28	5.97	5.84	
	PLACE3000213	4.79	5.55	10.8	5.12	5.16	5.05	
	PLACE3000215	1.88	5.02	5.71	4.74	5	3.03	
	PLACE3000218	0	1.63	1.18	0.97	0.62	0.31	
25	PLACE3000220	1.96	3.55	4.58	6.74	7.52	6.69	* +
	PLACE3000221	14.42	25.34	40.15	43.8	51.16	36.99	
	PLACE3000225	1.15	4.68	3.11	2.11	2.67	1.28	
	PLACE3000226	1.37	5.65	5.16	3.78	7.42	3.68	
	PLACE3000230	0.83	3.46	1.36	2	2.8	1.73	
30	PLACE3000231	1.31	1.97	2.37	4.86	3.95	4.12	** +
	PLACE3000235	1.12	1.75	3.89	3.95	4.21	3.39	
	PLACE3000242	2.6	5.11	9.24	9.46	10.97	8.29	
	PLACE3000244	1.05	3.2	1.81	1.85	1.81	0.64	
	PLACE3000253	0.7	3.75	1.64	2.67	2.11	1.27	
35	PLACE3000254	2.5	4.75	4.04	6.19	6.09	5.75	* +
	PLACE3000271	2.67	6.06	6.81	10.96	10.99	9.5	* +
	PLACE3000276	1.1	5.78	2.27	1.48	1.9	1.78	
	PLACE3000304	5.55	4.69	10.81	11.19	11.49	10.5	
40	PLACE3000309	0.43	1.67	1.87	2.43	2.94	2.78	* +
	PLACE3000310	2.19	2.19	3.73	4.84	4.81	3.4	
	PLACE3000320	1.02	3.65	1.8	2.54	2.37	2.32	
	PLACE3000322	1.31	4.23	6.63	7.5	7.8	6.09	
	PLACE3000330	24.05	24.44	41.08	31.87	35.83	29.17	
45	PLACE3000331	1.21	5.86	4.14	4.34	5.7	4.31	
	PLACE3000336	2.61	6.99	4.42	4.24	5.72	5.11	
	PLACE3000339	7.36	5.1	11.41	16.25	18.28	17.37	** +
	PLACE3000341	1.65	1.32	2.41	4.08	4.35	3.65	** +
	PLACE3000350	5.88	6.4	12.86	15.45	18.5	15.41	* +
50	PLACE3000352	1.54	3.88	2.13	2.37	2.25	1.71	
	PLACE3000353	5.38	9.72	11.8	19.12	22.98	15.5	* +
	PLACE3000362	0.62	4.92	4.72	3.61	5.33	3.39	
	PLACE3000363	2.19	5.13	2.32	1.89	3.28	2.07	
	PLACE3000365	1.34	6.11	3.37	3.34	4.05	2.12	
55	PLACE3000373	0.89	1.52	3.66	2.93	6.08	2.3	
	PLACE3000374	1.07	1.85	2.91	2.72	2.99	2.15	

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	PLACE3000387	0.31	3.32	1.04	1.24	1.65	1.29
	PLACE3000388	1.18	3.22	1.94	2.76	3.49	2.22
	PLACE3000399	2.12	4.66	6.28	7.42	9.84	6.05
5	PLACE3000400	3.08	5.44	11.87	7.97	10.77	7.82
	PLACE3000401	7.52	11.42	18.59	22.61	29.55	23.4 * +
	PLACE3000402	1.79	3.21	3.4	2.19	1.74	1.79
	PLACE3000405	3.37	3.74	5.82	5.54	7.22	6.01
	PLACE3000406	2.1	2.91	3.11	3.48	3.68	2.42
10	PLACE3000413	1.18	2.72	2.69	1.71	2.06	1.52
	PLACE3000416	1.05	4.03	4.04	3.43	2.67	2.72
	PLACE3000425	1.21	6.27	4.33	3.98	6.36	3.92
	PLACE3000437	4.79	10.85	29.89	16.69	25.26	19.14
	PLACE3000455	2.97	8.07	10.62	8.97	10.39	7.91
15	PLACE3000475	16.52	19.2	47.35	40.22	39.77	34.21
	PLACE3000477	5.44	4.79	5.56	8.05	5.52	8.42
	PLACE4000003	0.38	2.97	1.61	3.14	2.33	2.31
	PLACE4000008	15.19	11.38	16.76	13.05	14.26	8.84
20	PLACE4000009	1.17	6.19	3.39	3.93	3.37	1.82
	PLACE4000014	1.31	5.12	1.77	2.16	3.03	2.19
	PLACE4000029	6.33	8.48	35.37	23.93	32.21	24.25
	PLACE4000034	2.27	6.24	5.22	6.46	6.52	4.91
	PLACE4000049	3.39	3.35	5.21	3.85	5.82	4.86
25	PLACE4000052	1.41	3.36	2.2	2.62	2.64	2.02
	PLACE4000062	1.6	4.94	5.06	4.25	5.06	3.71
	PLACE4000063	2.59	6.87	5.19	4.86	4.81	3.73
	PLACE4000089	1.52	6.31	3.35	2.81	3.91	2.84
	PLACE4000093	0.44	5.6	1.61	1.28	1.65	1.98
30	PLACE4000100	2.72	6.13	4.75	4.33	3.62	3.94
	PLACE4000103	0.63	4.48	5.64	4.4	5.67	2.9
	PLACE4000106	3.2	5.33	6.63	7.1	5.13	7.21
	PLACE4000128	1.93	3.97	4.88	4.15	4.96	4.4
	PLACE4000129	0.74	3.26	1.64	1.57	2.11	1.78
35	PLACE4000131	7.14	10.85	41.43	32.45	41.08	31.22
	PLACE4000147	0.34	3.65	0.54	0.45	0.93	0.61
	PLACE4000156	2.47	6.08	8.06	7.83	13.47	9.07
	PLACE4000175	0.72	4.08	1.48	0.98	0.91	0.84
	PLACE4000190	14.55	18.47	70.34	49.15	74.82	60.76
40	PLACE4000192	1.3	2.27	3.6	2.36	2	1.25
	PLACE4000206	5.35	6.65	12.44	7.13	7.1	6.02
	PLACE4000211	3.34	4.64	22.23	11.68	12.35	13.44
	PLACE4000214	0.86	3.61	2.68	2.08	2.53	1.69
	PLACE4000222	0.93	5.28	4.36	4.13	4.75	3.5
45	PLACE4000223	0.46	4.51	1.79	1.37	1.22	0.38
	PLACE4000229	1.9	5.79	2.11	2.81	3.36	3.48
	PLACE4000230	1.11	5.89	6.51	3.61	6.81	5.15
	PLACE4000233	1.26	3.02	5.66	2.92	2.98	3.51
	PLACE4000239	2.35	3.68	4.17	4.19	3.97	3.35
50	PLACE4000247	0.52	2.37	3.38	2.64	3.1	2.35
	PLACE4000250	1.18	3.24	2.35	3.33	3.68	2.8
	PLACE4000252	1.06	4.99	2.25	1.92	1.75	1.64
	PLACE4000259	4.42	11.95	18.1	14.47	22.09	14.02
55	PLACE4000261	0.87	10.29	1.07	2.03	1.9	1.12

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	PLACE4000264	15.86	24.96	36.9	11.96	21.82	22.51	
	PLACE4000269	3.48	3.71	7.95	4.62	4.55	2.85	
	PLACE4000270	0.43	1.42	1.87	1.75	1.83	0.59	
5	PLACE4000281	17.84	20.97	44.05	32.93	28.37	28.87	
	PLACE4000300	0.67	2.06	2.04	3.21	2.88	3.58	* +
	PLACE4000320	1.33	5.86	3.1	2.84	5.32	3.21	
	PLACE4000323	1.63	7.43	5.13	4.03	4.65	4.82	
10	PLACE4000326	1.8	10.98	5.67	5.72	8.73	5.59	
	PLACE4000344	0.22	5.75	2.62	1.66	1.6	1.18	
	PLACE4000347	4.7	3.82	13.93	16.83	16.75	17.36	* +
	PLACE4000354	3.18	6.29	10.68	5.17	2.81	2.79	
	PLACE4000367	0.79	2.97	1.71	0.87	1.3	1.38	
15	PLACE4000369	1.35	3.97	2.36	1.99	1.96	0.82	
	PLACE4000379	2.44	6.66	5.44	5.94	7.55	5.07	
	PLACE4000387	0.88	5.86	2.11	1.28	0.84	1.12	
	PLACE4000392	0.42	5.58	1.32	1.81	1.02	1.63	
	PLACE4000399	10.99	17.08	75.17	59.11	80.22	58	
20	PLACE4000401	0.72	0.7	1.53	1.17	0.83	1.4	
	PLACE4000403	3.15	4.13	8.51	5.29	6.38	5.87	
	PLACE4000411	2.22	2.28	4	2.27	2.6	1.82	
	PLACE4000415	0.7	3.55	2.8	1.16	1.86	0.78	
	PLACE4000416	25.49	29.13	33.54	23.65	21.92	24.83	
25	PLACE4000424	1.61	5.59	3.33	3.27	3.92	2.51	
	PLACE4000431	3.89	7.39	21.01	17.68	28.21	16.79	
	PLACE4000443	0.07	4.33	2.15	1.52	2.83	1.14	
	PLACE4000445	3.94	5.43	9.98	7.62	6.99	6.27	
30	PLACE4000450	2.99	3.65	23.28	15.51	24.53	16.04	
	PLACE4000455	5.18	7.39	9.55	8	7.21	4.63	
	PLACE4000465	1.39	4.34	3.26	4.15	6.07	4.34	
	PLACE4000466	120.96	98.04	201.25	113.83	170.96	145.31	
	PLACE4000472	3.12	9.6	10.17	10.92	13.21	9.22	
35	PLACE4000487	3.18	7.83	16.5	14.66	16.62	15.05	
	PLACE4000489	0.93	4.69	3.41	1.95	3.88	1.69	
	PLACE4000494	1.15	1.6	4.07	2.74	3.1	2.08	
	PLACE4000502	6.3	5.39	10.92	11.65	15.08	6.37	
	PLACE4000521	2.5	3.44	16.06	12.78	20.63	11.2	
40	PLACE4000522	5.07	6.17	9.07	12.43	8.68	14.11	
	PLACE4000537	0.98	4.28	1.27	1.67	1.61	1.22	
	PLACE4000548	1.99	5.69	2.46	3.04	3.68	2.32	
	PLACE4000558	0.87	6.72	1.97	3.15	2.41	2.15	
	PLACE4000581	2.1	7.22	7.04	3.9	5.96	5.44	
45	PLACE4000590	0.4	0.61	0.15	0.4	0.81	-0.25	
	PLACE4000593	2.94	2.98	5.22	4.44	5.82	3.83	
	PLACE4000612	0.68	3.33	3.33	1.5	3.02	2.74	
	PLACE4000638	1.25	4.24	0.84	1.2	1.44	1.58	
	PLACE4000650	0.82	4.67	1.02	1.43	1.11	1.16	
50	PLACE4000651	2.42	6.4	7.48	5	7.01	6.07	
	PLACE4000654	0.98	5.7	2.47	1.35	2.48	1.47	
	PLACE4000670	0.5	4.06	2.92	0.76	1.29	0.67	
	PLACE4000685	6.35	8.68	13.83	13.46	14.26	13.77	
	PLACE4000687	0.37	3.02	1.11	2.2	1.4	1.12	
55	PLACE5000003	1.1	2.74	3.31	3.21	3.55	3.07	

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	PLACE5000005	12.43	16.53	27.36	24.54	24.57	24.76	
	PLACE5000019	0.4	4.15	1.13	0.59	1.89	0.79	
	PLACE5000021	0.74	4.59	1.61	0.39	0.93	0.32	
5	PLACE5000022	1.2	6.11	2.25	3.17	2.76	2.09	
	PLACE5000024	1.77	2.58	2.27	2.92	3.39	3.84	* +
	PLACE5000036	1.81	3.24	3.11	2.41	3.19	2.84	
	PLACE5000059	14.41	17.79	26.55	25.98	30.03	34.87	
10	PLACE5000076	1.41	3.61	2.22	4.04	3.96	2.54	
	PLACE5000117	7.44	12.48	15.66	16.87	18.78	20.64	
	PLACE5000143	0.85	6.45	2.11	1.67	2.85	2.73	
	PLACE5000152	0.42	4.49	1.23	1.61	1.95	1.57	
	PLACE5000154	18.23	23.5	45.06	21.81	25.65	31.8	
15	PLACE5000155	3.35	2.81	5.51	3.94	2.78	4.87	
	PLACE5000165	3.78	4.4	6.67	4.51	5.99	5.82	
	SKNMC1000004	9.7	11.62	16.77	10.19	12.16	13.96	
	SKNMC1000011	1.82	8.58	4.12	5.89	3.95	6.77	
	SKNMC1000013	0.51	6.69	1.13	1.21	2.14	1.44	
20	SKNMC1000014	1.28	4.18	3.22	3.77	6.37	3.96	
	SKNMC1000018	3.42	5.19	5.25	5.51	5.68	3.44	
	SKNMC1000020	0.95	4.03	3.46	3.6	4.68	4.56	
	SKNMC1000046	2	3.17	3.48	3.95	3.26	2.55	
	SKNMC1000050	4.99	8.04	10.32	5.4	6.28	6.12	
25	SKNMC1000062	9.79	12.6	20.18	19.2	15.42	18.73	
	SKNMC1000075	1.45	4.3	2.01	1.98	1.89	2.92	
	SKNMC1000082	1.12	4.39	2.13	1.85	1.78	2.39	
	SKNMC1000091	4.54	7.52	7.95	11.74	12.86	12.77	** +
30	SKNMC1000099	0.33	4.29	1.98	1.32	0.65	1.18	
	SKNMC1000104	1.13	4.24	3.45	1.47	3.14	2.43	
	SKNMC1000113	0.97	1.83	1.2	1.74	2.63	0.89	
	SKNMC1000119	1.73	2.64	5.07	4.48	5.34	4.67	
	SKNMC1000142	0.04	2.87	0.99	1.27	0.75	1	
35	SKNMC1000170	0.91	4.75	2.34	1.71	1.49	1.11	
	SKNMC1000178	3.02	8.39	7.08	5.77	9.65	9.02	
	SKNMC1000194	0.63	9.82	1.51	0.61	1.73	1.3	
	SKNMC1000198	1.35	11.01	3.33	2.65	2.1	2.88	
	SKNMC1000225	1.35	6.44	2.97	2.39	3.4	3.26	
40	SKNMC1000249	0.49	2.14	0.75	0.57	0.51	0.52	
	SPLEN1000007	0.74	2.15	2.11	1.7	2.26	1.99	
	SPLEN1000012	0.39	1.9	1.72	1.19	0.8	0.84	
	SPLEN1000014	1.78	4.4	4.9	5.75	4.33	3.99	
	SPLEN1000036	4.95	11.64	24.32	20.56	27.73	21.68	
45	SPLEN1000059	0.04	6.69	1.06	0.91	1.79	1.47	
	SPLEN1000068	1.68	10.81	5.71	5.79	5.17	5.64	
	SPLEN1000072	1	8.5	4.7	2.82	3	2.21	
	SPLEN1000101	20.01	18.4	45.64	29.93	25.24	12.63	
	SPLEN1000108	0.56	1.54	0.98	0.75	1.11	0.76	
50	SPLEN1000113	1.33	2.27	3.04	2.72	4.13	3.04	
	SPLEN1000114	2.97	4.19	6.03	3.59	4.76	6.32	
	SPLEN1000132	0.85	4	1.72	2.25	2.67	1.99	
	SPLEN1000135	3.13	8.76	14.93	11.12	15.28	10.52	
	SPLEN1000136	12.41	21.47	15.14	20.24	27.48	21.8	
55	SPLEN1000141	2.26	7.07	10.79	4.03	5.41	4.51	

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	SPLEN1000164	2.49	3.79	8.58	3.98	5.88	7.61	
	SPLEN1000166	0.4	2.9	2.96	1.67	1.19	1.68	
	SPLEN1000175	2.16	4.48	6.1	5.65	4.12	4.15	
5	SPLEN1000182	0.98	2.66	0.23	0.83	0.6	0.67	
	SPLEN1000185	3.41	8.49	8.54	11.38	10.43	11.95	
	THYMU1000004	10.22	14.07	20.43	22.34	22.76	23.6	
	THYMU1000009	9.48	10.13	14.9	13.48	23.86	22.1	
10	THYMU1000015	8.87	10.42	16.18	19.25	22.21	20.8	* +
	THYMU1000016	6.24	5.96	13.03	10.3	8.45	9.38	
	THYMU1000023	0.77	1.86	3.6	5.22	3.68	3.6	
	THYMU1000034	0.16	1.77	1.8	0.79	0.88	0.14	
	THYMU1000035	0.62	2.8	0.97	1.17	0.95	1.31	
15	THYMU1000037	1.53	4.15	2.11	2.06	2.81	1.45	
	THYMU1000042	5.97	10.24	12.23	12.03	13.98	13.28	
	THYMU1000047	2.72	6.03	6.72	6.04	7.77	7.23	
	THYMU1000080	0.56	4.31	2.6	3.26	1.85	2.11	
	THYMU1000094	2.77	3.47	7.91	9.17	8.35	4.55	
20	THYMU1000109	17.28	14.34	111.37	98.05	142.29	93.04	
	THYMU1000127	2.75	5.95	10.76	8.18	9.98	6.74	
	THYMU1000130	2.5	4.4	4.55	6.69	6.07	4.94	
	THYMU1000137	3.53	7.18	10.26	12.67	18.55	13.05	* +
	THYMU1000146	4.37	8.38	6.52	8.29	7.46	7.74	
25	THYMU1000159	5.43	9.51	16.37	12.4	15.15	13.27	
	THYMU1000163	5.85	12.26	37.58	45.53	58.37	36.93	
	THYMU1000167	2.39	3.02	4.73	4.89	6.79	3.97	
	THYMU1000186	0.69	1.05	1.45	1.31	2.45	0.66	
30	THYRO1000017	0.94	3.45	2.54	2.02	3.54	2.11	
	THYRO1000026	1.56	5.63	4.02	3.96	4.82	3.36	
	THYRO1000034	0.49	4.16	1.59	1.99	2	1.82	
	THYRO1000035	0.86	4.84	1.34	2.29	2.48	2.11	
	THYRO1000036	0.93	8.32	4	3.08	4.36	5.59	
35	THYRO1000040	2.58	7.02	4.76	4.66	4.83	4.93	
	THYRO1000061	2.01	1.91	3.07	3.53	3.8	2.61	
	THYRO1000067	1.98	2.8	5.12	3.37	4.14	3.3	
	THYRO1000070	1.26	2.09	3.59	2.65	3.85	3.45	
	THYRO1000072	1.33	3.37	4.22	2.54	4.08	2.06	
40	THYRO1000084	8.07	12.69	22.39	2.99	5.61	4.42	
	THYRO1000085	1.44	5.66	3.99	2.42	3.86	2.85	
	THYRO1000086	-0.05	5.46	1.74	0.89	1.18	1.15	
	THYRO1000087	0.72	3.86	1.01	0	0.58	0.17	
	THYRO1000092	2.32	5.1	4.66	3.75	4.43	4.5	
45	THYRO1000093	0.35	3.24	0.83	1.54	1.27	0.95	
	THYRO1000099	0.45	2.53	2.73	2.8	1.67	2.39	
	THYRO1000107	0.5	2.95	2.7	2.86	3.22	2	
	THYRO1000111	0.85	4.58	1.73	1.4	2.06	2.36	
50	THYRO1000121	1.33	5.72	2.52	1.94	2.4	2.95	
	THYRO1000124	0.27	5.55	0.64	0.86	0.89	0.64	
	THYRO1000129	0.36	2.1	0.11	0.94	1.11	0.92	
	THYRO1000130	1.82	3.11	3.13	3.85	3.01	2.39	
	THYRO1000132	2.4	3.62	9.43	11.14	6.99	6.26	
	THYRO1000134	1.5	4.07	3.22	4.06	3.65	3.73	
55	THYRO1000144	1.72	4.78	3.15	7.87	7.09	2.33	

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	THYRO1000155	1.6	4.1	1.45	1.77	1.9	2.23		
	THYRO1000156	1.13	6.53	3.62	2.45	4.29	2.58		
	THYRO1000163	3.62	8.42	5.28	4.76	6.63	2.24		
5	THYRO1000173	1.19	4.45	2.26	3.33	1.36	2.75		
	THYRO1000186	1.98	3.24	7.86	6.91	6.84	6.35		
	THYRO1000187	2.7	3.58	5.3	4.92	6.24	5.22		
	THYRO1000190	1.12	3.32	2.94	3.73	4.55	2.71		
	THYRO1000196	0.3	5.28	0.81	0.66	1.21	0.52		
10	THYRO1000197	2.05	7.28	4.69	4.08	6.24	3.89		
	THYRO1000199	0.76	6.28	4.13	1.93	2.08	1.98		
	THYRO1000206	8.47	6.92	9.25	8.44	11.6	7.5		
	THYRO1000221	1.9	3.17	4.42	4.02	5.87	4.54		
	THYRO1000222	3.65	4.26	4.23	4.68	4.96	4.93	*	+
15	THYRO1000228	0.81	3.67	2.85	2.24	3.04	2.94		
	THYRO1000241	1.76	3.7	6.29	4.62	5.54	4.01		
	THYRO1000242	0.63	4.16	4.46	2.49	2.56	2.62		
	THYRO1000246	1.61	5.5	3.9	3.43	4.7	3.91		
20	THYRO1000253	1.07	4.05	1.73	1.99	3.35	2.31		
	THYRO1000270	1.15	5.12	1.39	1.22	2.5	1.26		
	THYRO1000279	0.42	2.84	0.25	0.65	1.01	0.58		
	THYRO1000285	2.75	4.65	7.31	7.03	7.75	4.88		
	THYRO1000288	7.76	7.59	11.77	5.68	5.07	7.22		
25	THYRO1000296	4.18	6.04	6.22	7.4	11.24	8.96	*	+
	THYRO1000320	1.54	5.83	4.97	3.65	4.45	3.34		
	THYRO1000322	1.1	5.48	2.48	1.76	3.93	1.76		
	THYRO1000327	1.75	7.69	4.77	6.21	5.23	4.41		
	THYRO1000343	2.5	6.12	5.35	5.06	5.04	6.13		
30	THYRO1000345	1.36	7.34	11.92	7.82	5.84	9.49		
	THYRO1000358	1.82	3.39	3.08	1.92	2.32	1.54		
	THYRO1000368	0.76	2.39	2.73	1.43	2.82	0.58		
	THYRO1000375	3.2	7.03	4.79	7.38	6.09	9.77		
	THYRO1000381	0.92	2.88	2.19	3.87	3.11	2.74		
35	THYRO1000387	0.98	6.66	3.22	2.53	3.56	2.51		
	THYRO1000394	1.31	9.88	4.59	4.29	5.19	2.61		
	THYRO1000395	0.8	10.44	2.26	1.97	2.07	2.02		
	THYRO1000400	0.57	8.1	2.82	2.35	2.96	2.52		
40	THYRO1000401	0.86	1.94	2.5	1.87	1.16	1.57		
	THYRO1000407	1.97	2.3	1.36	1.37	1.58	0.55		
	THYRO1000420	1.8	2.67	4.46	3.52	3.53	3.39		
	THYRO1000438	1.78	4.37	3.26	2.94	3.33	3.15		
	THYRO1000452	2.62	7.99	6.45	3.71	5.75	4.38		
45	THYRO1000455	0.32	6.67	2.31	0.25	0.97	0.87		
	THYRO1000471	0.99	8.03	2.05	1.11	2.08	1.02		
	THYRO1000481	1.33	6.23	4.68	3.79	3.45	4.55		
	THYRO1000484	1.2	1.42	2.41	2.35	3	2.21		
	THYRO1000488	1.18	2.64	2.44	1.49	2.02	1.7		
50	THYRO1000501	1.12	4.01	2.78	3	1.92	1.82		
	THYRO1000502	0.34	3.7	1.69	1.79	1.44	1.2		
	THYRO1000505	0.13	4.64	1.19	1.14	1.02	0.6		
	THYRO1000535	11.1	20.54	39.24	54.13	69.59	62.96	*	+
	THYRO1000556	1.89	6.36	4.13	3.77	5.17	3.69		
55	THYRO1000558	0.25	2.82	1.12	1.16	0.81	0.61		

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	THYRO1000569	2.88	4.12	6.05	5.78	4.46	4.88
	THYRO1000570	2.31	3.28	8.46	8.53	6.04	3.49
	THYRO1000572	0.43	2.04	1.11	0.17	0.97	-0.42
5	THYRO1000573	0.69	4.02	1.73	2.02	2.2	1.78
	THYRO1000577	1.06	5	1.34	0.96	1.22	0.71
	THYRO1000580	0.79	3.72	3.01	2.82	2.2	1.79
	THYRO1000584	2.18	6.88	8.8	7.57	6.61	7.58
10	THYRO1000585	4.83	9.37	9.83	5.76	6.27	9.52
	THYRO1000596	0.22	0.93	1.19	0.44	1.36	0.21
	THYRO1000602	2.08	2.95	4.01	4.05	4.65	4.97
	THYRO1000605	0.37	3.01	0.98	2.13	2.14	1.56
	THYRO1000615	1.02	3.62	1.24	1.55	1.36	1.29
15	THYRO1000625	0.71	5.48	2.28	2.46	2.9	1.78
	THYRO1000636	3.67	5.65	6.9	6.53	7.84	6.67
	THYRO1000637	0.91	3.96	1.71	1.18	2.03	1.54
	THYRO1000641	0.38	4.19	2.49	1.36	1.67	1.64
20	THYRO1000657	2.99	3.69	5.42	7.67	12.28	3.86
	THYRO1000658	2.68	3.62	5.39	5.4	5.55	6.09
	THYRO1000662	1.1	3.19	2.09	2.42	2.69	1.66
	THYRO1000666	0.57	3.19	2.28	1.63	1.48	1.43
	THYRO1000676	1.37	4.53	2.01	1.75	1.83	1.56
25	THYRO1000678	0.52	5.86	0.99	1.29	1.4	0.53
	THYRO1000684	0.95	4.98	2.94	1.92	2.65	1.47
	THYRO1000694	2.08	6.64	4.65	2.8	2.48	3.59
	THYRO1000699	2.98	2.14	5.55	4.86	7.08	7.12
	THYRO1000712	1.88	4.25	5.9	6.25	6.75	7.78
30	THYRO1000715	5.74	5.67	27.37	21.74	28.63	16.99
	THYRO1000716	0.92	3.26	3.2	1.88	1.78	1.35
	THYRO1000717	1.58	5	4.36	2.98	4.63	1.91
	THYRO1000723	0.6	4.54	1.6	0.55	1.06	0.85
	THYRO1000734	-0.01	4.81	1.89	1.49	1.73	1.07
35	THYRO1000748	0.98	5.51	5.23	2.35	3.85	3.18
	THYRO1000755	1.74	3.26	4.32	4.33	3.47	4.38
	THYRO1000756	2.79	4.24	3.24	3.46	4.2	3.41
	THYRO1000776	0.48	2.17	3.02	3.36	3.99	3.34
	THYRO1000777	1.81	3.39	4.54	4.99	2.05	2.37
40	THYRO1000779	1.45	3.55	0.88	0.18	1.01	-0.26
	THYRO1000782	3.92	10.13	12.52	10.76	15.05	14.05
	THYRO1000783	0.12	5.51	1.2	1.11	1.41	0.92
	THYRO1000786	6.65	9.54	19.71	15.74	7.92	13.7
	THYRO1000787	0.23	1.88	1.67	1.31	1.54	0.78
45	THYRO1000792	1.51	3.13	2.29	3.09	3.13	2.11
	THYRO1000793	0.11	3.13	0.84	1.51	1.86	1.16
	THYRO1000795	1.23	6.03	3.54	2.76	3.1	3.05
	THYRO1000796	0.6	7.73	2.44	2.26	2.95	1.66
	THYRO1000798	1.89	5.82	2.51	2.59	3.57	3.53
50	THYRO1000800	9.26	17.2	24.74	17.74	20.68	21.06
	THYRO1000805	0.49	3.04	1.08	0.72	2.66	1.38
	THYRO1000815	2.54	3.49	9.48	7.61	5.47	7.87
	THYRO1000829	5.55	7.83	10.57	3.78	8.32	10.01
55	THYRO1000835	0.96	3.2	1.93	1.07	2.36	1.8
	THYRO1000843	1.09	11.48	3.56	3.69	4.41	3.62

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	THYRO1000846	0.76	5.71	1.32	2.67	1.62	1.26	
	THYRO1000852	1.59	6.02	5.63	2.8	4.7	3.32	
	THYRO1000855	3.14	5.02	6.63	9.03	15.1	10.07	* +
5	THYRO1000865	1.86	4.3	11.97	10.01	11.47	8.95	
	THYRO1000866	7.47	6.29	12.66	4.49	7.87	6.01	
	THYRO1000881	5.62	7.3	10.93	15.65	26.64	29.58	* +
	THYRO1000894	0.33	3.95	1.36	1.75	1.48	1	
	THYRO1000895	0.58	4.43	1.42	1.62	1.46	0.82	
10	THYRO1000916	1.22	5.49	3.43	2.43	3.13	2.29	
	THYRO1000917	16.19	25.26	34.11	30.37	37.42	35.89	
	THYRO1000926	0.78	3.13	1.27	1.76	1.57	0.82	
	THYRO1000934	0.08	3.1	1.34	0.43	1.38	1.46	
	THYRO1000951	0.52	2.46	1.26	2.33	2.11	1.9	
15	THYRO1000952	2.25	3.81	6.01	2.38	2.53	2.24	
	THYRO1000956	0.06	2.55	1.81	1.16	1.5	0.87	
	THYRO1000960	0.5	6.72	2.89	1.85	2.79	1.48	
	THYRO1000961	1.67	7.77	3.56	4.73	5.26	4.64	
20	THYRO1000964	0.42	11.59	0.76	1	1.27	1.06	
	THYRO1000971	1.82	9.9	3.56	3.29	3.33	2.19	
	THYRO1000974	2.87	8.83	7.53	9.87	11.79	8.71	
	THYRO1000975	1.5	2.19	3.8	4.02	3.68	3.68	
	THYRO1000983	6.42	8.31	11.63	12.67	8.49	7.12	
25	THYRO1000984	2.4	2.83	3.03	3.29	2.98	3.26	
	THYRO1000988	1.36	4.14	3.23	3.48	3.68	2.67	
	THYRO1000991	1.22	4.71	2.05	1.76	2.22	3.2	
	THYRO1000999	0.87	9.64	3.26	1.96	3.14	2.26	
	THYRO1001003	2.97	8.43	4.42	3.1	4.52	3.56	
30	THYRO1001015	0.6	6.29	2.04	2.22	1.79	1.66	
	THYRO1001016	1.73	2.26	3.34	2.06	1.85	1.24	
	THYRO1001022	0.9	1.86	0.86	1.68	1.25	1.41	
	THYRO1001031	4.65	3.97	4.55	5.03	7.03	6.16	
	THYRO1001033	1.18	3.34	2.46	2.86	3.45	2.02	
35	THYRO1001062	1.21	5.4	4.14	2.9	4.31	2.62	
	THYRO1001063	0.5	8.74	2.38	2.37	2.09	2.84	
	THYRO1001071	0.12	7.45	0.88	1.33	0.68	0.76	
	THYRO1001080	2.56	6.75	5.11	4.96	4.31	4.78	
	THYRO1001093	0.77	1.63	3.24	5.11	1.74	1.5	
40	THYRO1001100	0.52	1.89	2.05	1.89	1.21	0.78	
	THYRO1001102	2.61	3.6	5.7	4.4	4.95	6.93	
	THYRO1001104	3.67	6.54	6.55	8.77	8.01	11.18	
	THYRO1001109	1.81	6.02	2.68	3.06	2.58	1.99	
	THYRO1001113	11.41	17.42	32	21.81	26.65	18.72	
45	THYRO1001120	1.65	6.22	5.27	4.78	5.8	3.72	
	THYRO1001121	1.57	4.28	4.19	3.92	2.72	3	
	THYRO1001128	1.64	2.77	5.86	3.52	3.19	5.09	
	THYRO1001133	1.14	3.02	7.23	6.54	4.54	4.12	
	THYRO1001134	2.97	4.78	1.63	3.14	2.83	1.38	
50	THYRO1001142	0.3	2.69	0.63	1.3	1.71	0.22	
	THYRO1001173	8.37	12.87	7.72	11.14	9.92	10.62	
	THYRO1001175	3.26	6.63	5.51	3.46	4.62	3.52	
	THYRO1001177	1.36	5.85	5.93	4.66	7.27	7.97	
55	THYRO1001189	2.74	6.93	11.42	7.84	7.27	9.94	

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	THYRO1001194	1.05	2.62	4.96	4.89	4.57	2.31
	THYRO1001204	2.17	3.58	4.27	4.03	4.74	4
	THYRO1001205	5.76	10.65	20.23	18.54	19.57	20.9
5	THYRO1001213	1.21	4.69	4.44	3.12	3.21	2.33
	THYRO1001224	3.59	8.25	6.37	9.92	12.69	10.55 * +
	THYRO1001237	2.82	6.25	4.99	3.61	4.53	4.46
	THYRO1001242	9.74	11.65	19.04	20.02	19.98	20.46
10	THYRO1001258	2.08	5.45	3.58	3.33	2.05	2.66
	THYRO1001262	0.86	2.64	3.38	2.36	3.61	2.69
	THYRO1001266	0.15	2.39	1.02	0.97	1.64	0.66
	THYRO1001271	1.85	4.12	4.12	2.46	2.77	2.97
	THYRO1001287	7.3	8.3	39.26	30.14	43.68	26.2
15	THYRO1001290	0.38	3.25	1.14	1.15	1.35	0.36
	THYRO1001291	0.96	7.17	4.38	4.31	4.97	3.5
	THYRO1001297	3.05	8.04	6.14	6.85	7.47	9.18
	THYRO1001302	1.72	5.59	5.17	3.8	3.71	3.5
	THYRO1001313	1.61	2.33	2.91	2.91	2.62	1.48
20	THYRO1001320	1.76	2.52	5.31	5.07	5.74	4.83
	THYRO1001321	2.25	2.65	4.3	2.48	4.23	4.23
	THYRO1001322	1.34	3.93	3.34	1.75	2.67	2.01
	THYRO1001327	1.29	6.01	4.18	1.4	3.89	2.49
25	THYRO1001336	1.89	6.84	6.72	4.62	4.43	4.18
	THYRO1001347	0.43	4.12	3.35	1.85	2.81	0.65
	THYRO1001358	2.57	5.74	4.52	4.3	5.75	5.1
	THYRO1001363	0.8	2.15	1.52	2.09	2.24	2.28
	THYRO1001365	0.86	3	1.6	2.19	2.6	1.96
30	THYRO1001374	1.85	4.45	12.86	9.4	13.01	6.21
	THYRO1001401	1.76	5.33	4.89	5.39	7.86	6.29
	THYRO1001403	1.26	5.15	3.22	3.22	4.42	3.94
	THYRO1001405	6.99	12.5	10.86	6.69	8.56	10.63
	THYRO1001406	15.73	14.87	27.69	21.36	22.77	21.36
35	THYRO1001411	4.49	5.46	10.08	8.93	12.44	8.12
	THYRO1001420	11.55	15.25	47.52	42.01	44.49	49.87
	THYRO1001426	3.42	5.56	8.83	9.32	12.77	11.18
	THYRO1001430	6.97	6.54	10.84	11.13	11.7	13.81
	THYRO1001434	0.68	5.19	2.11	2.08	4.23	1.73
40	THYRO1001456	1.74	6.05	2.63	2.89	2.66	2.4
	THYRO1001457	1.71	4.72	2.04	2.95	4.7	2.67
	THYRO1001458	0.95	5.44	6.11	6.13	9.17	7.23
	THYRO1001459	4.54	5.07	9.42	7.18	9.87	14.21
45	THYRO1001471	0.91	2.07	1.93	2.36	2.91	1.64
	THYRO1001478	0.58	3.09	1.34	0.95	2.61	2.75
	THYRO1001480	5.4	10.53	13.62	14.79	15.94	15.57
	THYRO1001481	2.95	8.64	7.24	4.91	7.76	7.13
	THYRO1001487	1.36	5.51	3.52	4.1	2.67	3.48
50	THYRO1001495	2.06	5.57	5.43	5.06	9.4	7.55
	THYRO1001498	5.39	8.08	13.42	11.59	16.38	19.6
	THYRO1001510	1.67	2.88	1.59	1.65	2.57	3.35
	THYRO1001512	26.7	26.97	110.28	56.03	90.95	68.54
	THYRO1001519	5.92	7.77	11.05	8.91	5.75	10.38
55	THYRO1001522	2.02	4.7	5.79	4.15	4.69	5.51
	THYRO1001523	1.83	4.92	3.73	4.38	4.07	4.26

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	THYRO1001526	26.21	28.22	44.73	34.28	47.64	46.52	
	THYRO1001529	1.64	5.27	2.8	2.32	2.42	2.98	
	THYRO1001534	1.41	4.01	4.96	5.1	5.9	4.54	
5	THYRO1001537	7.4	5.17	12.33	5.97	7.42	7.23	
	THYRO1001541	2.14	3.88	8.27	7.76	8.7	6.73	
	THYRO1001545	1.26	3.84	2.9	4.95	3.57	3.16	
	THYRO1001559	4.52	6.34	8.04	9.06	10.5	10.54	* +
10	THYRO1001563	9.49	14.06	15.89	10	15.49	22.09	
	THYRO1001570	2.01	8.2	3.85	4.25	5.17	3.41	
	THYRO1001573	1.15	5.77	2.22	1.47	2.87	2.67	
	THYRO1001584	2.47	8.54	8.38	5.14	7.81	7.29	
	THYRO1001593	4.27	5.67	11.17	9.5	10.93	9.52	
15	THYRO1001595	3.14	4.53	7.06	5.97	6.35	7.29	
	THYRO1001596	4.71	5.48	7.44	6.45	5.86	2.51	
	THYRO1001602	1.49	3.26	3.52	4.95	5.22	3.41	
	THYRO1001605	1.58	4.48	3.22	3.2	3.43	2.42	
	THYRO1001608	1.87	9.45	5.1	5.04	8.23	4.7	
20	THYRO1001617	6.06	13.68	11.47	9.75	10.87	9.61	
	THYRO1001634	1.87	9.08	3.46	2.93	5.59	2.05	
	THYRO1001637	3.51	3.13	9.65	8.72	7.94	9.07	
	THYRO1001641	2.57	3.73	5.09	4.03	3.08	2.94	
	THYRO1001656	1.59	2.94	4.16	2.82	5.36	2.33	
25	THYRO1001658	22.34	29.19	40.11	34.98	33.16	42.01	
	THYRO1001661	1.4	5.83	2.31	2.93	3.31	2.05	
	THYRO1001671	0.67	7.36	2.68	1.89	1.34	1.8	
	THYRO1001672	1.1	9.24	2.1	1.14	1.52	1.66	
30	THYRO1001673	1.59	7.6	3.49	2.86	4.74	2.16	
	THYRO1001677	1.6	2.27	3.87	3.03	3.54	3.36	
	THYRO1001683	12.71	17.66	29.06	24.4	15.4	16.72	
	THYRO1001700	1.39	2.52	2.67	2.09	1.58	1.37	
	THYRO1001702	11.83	15.98	16.19	15.63	14.35	14.29	
35	THYRO1001703	1.63	6.74	4.25	4.72	3.27	4.21	
	THYRO1001706	1.7	6.47	3.01	2.96	5.6	3.53	
	THYRO1001721	1.84	5.66	3.2	2.73	6.37	2.77	
	THYRO1001725	5.3	6.55	9.69	8.97	8.65	8.29	
	THYRO1001730	17.72	20.4	40.1	30.61	26.56	34.8	
40	THYRO1001738	1.35	3.18	4.65	3.52	2.82	1.78	
	THYRO1001743	0.19	2.13	1.85	1.8	1.64	1.06	
	THYRO1001745	0.47	2.88	1.55	1.05	1.2	1.27	
	THYRO1001746	1.9	6.25	4.04	6.12	4.01	3.88	
45	THYRO1001770	15.49	20.38	35.39	41.65	44.42	40.17	* +
	THYRO1001772	1.12	4.88	3.64	4.78	4.24	3.06	
	THYRO1001778	3.89	6.68	9.89	14.67	13.47	14.25	* +
	THYRO1001793	3.85	3.77	9.43	10.3	10.42	4.92	
	THYRO1001796	1.35	2.28	2.28	3.45	4.22	3.24	* +
50	THYRO1001800	1.82	2.99	2.75	4.17	5.12	2.09	
	THYRO1001803	3.42	6.03	5.21	4.31	4.14	3.42	
	THYRO1001809	1.6	4.26	3.4	5.9	4.23	3.39	
	THYRO1001817	8.69	18.33	24.88	22.11	22.77	25.27	
	THYRO1001819	4.68	8.46	9.01	7.84	10.46	6.77	
55	THYRO1001828	21.89	24.53	104.32	106.68	121.95	68.55	
	THYRO1001854	6.67	6.12	12.45	13.43	15.86	13.31	

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	THYRO1001895	0.85	1.31	2.52	3.54	4.31	1.28	
	THYRO1001907	2.16	3.08	3.37	3.9	4.53	2.74	
	TRACH1000006	2.51	5.87	6.63	4.34	3.46	3.22	
5	TRACH1000013	1.53	4.65	3.68	2.55	3.33	2.65	
	TRACH1000074	2.65	6.75	6.09	7.5	7.26	4.77	
	TRACH1000095	0.28	5.66	2.23	2.46	1.48	1.11	
	TRACH1000102	2.42	6.66	4.09	5.79	5.04	3.65	
10	TRACH1000108	1.1	1.01	2.05	1.75	2.49	1.09	
	TRACH1000126	0.96	1.75	2.71	1.82	3.79	2.54	
	TRACH1000146	1.3	2.67	2.31	3.02	5.18	3.75	
	TRACH1000160	0.61	4.06	1.5	1.47	1.76	0.72	
	TRACH1000184	4.45	7.16	10.16	7.47	8.73	5.69	
15	VESEN1000004	0.69	5.55	3.19	2.56	2.95	2.02	
	VESEN1000007	0.93	5.32	2.94	2.38	3.45	2.94	
	VESEN1000013	5.96	10.11	16.73	10.76	11.25	13.88	
	VESEN1000028	5.2	7.5	9.88	13.18	11.71	14.08	* +
	VESEN1000059	1.55	2.88	2.1	3.38	2.82	2.27	
20	VESEN1000100	1.96	3.22	3.35	3.49	4.58	3.59	
	VESEN1000107	0.88	4.84	2.88	3.12	2.9	2.48	
	VESEN1000117	1.63	6.43	2.46	2.16	2.7	1.79	
	VESEN1000122	1.52	5.34	1.24	4.79	4.51	4.5	
25	VESEN1000137	0.76	5.47	1.92	1.75	3.33	1.65	
	VESEN1000195	7.79	7.93	11.67	8.42	7.51	10.27	
	VESEN1000215	1.48	3.03	2.06	2.67	3.84	1.87	
	VESEN1000279	8.71	11.32	18.49	22.93	23.38	34.68	* +
	VESEN1000363	3.52	6.07	9.99	7.2	9.06	4.59	
30	VESEN1000388	2.55	6.48	3.31	4.17	3.75	6.7	
	VESEN1000394	0.44	7.11	2.33	2.37	2.55	2.36	
	VESEN1000410	1.11	5	1.78	2.36	2.71	3.69	
	VESEN1000411	2.37	4.95	5.08	6.76	7.55	9	* +
	VESEN1000415	1.54	2.64	4.03	5.57	3.92	5.29	
35	VESEN1000440	7	5.53	7.81	3.79	9.4	12.22	
	VESEN1000452	1.22	3.65	2.33	2.91	3.97	4.11	
	VESEN1000539	191.54	185.28	334.6	389.84	403.89	547.31	* +
	VESEN1000554	0.67	6.47	1.43	1.47	2.55	1.58	
	VESEN1000557	4.22	7.94	7.73	6.55	9.07	10	
40	VESEN1000575	7.49	9.75	16.33	11.95	11.73	14.8	
	VESEN1000585	1.69	4.49	3.37	2.53	2.93	3.08	
	VESEN1000592	1.58	2.31	1.58	2.02	1.83	1.46	
	VESEN1000658	1.96	3.56	4.45	5.86	3.91	4.91	
	VESEN1000669	8.43	10.02	16.35	15.06	14.17	15.51	
45	VESEN1000743	0.97	3.3	2.52	1.99	3.37	3.21	
	VESEN1000752	37.43	51.51	72.35	49.32	57.03	57.96	
	VESEN1000761	13.48	18.17	19.37	24.6	33.21	31.28	* +
	VESEN2000039	10.45	15.98	15.56	13.56	18.3	20.1	
50	VESEN2000102	0.4	3.99	1.6	1.21	1.51	1.61	
	VESEN2000164	2.45	3.52	4.8	5.55	4.36	3.66	
	VESEN2000175	0.57	2.64	1.94	3.03	2.05	2.59	
	VESEN2000186	3.77	5.53	6.53	6.68	3.87	2.47	
	VESEN2000199	8.94	13.26	21.75	19.58	24.45	24.12	
55	VESEN2000200	0.5	4.97	2.78	3.03	3.1	1.6	
	VESEN2000204	0.48	12.7	1.02	0.98	1.2	0.33	

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	VESEN2000218	6.66	20.26	19.48	21.37	20.75	18.86		
	VESEN2000230	0.84	7.4	1.45	2.74	1.7	2.41		
	VESEN2000272	2.29	4	8.92	7	8.31	5.88		
5	VESEN2000299	1.99	2.97	3.2	3.3	3.77	3.31		
	VESEN2000323	4.51	8.12	8.37	8.91	9.5	9.36		
	VESEN2000327	3.16	5.8	4.42	3.62	7.66	5.07		
	VESEN2000328	5.44	8.02	11.88	8.73	15.35	14.36		
10	VESEN2000330	6.39	15.42	14.7	14.59	27.73	18.86		
	VESEN2000336	0.82	8.97	2.54	3.46	3.83	2.88		
	VESEN2000354	1.56	8.24	2.48	1.53	2.71	2.1		
	VESEN2000378	7.17	8.87	14.57	13.23	11.14	10.3		
	VESEN2000379	19.87	23.02	44.55	49.13	42.81	32.61		
15	VESEN2000397	0.72	2.38	1.24	1.36	2.06	1.54		
	VESEN2000416	2.83	3.88	4.41	5.74	5.31	5.71	*	+
	VESEN2000420	1.08	3.58	1.94	0.95	1.21	1.13		
	VESEN2000430	0.51	6.68	1.53	2.06	1.79	1.8		
	VESEN2000448	0.51	6.87	1.73	2.12	2.69	1.5		
20	VESEN2000449	2.43	8.07	6.59	8.3	11.31	8.21		
	VESEN2000456	0.74	0.87	2.11	1.54	1.22	0.87		
	VESEN2000562	4.07	3.42	17.42	13.67	22.82	14.47		
	VESEN2000573	0.18	1.75	1.75	1.04	1.21	1.13		
	VESEN2000604	1.73	3.44	2.24	2.04	1.67	2.15		
25	VESEN2000614	4.16	9.02	14.64	13.54	16.27	12.27		
	VESEN2000638	0.48	5.92	1.98	1.33	1.91	1.68		
	VESEN2000641	0.83	3.69	1.34	1.95	2.21	1.43		
	VESEN2000645	2.18	5.29	5.38	5.91	5.73	5.5		
30	Y79AA1000013	2.57	2.7	4.33	3.45	3.8	3.94		
	Y79AA1000030	1.79	4.06	4.52	3.24	3.85	2.47		
	Y79AA1000033	2.87	6	8.4	8.37	10.17	5.83		
	Y79AA1000037	1.38	3.36	5.71	4.84	6.82	4.49		
	Y79AA1000041	1.05	5.16	3.79	4.73	3.65	2.06		
35	Y79AA1000059	1.69	5	4.09	3.88	4.51	2.82		
	Y79AA1000065	24.06	28.99	52.25	82.48	101.48	98.73	**	+
	Y79AA1000081	39.47	49.78	73.62	113.19	114.49	98.22	**	+
	Y79AA1000127	4.08	4.21	5.8	8.42	10.03	7.39	*	+
	Y79AA1000130	2.24	2.48	5.76	6.61	8.1	8.03	*	+
40	Y79AA1000131	507.64	569.21	946.04	769.75	725.35	342.07		
	Y79AA1000134	1.99	4.93	4.21	5.63	4.75	5.38		
	Y79AA1000143	3.58	8.79	4.83	9.98	10.98	11.04	*	+
	Y79AA1000144	4.63	10.79	10.59	11.02	11.62	11		
	Y79AA1000150	18.39	22.18	84.69	93.5	117.62	78.89		
45	Y79AA1000153	183.67	191.4	436.64	423.46	442.52	386.45		
	Y79AA1000166	2.13	2.25	4.15	3.52	4.97	3.6		
	Y79AA1000179	2.58	3.76	4.2	6.85	7.58	3.89		
	Y79AA1000181	1.96	3.92	4.2	4.82	5.66	3.79		
	Y79AA1000202	22.93	24.47	55.57	91.68	86.86	83.22	**	+
50	Y79AA1000207	5.22	7.51	9.82	14.95	16.24	12.62	*	+
	Y79AA1000214	14.94	22.18	33.76	50.43	60.78	41.96	*	+
	Y79AA1000222	11.8	14.89	21.69	49.21	58.01	68.86	**	+
	Y79AA1000226	11.04	14.94	34.41	22.86	33.54	30.03		
	Y79AA1000227	5.95	4.52	7.25	8.98	9.51	9.62	*	+
55	Y79AA1000230	1.09	1.49	2.02	2.07	2.88	2.59		

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	Y79AA1000231	5.99	9.04	15.81	14.63	23.77	17.1	
	Y79AA1000239	15.47	20.55	25.65	18.95	24.01	22.11	
	Y79AA1000258	2.64	5.17	6.72	5.87	4.95	5.84	
5	Y79AA1000268	2.65	5.48	5.09	4.33	5.76	4.01	
	Y79AA1000269	4.32	7.88	7.86	8	6.86	8.24	
	Y79AA1000270	5.28	8.35	11.58	13.17	17.58	16.23	* +
	Y79AA1000280	1.74	4.17	4.9	5.29	3.1	5.27	
10	Y79AA1000285	3.44	4.21	5.91	4.01	6.86	5.22	
	Y79AA1000295	0.75	3.06	4.85	4.32	4.23	4.45	
	Y79AA1000307	2.88	3.91	5.06	9.35	7.58	11.25	* +
	Y79AA1000313	3.11	9.02	9.85	10.61	12.84	13.36	
	Y79AA1000314	4.23	10.74	9.19	6.93	6.53	7.51	
15	Y79AA1000328	4.65	10.05	2.64	7.73	9.28	8.68	
	Y79AA1000334	1.43	4.22	3.55	2.68	2.81	3.46	
	Y79AA1000342	10.65	10.05	26.47	23.7	19.13	28.35	
	Y79AA1000346	7.61	8.17	7.9	20.1	22.06	20.18	** +
20	Y79AA1000347	6.94	7.96	12.42	18.78	16.47	18.48	** +
	Y79AA1000349	6.93	9.63	12.67	12.31	11.96	14.75	
	Y79AA1000355	3.17	8.28	8.94	8.84	13.55	8.77	
	Y79AA1000368	5.24	8.39	24.43	22.48	35.67	22.55	
	Y79AA1000388	22.9	32.66	62.37	94.17	128.35	109.08	** +
25	Y79AA1000392	3.02	6.81	3.76	3.42	2.73	3.78	
	Y79AA1000405	3.98	5.97	8.25	7.14	8.17	9.32	
	Y79AA1000410	6.01	7.87	15.72	13.79	17.05	14.95	
	Y79AA1000420	1.54	4.78	3.13	3.32	3.95	5.1	
	Y79AA1000423	1.38	7.08	5.59	5.22	6.04	10.27	
30	Y79AA1000426	3.61	9.44	8.66	4.24	4.43	5.22	
	Y79AA1000432	0.8	4.79	2.16	1.91	2.01	2.34	
	Y79AA1000453	23.94	30.67	47.79	39.74	50.65	58.24	
	Y79AA1000465	4.12	6.02	6.65	4.77	4.14	7.69	
	Y79AA1000469	11.59	9.61	18.04	13.82	16.21	17.18	
35	Y79AA1000480	1.24	4.37	2.78	3.33	3.57	2.79	
	Y79AA1000502	5.31	7.97	12.58	10.49	11.35	15.26	
	Y79AA1000521	1.24	4.4	4.13	2.51	3.61	2.7	
	Y79AA1000534	3.22	8.13	8.92	11.97	14.41	13.46	* +
	Y79AA1000538	3.58	6.95	8.79	9.52	12.12	8.41	
40	Y79AA1000539	12.76	14.96	53.11	42.61	68.56	50.97	
	Y79AA1000540	1.32	3.59	1.61	2.54	2.97	3.21	
	Y79AA1000560	160.46	140.99	339.33	380.8	313.21	220.43	
	Y79AA1000574	1	2.92	1.65	1.98	2.04	1.59	
45	Y79AA1000584	2.07	4.55	4.97	4.62	5.39	4.04	
	Y79AA1000589	10.74	13.67	81.43	59.09	95.35	68.5	
	Y79AA1000598	1.43	7.64	2.17	1.85	3.88	3.18	
	Y79AA1000600	2.7	10.02	7.93	13.64	15.64	12.84	* +
	Y79AA1000609	1.18	5.16	1.44	2.28	2.77	1.55	
50	Y79AA1000618	1.85	10.59	5.76	7.4	9.5	9.37	
	Y79AA1000627	1.91	3.93	4.57	3.27	3.02	2.43	
	Y79AA1000636	5.16	5.7	9.9	15.57	11.52	5.38	
	Y79AA1000649	9.45	10.97	12.73	18.7	11.56	20.54	
	Y79AA1000656	15.32	20.21	96.75	80.17	115.97	82.61	
55	Y79AA1000673	1.02	5.86	2.14	1.39	3.13	2.4	
	Y79AA1000674	11.88	21.96	78.28	59.4	98.22	62.67	

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	Y79AA1000678	2.48	8.91	3.88	3.01	4.15	2.45	
	Y79AA1000682	17.99	53.99	93.7	102.53	110.87	118.22	
	Y79AA1000683	1.87	2.66	3.21	4.27	2.59	2.17	
5	Y79AA1000697	21.76	27.52	43.01	21.93	24.76	27.31	
	Y79AA1000700	5.07	7.1	7.08	7.51	6.93	9.97	
	Y79AA1000702	5.13	14.57	13.31	41.48	56.57	63.15	** +
	Y79AA1000704	1.34	5.24	1.14	1.5	2.1	1.18	
10	Y79AA1000705	1.86	9.7	6.24	6.06	7.98	6.45	
	Y79AA1000717	6.18	12.39	9.42	9.73	11.1	8.7	
	Y79AA1000722	5.61	8.6	8.65	26.26	34.81	34.31	** +
	Y79AA1000724	6.42	9.77	18.55	26.57	21.7	11.95	
	Y79AA1000726	0.77	1.24	0.83	1.46	2.01	0.71	
15	Y79AA1000734	2.05	4.46	4.92	3.57	3.3	2.94	
	Y79AA1000748	0.88	4.38	1.77	2.14	2.99	1.56	
	Y79AA1000750	4.17	8.47	20.58	18.11	20.02	18.62	
	Y79AA1000752	1.25	5.13	2.33	2.23	3.38	3.38	
	Y79AA1000774	2.11	6.23	4.24	4.28	5.79	4.21	
20	Y79AA1000776	1.2	4.37	1.9	2.13	1.83	2.11	
	Y79AA1000777	4.36	5.84	9.63	10.05	6.99	6.01	
	Y79AA1000778	1.72	3.77	3.79	3.87	4.19	1.44	
	Y79AA1000782	2.08	4.18	3.72	3.53	2.89	2.96	
	Y79AA1000784	7.04	10.01	7.78	13.87	15.58	14.26	** +
25	Y79AA1000794	0.61	5.21	1.88	2.92	1.69	1.23	
	Y79AA1000800	1.59	5.44	3.82	3.38	2.97	3.39	
	Y79AA1000802	0.64	4.18	1.15	2.52	1.77	2.1	
	Y79AA1000805	2.29	4.03	2.63	2.43	2.11	2.6	
30	Y79AA1000814	2.73	3.9	4.14	4.98	7.09	6.76	* +
	Y79AA1000823	7.91	9.99	12.07	12.02	12.42	6.56	
	Y79AA1000824	0.98	2.47	1.84	2.75	2.26	0.79	
	Y79AA1000827	1.6	4.02	7.27	6.71	8.91	6.14	
	Y79AA1000831	7.04	10.49	17.32	26.61	30.43	27.82	** +
35	Y79AA1000833	62.14	67.46	191.76	270.42	308.16	248.21	* +
	Y79AA1000850	1.69	5.68	2.72	4.92	4.59	4.21	
	Y79AA1000856	3.49	6.78	6.31	9.28	6.01	8.51	
	Y79AA1000862	2.22	2.76	2.44	3.08	2.87	2.59	
	Y79AA1000876	7.46	10.04	17.91	27.36	27.61	25.46	** +
40	Y79AA1000888	4.59	5.07	28.1	24.51	38.78	22.48	
	Y79AA1000902	4.65	5.74	8.44	12.18	12.32	7.68	
	Y79AA1000935	3.53	5.99	6.69	8.28	10.07	9.18	* +
	Y79AA1000959	0.74	6.29	4.35	6.71	5.77	6.07	
	Y79AA1000962	1.22	4.45	3.18	2.9	2.41	1.79	
45	Y79AA1000963	18.6	26.86	35.93	31.61	42.17	49.13	
	Y79AA1000966	18.52	19.25	98.18	77.47	116.12	61.1	
	Y79AA1000967	8.62	8.82	33.82	34.47	40.36	29.3	
	Y79AA1000968	3.32	5.67	6.89	8.86	9.4	7.96	* +
	Y79AA1000969	0.91	3.18	3.04	2.66	2.91	1.41	
50	Y79AA1000976	1.43	4.72	3.02	2.55	3.51	1.43	
	Y79AA1000978	1.99	5.6	7.26	6.9	10.54	5.56	
	Y79AA1000985	9.39	12.84	40.49	38.26	44.3	27.89	
	Y79AA1000989	21.59	22.49	46.19	51.84	58.65	55.19	* +
	Y79AA1000991	22.11	22.21	110.42	72.46	96.96	82.23	
55	Y79AA1001013	59.2	62.64	140.9	174.85	214.13	201.9	* +

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	Y79AA1001014	2.27	4.16	4.1	4.8	5.2	6.55		
	Y79AA1001019	3.37	5.89	7.74	9.24	9.02	9.43	*	+
	Y79AA1001020	5.37	7.82	9.43	12.31	11.11	10.86	*	+
5	Y79AA1001023	0.83	6.11	2.29	1.22	1.95	1.54		
	Y79AA1001030	4.23	8.79	10.87	11.14	10.72	12.43		
	Y79AA1001035	0.19	2.88	0.03	14.44	8.19	17.16	*	+
	Y79AA1001041	1.78	2.46	2.36	2.93	2.45	2.78		
	Y79AA1001043	11.65	12.62	15.22	8.64	12.01	14.71		
10	Y79AA1001048	1.1	4.78	3.73	4.05	4.52	4.21		
	Y79AA1001056	4.56	7.82	11.04	8.27	7.11	9.94		
	Y79AA1001061	1.53	7.79	5.28	6.13	7.46	6.66		
	Y79AA1001062	2.62	6.14	5.02	4.44	6.01	4.67		
	Y79AA1001068	3.46	6.39	7.29	6.61	8.69	7.05		
15	Y79AA1001073	8.19	13.08	17.46	24.14	22.1	29.81	*	+
	Y79AA1001077	7.1	7.08	17.15	14.69	14.74	17.08		
	Y79AA1001078	3.11	8.34	11.07	5.01	12.15	12.92		
	Y79AA1001081	3.59	5.61	4.94	9.62	9.98	10.5	**	+
20	Y79AA1001088	27.75	38.61	69.33	93.1	88.97	113.04	*	+
	Y79AA1001089	4.64	7.8	11.92	22.67	22.6	27.73	**	+
	Y79AA1001090	1.38	4.15	2.2	3.58	2.83	2.35		
	Y79AA1001105	3.7	5.23	15.81	12.52	22.1	13.35		
	Y79AA1001142	8.53	13.38	15.85	14.28	11.42	22.32		
25	Y79AA1001145	2.22	4.68	5.13	4.97	6.26	5.87		
	Y79AA1001162	2.27	2.91	1.62	1.62	4.56	4		
	Y79AA1001167	0.86	2.76	2.38	1.12	2.35	0.77		
	Y79AA1001176	0.57	3.33	1.14	2.02	1.68	0.88		
	Y79AA1001177	1.21	5.5	2.22	2.35	3.01	1.99		
30	Y79AA1001179	6.81	8.66	16.73	22.82	22.64	20.07	*	+
	Y79AA1001185	1.33	5.3	4.55	3.65	4.49	5.8		
	Y79AA1001201	5.69	11.3	16.13	14.57	15.21	19.38		
	Y79AA1001205	1.87	3.28	2.85	5.87	4.85	4.09	*	+
	Y79AA1001211	1.64	4.75	6.93	4.83	4.36	4.15		
35	Y79AA1001212	3.55	6.93	15.91	13.74	15	11.65		
	Y79AA1001216	52.59	51.46	93.73	76.52	97.53	109.55		
	Y79AA1001228	6.1	11.21	9.34	8.99	12.19	10.24		
	Y79AA1001233	0.68	11.46	2.39	0.92	1.66	1.09		
	Y79AA1001236	4.46	12.86	9.25	11.4	10.66	13.08		
40	Y79AA1001239	4.62	13.93	9.94	11.53	12.15	12.94		
	Y79AA1001240	8.74	8.6	13.75	9.13	6.68	3.01		
	Y79AA1001255	10.37	12.22	22.61	12.47	7.51	6.57		
	Y79AA1001264	3.63	5.15	4.49	7.73	8.59	8.75	**	+
45	Y79AA1001272	10.81	13.63	17.47	21.56	20.67	21.32	*	+
	Y79AA1001281	0.45	4.95	1.89	1.42	1.81	0.95		
	Y79AA1001299	2.49	11.34	9.06	9.9	9.26	9.81		
	Y79AA1001312	2.49	10.36	5.17	2.15	4.77	4.14		
	Y79AA1001319	3.34	11.88	5.27	7.23	6.05	7.15		
	Y79AA1001323	1.22	1.16	2.09	1.11	1.55	0.89		
50	Y79AA1001328	2.04	3.18	3.62	4.66	4.48	4.05	*	+
	Y79AA1001343	154.19	151.55	345.05	304.88	394.54	265.65		
	Y79AA1001351	0.81	2.77	1.67	0.03	1.26	0.96		
	Y79AA1001364	1.65	6.07	4.03	3.39	4.43	3.6		
55	Y79AA1001367	2.16	7.41	2.93	3.09	5.34	3.19		

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	Y79AA1001384	0.5	5.14	1.98	0.73	1.15	0.94	
	Y79AA1001391	0.59	3.73	2.88	1.35	1.65	1.2	
	Y79AA1001394	3.12	4.66	12.92	10.94	9.56	10.94	
5	Y79AA1001402	2.77	3.7	5.95	5.65	5.09	4.14	
	Y79AA1001410	0.82	2.78	2.33	2.06	2.31	2.25	
	Y79AA1001414	2.76	7.5	7.59	11.08	10.73	10.06	* +
	Y79AA1001426	0.61	4.36	2.61	1.5	1.43	1.82	
	Y79AA1001427	14.22	13.44	86.36	59.92	88.36	63.53	
10	Y79AA1001430	11.28	16.98	20.98	29.04	34.03	34.38	** +
	Y79AA1001439	16.22	21.53	33.42	45.02	43.74	43.1	* +
	Y79AA1001485	1.65	2.51	4.38	4.85	3.88	3.57	
	Y79AA1001493	1.29	2.3	3.43	2.43	2.35	2.46	
15	Y79AA1001511	4.79	8.57	11.05	9.39	9.11	6.47	
	Y79AA1001523	2.64	6.57	5.08	8.74	7.37	6.1	
	Y79AA1001530	7.46	11.69	22	41.43	36.37	36.07	** +
	Y79AA1001532	5.12	7.35	6.69	10.49	14.82	12.9	* +
	Y79AA1001533	1.84	4.89	2.53	4.15	4	4.19	
20	Y79AA1001541	2.82	5.89	7.54	7.23	5.08	7.34	
	Y79AA1001548	4.25	4.84	9.82	10.46	7.37	7.1	
	Y79AA1001555	2	2.55	3.65	4.7	5.28	4.25	* +
	Y79AA1001562	7.76	10.11	17.15	14.07	16.16	10.83	
	Y79AA1001581	2	5.05	4.47	5.1	7.01	3.54	
25	Y79AA1001585	3.18	7.38	10.96	9.72	10.93	8.05	
	Y79AA1001592	2.61	7.38	5.97	8.15	8	7.02	
	Y79AA1001594	0.76	4.73	3.85	1.96	3.24	1.73	
	Y79AA1001603	56.74	70.81	153.14	131.56	112.16	107.66	
	Y79AA1001613	3.74	3.52	14.81	13.12	15.36	10.66	
30	Y79AA1001630	0.71	2.36	1.73	1.14	2.64	0.67	
	Y79AA1001647	1.96	3.57	2.47	4.14	4.32	2.65	
	Y79AA1001664	4.67	8.39	11.43	8.96	10.01	8.73	
	Y79AA1001665	1.39	6.4	3.73	4.67	4.71	3.75	
	Y79AA1001679	8.92	15.94	20.71	20.53	26.67	25.35	
35	Y79AA1001692	1.87	5.55	3.95	3.99	3.95	3.51	
	Y79AA1001696	1.97	6.49	2.77	1.83	2.63	2.55	
	Y79AA1001705	6.09	6.44	10.39	7.62	7.92	7.85	
	Y79AA1001711	16.17	12.34	29.74	13.73	23.83	21	
	Y79AA1001717	0.72	2.99	1.29	1.68	3.13	1.14	
40	Y79AA1001719	2.5	5.79	6.44	6.15	6.07	6.43	
	Y79AA1001727	6.87	12.13	14.99	8.73	14.71	8.77	
	Y79AA1001750	10.21	13.63	21.67	21.92	32.29	24.33	
	Y79AA1001760	25.24	27.31	122.97	113.56	155.17	83.24	
45	Y79AA1001777	1.17	3.59	1.6	2.49	1.75	1.28	
	Y79AA1001781	0.31	2.3	0.42	1.62	1.84	1.42	
	Y79AA1001787	1	3.94	3.54	5.51	5.18	5.15	
	Y79AA1001793	16.23	15.19	91.7	60.44	87.21	75.35	
	Y79AA1001795	1.23	3.84	2.24	2.05	2.45	2.8	
50	Y79AA1001799	4.9	8.35	6.99	10.7	10.72	11.26	* +
	Y79AA1001800	2.25	8.3	10.1	8.49	10.51	9.9	
	Y79AA1001801	1.77	6.44	4.87	7.67	5.91	7.33	
	Y79AA1001803	0.74	2.15	1.72	1.85	1.68	1.17	
	Y79AA1001805	6.05	6.88	12.15	10.21	8.32	11.15	
55	Y79AA1001807	3.37	6.33	12.56	11.76	17.8	16.79	

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	Y79AA1001827	1.7	4.41	3.12	3.43	3.6	2.52	
	Y79AA1001846	1.82	6.52	5.51	6.52	5.09	5.07	
	Y79AA1001848	0.86	5.57	2.75	5.98	4.78	5.14	
5	Y79AA1001853	1.38	6.16	2.76	3.24	4.56	3.63	
	Y79AA1001863	0.86	5	2.53	2.93	3.83	3.85	
	Y79AA1001866	2.29	3.2	5.81	3.53	3.98	3.46	
	Y79AA1001874	0.12	2.18	-0.21	1.17	0.75	0.51	
10	Y79AA1001875	9.33	12.67	13.09	11.05	17.79	18.63	
	Y79AA1001907	68.02	70.94	96.4	118.34	86.75	104.86	
	Y79AA1001908	0.64	8.4	2.29	1.92	2.59	2.31	
	Y79AA1001923	1.61	6.64	3.03	3.86	3.76	3.35	
	Y79AA1001927	19.1	22.05	36.94	42.46	45.29	48.81	* +
15	Y79AA1001930	4.07	6.65	8.07	7.92	12.42	12.21	
	Y79AA1001932	2.84	4.41	8.47	11.51	9.1	8.57	
	Y79AA1001933	2.14	3.27	3.69	4.34	7.99	6.65	* +
	Y79AA1001942	1.58	3.45	2.69	2.94	2.13	2.41	
	Y79AA1001963	9.6	9.37	46.06	38.48	49.64	47.27	
20	Y79AA1001968	18.61	27.73	37.44	42.93	44.16	55.23	* +
	Y79AA1001983	1.81	6.35	4.28	3.97	5.86	4.47	
	Y79AA1002000	2.55	5.35	4.55	4.42	3.21	2.83	
	Y79AA1002004	13.1	18.87	27.47	23.72	29.45	40.93	
25	Y79AA1002008	2.51	3.73	3.79	4.54	2.19	2.85	
	Y79AA1002012	1.37	3.22	2.81	3.22	2.29	2.87	
	Y79AA1002017	1.34	2.53	2.46	3.51	3.07	2.82	
	Y79AA1002022	2.99	4.94	5.93	7.32	7.51	6.01	
	Y79AA1002027	2.02	6.33	2.67	2.69	4.03	4.09	
30	Y79AA1002050	2.53	8.12	4.22	6.68	6.91	5.11	
	Y79AA1002058	13.69	21.8	70.12	59.07	70.89	55.33	
	Y79AA1002060	6.38	13.17	20.54	17.14	21.12	24.23	
	Y79AA1002062	4.33	5.18	8.15	8.54	6.66	5.51	
	Y79AA1002065	33.54	39.97	72.6	49.46	30.04	41.81	
35	Y79AA1002067	10.11	11.64	17.24	16.25	9.42	8.13	
	Y79AA1002069	0.97	1.79	0.54	1.55	1.44	0.66	
	Y79AA1002070	10.16	33.47	44.36	52.16	71.15	73.35	* +
	Y79AA1002074	38.55	74.38	179.6	165.55	282.48	224.96	
	Y79AA1002076	0.48	9.71	2.89	2.86	3.34	1.91	
40	Y79AA1002083	1.2	7.48	2.03	2.73	1.75	2.06	
	Y79AA1002084	1.79	2.59	4.54	3.73	3.73	2.98	
	Y79AA1002086	0.96	1.78	1.71	2.77	1.88	1.43	
	Y79AA1002087	11.18	14.9	27.67	33.34	30.01	23.08	
	Y79AA1002089	1.18	3.46	2.13	1.46	2.92	3.26	
45	Y79AA1002093	2.19	5.48	5.25	5.28	5.68	6.17	
	Y79AA1002101	1.11	8.58	2.98	6.54	5.58	6.6	
	Y79AA1002103	1.47	10.22	3.39	4.43	6.49	4.7	
	Y79AA1002115	4.34	9.78	7.37	7.45	7.03	6.95	
	Y79AA1002121	1.55	2.16	2.18	1.67	2.55	2.31	
50	Y79AA1002125	6.67	7.08	9.29	8.81	6.4	7.6	
	Y79AA1002129	1.64	6.23	7.84	5.41	2.2	4.93	
	Y79AA1002131	0.9	3.25	0.78	0.77	1.29	1.15	
	Y79AA1002139	0.69	5.02	1.04	1.83	1.53	1.34	
55	Y79AA1002144	25.99	29.62	51.01	42.61	51.16	43.17	
	Y79AA1002177	1.72	5.97	4.33	4.79	3.09	4.73	

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	Y79AA1002183	10.44	13.89	17.69	27.61	29.67	28.92	**	+
	Y79AA1002202	3.97	7.15	8.34	18.27	10.12	17.85	*	+
	Y79AA1002204	0.53	0.99	1.56	1.7	2.2	1.54		
5	Y79AA1002206	2.63	5.36	7.28	4.35	2.95	1.49		
	Y79AA1002208	4.26	6.54	3.94	6.88	6.3	3.96		
	Y79AA1002209	1.8	6.34	2.88	4.38	3.74	4.57		
	Y79AA1002210	0.41	4.14	2.09	1.8	2.24	1.65		
	Y79AA1002211	2.25	5.39	3.85	5.71	5.3	4.5		
10	Y79AA1002213	1.15	4.13	6.53	7.38	7.54	7.43		
	Y79AA1002215	18.7	18.69	26.61	17.72	15.59	9.62		
	Y79AA1002220	3.78	3.38	2.87	4.89	4.19	4.14	*	+
	Y79AA1002226	8.54	8.9	9.75	13.06	14.2	4.41		
15	Y79AA1002229	1.35	3.88	3.38	2.95	2.79	2.67		
	Y79AA1002234	3.24	6.82	3.94	4.29	7.74	6.88		
	Y79AA1002235	5.6	7.55	6.43	8.78	9.74	9.47	*	+
	Y79AA1002246	0.59	5.06	2.41	3.94	2.54	4.27		
	Y79AA1002258	0.72	7.26	2.92	3.99	4.19	2.7		
20	Y79AA1002279	17.79	19.12	27.8	16.52	19.13	11.5		
	Y79AA1002292	1.68	2.1	3.22	2.96	3.91	2.73		
	Y79AA1002298	0.76	2.52	1.32	2.03	2.77	1.06		
	Y79AA1002307	1.05	4.35	1.79	0.76	1.05	1.2		
	Y79AA1002309	1.15	4.19	2.3	2.21	1.78	2.55		
25	Y79AA1002311	2.84	7.35	3.43	5.71	6.04	5.45		
	Y79AA1002334	1.72	6.54	2.95	4.77	4.19	3.35		
	Y79AA1002351	1.27	5.5	2.89	3.5	3.38	3.06		
	Y79AA1002355	12.83	12.25	28.96	22.94	22.07	21.02		
30	Y79AA1002361	2.22	2.27	3.26	2.47	4.54	1.55		
	Y79AA1002365	0.66	2.04	2.26	1.97	3.51	2.25		
	Y79AA1002373	1.17	3.93	2.42	1.59	1.97	1.43		
	Y79AA1002376	110.81	135.82	249.8	205.99	213.25	191.69		
	Y79AA1002378	1.9	4.8	4.91	2.2	3.6	3		
35	Y79AA1002381	8.65	14.11	19.19	18.84	21.52	17.97		
	Y79AA1002388	7.05	9.99	18.24	15.88	21.51	19.99		
	Y79AA1002399	1.79	4.25	3.74	4.62	4.08	3.47		
	Y79AA1002407	3.05	4.16	3.13	4.66	5.77	4.5	*	+
	Y79AA1002413	3.21	6.78	8.05	6.46	8.32	6.87		
40	Y79AA1002416	1.46	5	2.74	2.49	3.44	3.55		
	Y79AA1002429	5.5	8.15	7.27	8	11.11	8.01		
	Y79AA1002431	0.92	4.43	0.48	0.79	1.78	0.89		
	Y79AA1002433	1.27	5.9	3.24	4.8	3.84	5.58		
45	Y79AA1002445	4.01	5.34	5.76	3.1	4.89	5.41		
	Y79AA1002461	0.63	2.45	1.79	1.19	2.71	1.41		
	Y79AA1002466	39.02	70.71	94.5	91.12	82.27	94.71		
	Y79AA1002471	4.44	6.67	6.08	7.43	8.06	10.49		
	Y79AA1002472	2.41	6.16	5.99	6.8	8.39	4.06		
50	Y79AA1002474	1.93	8.27	4.31	4.89	6.52	7.13		
	Y79AA1002482	3.52	6.66	10.37	9.02	11.81	8.69		
	Y79AA1002487	1.38	4.12	2.46	1.96	3.01	2.56		
	Y79AA1002490	10.37	9.91	16.35	11.11	12.88	16.86		
	Y79AA1002493	1.96	4.07	6.14	6.5	8.9	4.1		
55	ZRV6C1006278	0.61	4.08	2.22	1.81	1.58	2.11		

Table 367

Difference in the expression level of each clone in response to TNF stimulation or IL-1 stimulation

Before stimulation, IL1 1h, and IL1 7h represent relative levels of expression in the absence of the stimulation, 1 hour after the IL-1 stimulation, and 7 hours after the stimulation, respectively. TNF 1h, TNF 3h, and TNF 7h represent relative levels of expression 1 hour after the TNF stimulation, 3 hours after the stimulation, and 7 hours after the stimulation, respectively. Correlation coefficients 1 and 2 indicate the correlation coefficients in the calibration curves prepared based on the data for the internal standard in reaction systems A and B, respectively.

Clone	IL1		TNF			Correlation coefficients			
	before stimulation	1h	7h	1h	3h	7h	1	2	
NT2RM1000858	5.6	7.6	3.8	4.7	2.1	1.7	0.98	0.94	
NT2RM1000462	0.9	0.9	0.5	0.7	0.1	0	1	1	
NT2RM1000855	1	1.3	1	1.1	0.4	0.4	1	1	
NT2RM1000789	1	0.9	0.4	1	0.4	0.6	0.96	0.98	
NT2RM2000306	0.7	1.1	0.3	1.1	0.3	0.1	1	0.98	
NT2RM2000514	0.2	0.2	0.6	0.2	0.1	0.2	0.98	0.96	
NT2RM2001126	0.5	0	0.4	0.3	0.3	1.2	0.99	0.99	
NT2RM2001902	1.3	1.6	0.6	1.3	0.8	0.8	1	1	
NT2RM2001738	1.6	1.8	1.5	1.7	0.8	0.9	0.98	1	
NT2RM2000582	0.2	0.1	0	0.7	0.1	0.1	0.99	0.99	
NT2RM2000773	1.1	1.2	1.4	2	1	0.8	0.95	1	
NT2RM2001626	0.4	0.2	0.6	0.7	0.1	0.7	1	1	
NT2RM2001643	1.6	3.1	1.2	2.4	0.7	0.8	1	1	
NT2RM2001792	0.2	0	0	0.3	0.1	0.1	0.98	0.97	
NT2RM2000589	0.2	0.1	0	0.1	0	0	1	0.99	
NT2RM2000588	0.6	0.7	0.1	0.8	0.2	0.2	1	1	
NT2RM2002109	0	0	0	0.2	0.1	0	0.99	0.99	
NT2RM4000284	6.5	9.1	4.8	10.1	3.4	3	1	1	
NT2RM4001735	3.8	4.6	2.1	5	1.6	1.4	1	1	
NT2RM4000100	0.5	0.6	0.2	0.5	0.3	0.3	0.95	0.95	
NT2RM4000417	0.2	0	0	0.2	0.1	0	0.99	0.98	
NT2RM4000761	3.2	3.2	2.2	2.6	0.7	0.7	0.95	1	
NT2RM4001843	1.5	1.8	1.7	2.8	1.2	0.6	0.98	1	
NT2RP1000239	2.1	3.2	1.2	2.1	0.5	0.6	1	0.99	
NT2RP1000465	0.9	0.3	0.3	0.9	0.2	0.1	0.97	0.96	
NT2RP1000679	0.3	0.3	0.4	0.9	0.2	0.3	0.97	1	
NT2RP1001031	1.4	1.4	0.4	1.2	0.1	0.3	1	0.98	
NT2RP2001200	2	1.5	0.8	2.2	0.7	0.7	0.99	1	
NT2RP2001562	2.7	2.4	0.7	3.6	0.4	1.1	1	0.94	
NT2RP2001948	1.1	1.5	0.7	1.8	0.6	0.7	0.97	0.99	
NT2RP2002015	1.3	1.7	0.7	1.8	0.6	0.5	0.99	1	
NT2RP2003390	2	1.7	1.3	2.3	0.6	0.5	0.99	0.99	
NT2RP2003664	0.4	0.1	0.1	0.8	0.1	0	0.99	0.99	
NT2RP2005597	1.2	1.4	0.5	2.7	2.2	2.2	0.96	0.99	
NT2RP2001469	1.7	1.4	1.2	2	0.6	0.6	1	1	
NT2RP2000240	0.9	0.9	0.3	1.4	0.7	0.3	1	1	
NT2RP2000610	2.4	2.2	2.1	2.7	1.5	1.6	0.93	0.96	

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	NT2RP2001276	1	0.4	0.4	0.8	0.2	0.7	0.95	1
	NT2RP2001817	1.2	0.8	0.5	1.9	0.7	0.7	1	1
	NT2RP2004069	0.6	0.6	0.4	0.8	0.5	0.3	0.93	0.97
5	NT2RP2004108	0.3	0.2	0.6	1.1	0.4	0.5	0.96	1
	NT2RP2005391	0.7	0.5	0.1	1.2	0.3	0.3	1	0.99
	NT2RP2006092	1.6	1.2	0.9	2.1	0.6	0.7	0.97	1
	NT2RP2006134	1.2	1.5	0.7	1.9	1	0	0.91	1
10	NT2RP2000818	0.9	0.3	0.3	1.6	0.3	0.3	0.95	1
	NT2RP2000092	1.8	1.8	0.8	2	1	1	0.99	0.98
	NT2RP2000092	1.1	1.1	0.5	1.4	0.6	0.6	0.99	0.97
	NT2RP2001538	2.1	1.9	1.8	2.5	0.6	0.8	0.98	1
	NT2RP2006476	2.1	2.2	1.4	3.2	1.6	2	0.97	0.98
15	NT2RP3000616	0.1	0.1	0	0	0	0	1	1
	NT2RP3000721	2.2	2.8	0.7	2.4	0.4	0.4	1	0.98
	NT2RP3001044	1.5	1.9	0.6	2	0.7	0.4	1	1
	NT2RP3001240	0.8	1	0.8	1.5	0.6	0.7	0.97	0.99
	NT2RP3001592	0.3	0.8	0.8	1.1	0	0	0.94	0.93
20	NT2RP3002448	4.6	4.2	2.5	4.5	0.8	1.2	1	0.98
	NT2RP3002721	1.3	1.6	0.5	1.4	0.3	0.3	1	0.99
	NT2RP3002738	0.1	0	0.1	1.9	0.1	0.1	0.99	1
	NT2RP3002790	1.6	2	0.6	1.7	0.6	0.5	0.98	1
	NT2RP3002836	1.7	3	0.9	2.4	1.6	0.7	1	1
25	NT2RP3003354	0.9	0.7	0.5	0.6	0.4	0.5	0.99	0.92
	NT2RP3003614	0.5	0.4	0	0.3	0.3	0.2	0.99	0.99
	NT2RP3004075	0.8	1.4	0.7	1	0.4	0.4	1	1
	NT2RP3004130	0.3	0.4	0	0.2	0.1	0	0.93	0.96
	NT2RP3004133	1.9	3.5	0.6	3.8	1	1.3	0.99	1
30	NT2RP3004321	0.2	0.2	0	1.4	0.4	0.2	1	0.99
	NT2RP3004406	1.3	0.2	0.2	0.7	0.1	0	1	1
	NT2RP3004552	0.1	0.1	0.1	0.1	0	0	1	1
	NT2RP3004557	1.3	1.1	2.2	2.6	1.5	1.4	0.98	0.94
	NT2RP3004647	1.2	2.1	0.6	1.2	1	0.5	1	1
35	NT2RP3000201	2.3	2.9	0.4	1	1.3	0.5	1	0.98
	NT2RP3000820	1.2	1.6	0.9	1.2	0.6	0.5	1	1
	NT2RP3000818	1.4	1.5	0.7	1.8	0.5	0.7	1	0.99
	NT2RP3001159	1.2	2.5	1.2	1.4	0.6	0.7	0.99	0.99
	NT2RP3002281	1.6	2	1.2	1.8	1	1.2	0.99	1
40	NT2RP3002571	3.9	1.8	1.2	5.2	1.4	0.8	0.99	0.97
	NT2RP3002983	1.4	1.7	0.5	1.4	0.4	0.3	1	1
	NT2RP3003473	0.8	0.9	1	0.7	0.4	0.5	1	0.99
	NT2RP3001976	0.6	1.1	0.1	0.7	0.4	0.1	1	0.99
	NT2RP3002286	1.4	1.8	1	1.6	0.6	0.5	1	0.99
45	NT2RP3002353	7.7	6.4	2.2	8.7	1.1	1.3	0.94	0.99
	NT2RP3004025	1.9	2	1	2.1	1	1	0.96	0.98
	NT2RP3004119	0.8	1.1	0.4	0	0	0.2	1	0.99
	NT2RP3000171	0.7	1.3	0.6	1	0.4	0.3	0.99	1
	NT2RP3000676	1.2	1.9	0.7	1.1	1.3	0.5	0.99	1
50	NT2RP3000921	0.2	0.1	0	0.2	0.1	0	1	0.99
	NT2RP3002015	0.8	0.6	0.4	0.7	0.1	0.1	0.99	0.99
	NT2RP3004294	0	0	0	0.1	0.1	0	1	1
	NT2RP3004345	0.6	0.4	0.2	0.9	0.2	0.5	1	1
55	NT2RP3000148	1.7	2.5	0.8	2	0.8	0.8	1	1

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	NT2RP3000232	0.6	0.8	0.4	0.3	0	0	1	0.99
	NT2RP3001650	2.3	1.5	1.6	1.7	1	1.3	1	1
	NT2RP3002411	0.5	0.4	0.1	0.5	0.2	0.1	1	1
5	NT2RP4001001	0.8	1.3	0.7	1	0.7	0.4	0.97	0.97
	NT2RP4001877	1.5	0.9	1.1	1.2	0.5	0.7	1	0.99
	NT2RP4002451	0.7	1	0.6	0.7	0.2	0.3	0.91	0.95
	NT2RP4000634	1	1	0.3	0.9	0.3	0.4	0.99	1
10	NT2RP4002187	0.4	0.4	0.1	0.7	0.3	0.2	1	0.99
	NT2RP4002715	1.5	1.6	0.7	1.5	0.4	0.3	1	0.99
	MAMMA1000986	3.9	4.1	1.9	4.2	1.8	1.4	0.99	1
	MAMMA1001237	0	0	1.6	0.2	0	0	0.99	0.98
	MAMMA1001978	3.5	3.4	2.3	6	3.4	2.5	0.97	0.98
15	MAMMA1002080	0.4	0	0	0.4	0.1	0	1	0.99
	MAMMA1002234	4	4.4	3	7.7	1.9	3	0.97	1
	MAMMA1000614	4.8	1	15.5	5.6	3.9	4.8	0.95	0.93
	MAMMA1000141	7.1	11.5	3.5	14.8	6.5	3.7	1	0.98
	MAMMA1000706	7.2	9.3	3.9	3.7	2.3	2.6	0.98	0.99
20	MAMMA1000788	3	3.8	2.8	8.9	4.8	4.2	0.92	0.98
	MAMMA1000994	0.3	0	0	0.4	0	0	1	1
	MAMMA1001310	4.1	6.1	3.8	8	2.5	3.6	0.99	0.95
	MAMMA1001344	2.7	4.4	2.2	3.2	2.6	2.1	1	0.99
	MAMMA1001957	2.3	2.7	1.9	1.7	1	1.8	0.99	1
25	MAMMA1002070	0.1	0.1	0	0.8	0.4	0.2	1	0.99
	MAMMA1002586	1.7	1.6	1.2	1.3	0.4	0.3	0.94	1
	MAMMA1000102	2.1	2.3	1.4	3.3	1.6	1.6	1	1
	MAMMA1001066	2.8	2.6	1.8	5.3	0.7	1.2	1	0.98
	MAMMA1001094	2.3	2.9	2	3.3	2.1	2.5	0.96	0.9
30	MAMMA1001609	2	3	1.2	2.7	1.7	2.2	0.99	0.97
	PLACE1002547	2	1.7	1.2	4.1	1.2	2	0.95	1
	PLACE1003573	0	0	0	0.1	0	0	1	0.98
	PLACE1004199	0.1	0.2	0	0	0	0	0.99	0.97
	PLACE1004305	0	0	0	0.3	0	0.2	0.96	0.99
35	PLACE1004450	0.9	0.3	0	0.1	0	0	0.98	0.98
	PLACE1005031	0.9	0	0	0.5	0	0	0.98	0.99
	PLACE1007845	0.8	1	0.4	0.4	0.1	0.1	1	0.98
	PLACE1008984	1.4	1.2	0.4	1.9	0.6	0.5	0.98	0.98
	PLACE1011116	2.6	1.5	1.6	1.6	0.3	0.4	1	1
40	PLACE1000986	0.6	0.2	0.2	0.3	0.1	0.1	1	0.98
	PLACE1004492	1.9	1.9	1.5	3.3	1	1	1	0.97
	PLACE1005569	2.6	0.4	0	1.1	0.3	0.1	0.98	0.99
	PLACE1005601	1.7	1.3	1	2.3	0.6	0.3	0.93	1
	PLACE1006079	0.6	0.3	0	0.1	0.1	0	0.98	0.99
45	PLACE1007077	1.1	0	0	0.3	0.1	0	0.97	0.98
	PLACE1008744	0.4	0.1	0.1	1.1	0.1	0	0.98	1
	PLACE1011181	0.6	0.3	0.5	1.6	0.3	0.5	0.98	0.99
	PLACE1005539	0.4	0	0.2	0.3	0.2	0	1	0.93
	PLACE1008282	1.1	0.7	0.6	1.2	0.4	0.4	0.98	1
50	PLACE1010713	0.6	0.7	0	1.4	0.5	0.4	0.99	0.95
	PLACE1010011	1.2	1.4	0.2	2.7	1.5	1.7	1	0.99
	PLACE3000213	1.9	0.2	0.1	0.8	0.1	0	0.99	1
	PLACE1002080	6.7	3.9	0.3	1.7	0.8	0.5	0.95	0.98
55	SKNMC1000082	1.3	0.1	1.1	0.7	0	0	1	1

	Y79AA1000127	1.8	1.8	1.1	2.1	0.5	0.6	1	1
	Y79AA1000226	1.4	0.8	0.6	0.9	0.3	0.4	0.99	0.99
5	Y79AA1000776	0.3	0.1	0	1.1	0.3	0.5	0.99	0.99
	Y79AA1000876	1.1	1.5	1.2	1.3	0.5	0.8	0.97	1
	Y79AA1001056	1.7	1.7	0.8	1.4	0.9	0.7	1	1
	Y79AA1000777	3.1	3.1	1.2	3.8	0.7	0.5	0.98	0.99
10	Y79AA1000030	1	1.3	0.2	1.3	0	0.6	0.98	0.96
	Y79AA1001212	1.5	1.2	1	2	0.8	0.5	1	0.99
	Y79AA1001427	2.3	3	0.6	2	0.8	0.4	1	1
	Y79AA1001530	0.9	0.9	0.5	1.1	0.4	0.4	1	1
	Y79AA1001592	0.6	0.2	0	0.7	0	0	0.97	1
15	Y79AA1001727	0.8	0.4	0.2	0.9	0.2	0.1	1	1
	Y79AA1001803	0.1	0	0	0.2	0.1	0	0.97	0.99
	Y79AA1002373	0	0	0	0	0	0	0.99	1
	Y79AA1002376	0.9	0.1	0	1.2	0.1	0.4	0.98	1
20	Y79AA1001523	0.5	0.5	0.3	0.6	0.3	0.1	1	0.98
	Y79AA1000888	1.1	1	0.7	1.4	0.7	0.5	1	1
	Y79AA1002129	0.2	0.2	0.1	0.5	0.2	0.2	0.99	1

25 [0285] The present invention has provided a total of 830 novel full length cDNA clones. As has not yet proceeded the isolation of full length cDNA within the human, the invention has a large significance. Those proteins such as secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription are known to be associated with many diseases. Those genes and proteins associating with diseases are useful for developing medicines as they can be used as a diagnostic marker, or a target for gene therapy or developing

30 medicines that is capable of regulating their expression and activity. Especially, the cDNA clones encoding a secretion protein are extremely important for medicinal industry since the protein itself is expected to be effective as a medicine, and also the gene may have potential to be associating with many diseases. Moreover, those proteins such as membrane proteins, and proteins associated with signal transduction, glycoprotein, transcription, and diseases, and the genes encoding the proteins may be used as a disease marker. These cDNA clones are also important for medicinal

35 industry as they may be effective for treating diseases through the regulation of the expression and activity of their encoded proteins.

Table 368

40 The names of the representative sequences of the clusters (groups) and the corresponding SEQ IDs.

	HRIFA000016a : 1573	HRIFA017855a : 1979
45	HRIFA000071a : 1574	HRIFA017921a : 1980
	HRIFA000116a : 1575	HRIFA018075a : 1981
	HRIFA000123a : 1576	HRIFA018092a : 1982
	HRIFA000264a : 1577	HRIFA018131a : 1983
	HRIFA000284a : 1578	HRIFA018134a : 1984
50	HRIFA000327a : 1579	HRIFA018238a : 1985
	HRIFA000415a : 1580	HRIFA018262a : 1986
	HRIFA000432a : 1581	HRIFA018287a : 1987
	HRIFA000446a : 1582	HRIFA018447a : 1988
55	HRIFA000553a : 1583	HRIFA018580a : 1989
	HRIFA000564a : 1584	HRIFA018666a : 1990
	HRIFA000631a : 1585	HRIFA018688a : 1991

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	HRIFA000683a : 1586	HRIFA018754a : 1992
	HRIFA000695a : 1587	HRIFA018794a : 1993
	HRIFA000776a : 1588	HRIFA018827a : 1994
5	HRIFA000814a : 1589	HRIFA018849a : 1995
	HRIFA000822a : 1590	HRIFA018870a : 1996
	HRIFA000845a : 1591	HRIFA018904a : 1997
	HRIFA000899a : 1592	HRIFA018931a : 1998
	HRIFA000974a : 1593	HRIFA018993a : 1999
10	HRIFA001099a : 1594	HRIFA019105a : 2000
	HRIFA001132a : 1595	HRIFA019136a : 2001
	HRIFA001138a : 1596	HRIFA019175a : 2002
	HRIFA001179a : 1597	HRIFA019185a : 2003
	HRIFA001200a : 1598	HRIFA019262a : 2004
15	HRIFA001201a : 1599	HRIFA019412a : 2005
	HRIFA001337a : 1600	HRIFA019437a : 2006
	HRIFA001341a : 1601	HRIFA019466a : 2007
	HRIFA001413a : 1602	HRIFA019490a : 2008
20	HRIFA001439a : 1603	HRIFA019498a : 2009
	HRIFA001489a : 1604	HRIFA019532a : 2010
	HRIFA001558a : 1605	HRIFA019651a : 2011
	HRIFA001712a : 1606	HRIFA019867a : 2012
	HRIFA001720a : 1607	HRIFA019869a : 2013
25	HRIFA001866a : 1608	HRIFA019958a : 2014
	HRIFA001942a : 1609	HRIFA019960a : 2015
	HRIFA001971a : 1610	HRIFA020109a : 2016
	HRIFA001972a : 1611	HRIFA020144a : 2017
	HRIFA001975a : 1612	HRIFA020163a : 2018
30	HRIFA001984a : 1613	HRIFA020184a : 2019
	HRIFA002037a : 1614	HRIFA020272a : 2020
	HRIFA002063a : 1615	HRIFA020335a : 2021
	HRIFA002102a : 1616	HRIFA020349a : 2022
	HRIFA002195a : 1617	HRIFA020453a : 2023
35	HRIFA002284a : 1618	HRIFA020466a : 2024
	HRIFA002309a : 1619	HRIFA020661a : 2025
	HRIFA002384a : 1620	HRIFA020693a : 2026
	HRIFA002503a : 1621	HRIFA020707a : 2027
	HRIFA002689a : 1622	HRIFA020748a : 2028
40	HRIFA002694a : 1623	HRIFA020862a : 2029
	HRIFA002743a : 1624	HRIFA020883a : 2030
	HRIFA002762a : 1625	HRIFA020965a : 2031
	HRIFA002766a : 1626	HRIFA021007a : 2032
	HRIFA002787a : 1627	HRIFA021040a : 2033
45	HRIFA002805a : 1628	HRIFA021061a : 2034
	HRIFA002891a : 1629	HRIFA021069a : 2035
	HRIFA002919a : 1630	HRIFA021136a : 2036
	HRIFA002980a : 1631	HRIFA021213a : 2037
50	HRIFA002985a : 1632	HRIFA021224a : 2038
	HRIFA003055a : 1633	HRIFA021323a : 2039
	HRIFA003063a : 1634	HRIFA021398a : 2040
	HRIFA003093a : 1635	HRIFA021399a : 2041
	HRIFA003169a : 1636	HRIFA021445a : 2042
55	HRIFA003340a : 1637	HRIFA021448a : 2043

	HRIFA003357a : 1638	HRIFA021494a : 2044
	HRIFA003379a : 1639	HRIFA021499a : 2045
	HRIFA003402a : 1640	HRIFA021543a : 2046
5	HRIFA003504a : 1641	HRIFA021594a : 2047
	HRIFA003592a : 1642	HRIFA021611a : 2048
	HRIFA003635a : 1643	HRIFA021620a : 2049
	HRIFA003640a : 1644	HRIFA021637a : 2050
10	HRIFA003883a : 1645	HRIFA021651a : 2051
	HRIFA003892a : 1646	HRIFA021754a : 2052
	HRIFA003946a : 1647	HRIFA021781a : 2053
	HRIFA004006a : 1648	HRIFA021787a : 2054
	HRIFA004034a : 1649	HRIFA021794a : 2055
15	HRIFA004112a : 1650	HRIFA021855a : 2056
	HRIFA004145a : 1651	HRIFA021886a : 2057
	HRIFA004162a : 1652	HRIFA021906a : 2058
	HRIFA004401a : 1653	HRIFA021985a : 2059
	HRIFA004426a : 1654	HRIFA022055a : 2060
20	HRIFA004490a : 1655	HRIFA022065a : 2061
	HRIFA004523a : 1656	HRIFA022106a : 2062
	HRIFA004663a : 1657	HRIFA022139a : 2063
	HRIFA004696a : 1658	HRIFA022156a : 2064
	HRIFA004714a : 1659	HRIFA022166a : 2065
25	HRIFA004745a : 1660	HRIFA022177a : 2066
	HRIFA004780a : 1661	HRIFA022182a : 2067
	HRIFA004852a : 1662	HRIFA022203a : 2068
	HRIFA004919a : 1663	HRIFA022227a : 2069
30	HRIFA005072a : 1664	HRIFA022234a : 2070
	HRIFA005102a : 1665	HRIFA022249a : 2071
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Table 369

The names of the internal sequences that are used in the selection of the clones from the representative sequences, and the corresponding SEQ IDs.

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	HRIFA022923a : 2429	HRIRA006263a : 2508
	HRIFA023027a : 2430	HRIRA006324a : 2509
	HRIFA023218a : 2431	HRIRA006517a : 2510
35	HRIFA023363a : 2432	HRIRA006580a : 2511
	HRIFA023434a : 2433	HRIRA007665a : 2512
	HRIFA023444a : 2434	HRIRA007680a : 2513
	HRIFA023551a : 2435	HRIRA008129a : 2514
	HRIFA023558a : 2436	HRIRA008152a : 2515
40	HRIFA023641a : 2437	HRIRA008276a : 2516
	HRIFA023798a : 2438	HRIRA008329a : 2517
	HRIFA024330a : 2439	HRIRA008854a : 2518
	HRIFA024338a : 2440	HRIRA008896a : 2519
	HRIFA024384a : 2441	HRIRA008958a : 2520
45	HRIFA024644a : 2442	HRIRA009551a : 2521
	HRIFA025170a : 2443	HRIRA009828a : 2522
	HRIFA025496a : 2444	HRIRA010472a : 2523
	HRIFA025565a : 2445	HRIRA012442a : 2524
	HRIFA025651a : 2446	HRIRA012921a : 2525
50	HRIFA026224a : 2447	HRIRA013325a : 2526
	HRIFA026729a : 2448	HRIRA013644a : 2527
	HRIFA026925a : 2449	HRIRA013675a : 2528
	HRIFA028501a : 2450	HRIRA013702a : 2529
	HRIFA029454a : 2451	HRIRA013757a : 2530
55	HRIFA030181a : 2452	HRIRA013951a : 2531

HRIFA032701a : 2453	HRIRA014256a : 2532
HRIFA032801a : 2454	HRIRA014380a : 2533
HRIFA033384a : 2455	HRIRA015831a : 2534
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HRIFA033930a : 2457	HRIRA016124a : 2536
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HRIFA035542a : 2460	HRIRA020304a : 2539
HRIFA035577a : 2461	HRIRA000579a : 2540
<u>HRIFA036630a : 2462</u>	

[0286] The internal sequences include EST, HRIFA(the representative sequence of the 5'-end), and HRIRA (the representative sequence of the 3'-end).

Table 370

clone	the name of full-length nucleotide sequences	SEQ ID NO of the full-length nucleotide sequences	SEQ ID NO of the deduced amino acid sequences	SEQ ID NO
HEMBA1000006	C-HEMBA1000006	2547	2548	
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HEMBA1000128	C-HEMBA1000128	2553	2554	
HEMBA1000275	C-HEMBA1000275	2555	2556	
HEMBA1000300	C-HEMBA1000300	2557		
HEMBA1000349	C-HEMBA1000349	2558	2559	
HEMBA1000443	C-HEMBA1000443	2560	2561	
HEMBA1000590	C-HEMBA1000590	2562	2563	
HEMBA1000634	C-HEMBA1000634	2564	2565	
HEMBA1000713	C-HEMBA1000713	2566	2567	
HEMBA1000745	C-HEMBA1000745	2568	2569	
HEMBA1000907	C-HEMBA1000907	2570	2571	
HEMBA1000940	C-HEMBA1000940	2572	2573	
HEMBA1000962	C-HEMBA1000962	2574	2575	
HEMBA1001221	C-HEMBA1001221	2576	2577	
HEMBA1001228	C-HEMBA1001228	2578	2579	
HEMBA1001297	C-HEMBA1001297	2580		
HEMBA1001390	C-HEMBA1001390	2581	2582	
HEMBA1001563	C-HEMBA1001563	2583		
HEMBA1001621	C-HEMBA1001621	2584	2585	
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HEMBA1001878	C-HEMBA1001878	2588	2589	
HEMBA1002131	C-HEMBA1002131	2590	2591	
HEMBA1002163	C-HEMBA1002163	2592	2593	
HEMBA1002164	C-HEMBA1002164	2594	2595	
HEMBA1002167	C-HEMBA1002167	2596	2597	
HEMBA1002178	C-HEMBA1002178	2598	2599	
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	HEMBA1002195	C-HEMBA1002195	2602	2603
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5	HEMBA1002316	C-HEMBA1002316	2607	2608
	HEMBA1002420	C-HEMBA1002420	2609	2610
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	HEMBA1002524	C-HEMBA1002524	2613	2614
	HEMBA1002551	C-HEMBA1002551	2615	2616
10	HEMBA1002767	C-HEMBA1002767	2617	2618
	HEMBA1002992	C-HEMBA1002992	2619	2620
	HEMBA1003047	C-HEMBA1003047	2621	2622
	HEMBA1003072	C-HEMBA1003072	2623	2624
	HEMBA1003101	C-HEMBA1003101	2625	2626
15	HEMBA1003230	C-HEMBA1003230	2627	2628
	HEMBA1003294	C-HEMBA1003294	2629	
	HEMBA1003315	C-HEMBA1003315	2630	2631
	HEMBA1003392	C-HEMBA1003392	2632	2633
20	HEMBA1003399	C-HEMBA1003399	2634	2635
	HEMBA1003487	C-HEMBA1003487	2636	2637
	HEMBA1003530	C-HEMBA1003530	2638	2639
	HEMBA1003602	C-HEMBA1003602	2640	2641
	HEMBA1003732	C-HEMBA1003732	2642	2643
25	HEMBA1003945	C-HEMBA1003945	2644	2645
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	HEMBA1004250	C-HEMBA1004250	2648	2649
	HEMBA1004391	C-HEMBA1004391	2650	2651
	HEMBA1004444	C-HEMBA1004444	2652	2653
30	HEMBA1004454	C-HEMBA1004454	2654	2655
	HEMBA1004505	C-HEMBA1004505	2656	2657
	HEMBA1004797	C-HEMBA1004797	2658	2659
	HEMBA1004982	C-HEMBA1004982	2660	2661
	HEMBA1005070	C-HEMBA1005070	2662	2663
35	HEMBA1005084	C-HEMBA1005084	2664	2665
	HEMBA1005145	C-HEMBA1005145	2666	2667
	HEMBA1005430	C-HEMBA1005430	2668	2669
	HEMBA1005449	C-HEMBA1005449	2670	2671
40	HEMBA1005489	C-HEMBA1005489	2672	2673
	HEMBA1005522	C-HEMBA1005522	2674	2675
	HEMBA1005545	C-HEMBA1005545	2676	2677
	HEMBA1005698	C-HEMBA1005698	2678	2679
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	HEMBA1005945	C-HEMBA1005945	2683	2684
	HEMBA1006016	C-HEMBA1006016	2685	
	HEMBA1006171	C-HEMBA1006171	2686	2687
	HEMBA1006299	C-HEMBA1006299	2688	2689
50	HEMBA1006311	C-HEMBA1006311	2690	2691
	HEMBA1006335	C-HEMBA1006335	2692	2693
	HEMBA1006430	C-HEMBA1006430	2694	2695
	HEMBA1006482	C-HEMBA1006482	2696	2697
	HEMBA1006572	C-HEMBA1006572	2698	2699
55	HEMBA1006707	C-HEMBA1006707	2700	2701

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	HEMBA1006724	C-HEMBA1006724	2702	2703
	HEMBA1006902	C-HEMBA1006902	2704	2705
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5	HEMBA1006960	C-HEMBA1006960	2708	2709
	HEMBA1007013	C-HEMBA1007013	2710	2711
	HEMBA1007057	C-HEMBA1007057	2712	2713
	HEMBA1007241	C-HEMBA1007241	2714	
	HEMBA1007291	C-HEMBA1007291	2715	2716
10	HEMBA1007332	C-HEMBA1007332	2717	
	HEMBB1000276	C-HEMBB1000276	2718	
	HEMBB1000447	C-HEMBB1000447	2719	2720
	HEMBB1000642	C-HEMBB1000642	2721	
	HEMBB1000668	C-HEMBB1000668	2722	2723
15	HEMBB1000679	C-HEMBB1000679	2724	2725
	HEMBB1000881	C-HEMBB1000881	2726	2727
	HEMBB1000905	C-HEMBB1000905	2728	2729
	HEMBB1001026	C-HEMBB1001026	2730	2731
20	HEMBB1001048	C-HEMBB1001048	2732	2733
	HEMBB1001200	C-HEMBB1001200	2734	
	HEMBB1001407	C-HEMBB1001407	2735	2736
	HEMBB1001530	C-HEMBB1001530	2737	2738
	HEMBB1001573	C-HEMBB1001573	2739	2740
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	HEMBB1001847	C-HEMBB1001847	2743	2744
	HEMBB1001978	C-HEMBB1001978	2745	2746
	HEMBB1002162	C-HEMBB1002162	2747	2748
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30	HEMBB1002245	C-HEMBB1002245	2750	2751
	HEMBB1002427	C-HEMBB1002427	2752	2753
	HEMBB1002465	C-HEMBB1002465	2754	2755
	HEMBB1002663	C-HEMBB1002663	2756	2757
	HEMBB1002693	C-HEMBB1002693	2758	2759
35	MAMMA1000046	C-MAMMA1000046	2760	
	MAMMA1000118	C-MAMMA1000118	2761	2762
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	MAMMA1000449	C-MAMMA1000449	2765	
40	MAMMA1000457	C-MAMMA1000457	2766	2767
	MAMMA1000591	C-MAMMA1000591	2768	2769
	MAMMA1000681	C-MAMMA1000681	2770	2771
	MAMMA1001043	C-MAMMA1001043	2772	2773
	MAMMA1001893	C-MAMMA1001893	2774	2775
45	NT2RM2000241	C-NT2RM2000241	2776	2777
	NT2RM2000306	C-NT2RM2000306	2778	2779
	NT2RM2000410	C-NT2RM2000410	2780	2781
	NT2RM2000423	C-NT2RM2000423	2782	2783
	NT2RM2000497	C-NT2RM2000497	2784	2785
50	NT2RM2000514	C-NT2RM2000514	2786	2787
	NT2RM2000622	C-NT2RM2000622	2788	2789
	NT2RM2001126	C-NT2RM2001126	2790	2791
	NT2RM2001902	C-NT2RM2001902	2792	2793
	NT2RM2001939	C-NT2RM2001939	2794	2795
55	NT2RM2001941	C-NT2RM2001941	2796	2797

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	NT2RM4000198	C-NT2RM4000198	2798	2799
	NT2RM4000284	C-NT2RM4000284	2800	2801
	NT2RM4000295	C-NT2RM4000295	2802	2803
5	NT2RM4000326	C-NT2RM4000326	2804	2805
	NT2RM4000444	C-NT2RM4000444	2806	2807
	NT2RM4000587	C-NT2RM4000587	2808	2809
	NT2RM4000648	C-NT2RM4000648	2810	2811
10	NT2RM4000997	C-NT2RM4000997	2812	2813
	NT2RM4001321	C-NT2RM4001321	2814	2815
	NT2RM4001325	C-NT2RM4001325	2816	2817
	NT2RM4001735	C-NT2RM4001735	2818	2819
	NT2RM4002352	C-NT2RM4002352	2820	2821
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	NT2RP1000050	C-NT2RP1000050	2824	2825
	NT2RP1000181	C-NT2RP1000181	2826	2827
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	NT2RP1000325	C-NT2RP1000325	2832	2833
	NT2RP1000448	C-NT2RP1000448	2834	2835
	NT2RP1000551	C-NT2RP1000551	2836	2837
	NT2RP1000579	C-NT2RP1000579	2838	2839
25	NT2RP1000613	C-NT2RP1000613	2840	2841
	NT2RP1000903	C-NT2RP1000903	2842	2843
	NT2RP1000981	C-NT2RP1000981	2844	2845
	NT2RP1001004	C-NT2RP1001004	2846	2847
	NT2RP1001020	C-NT2RP1001020	2848	2849
30	NT2RP1001563	C-NT2RP1001563	2850	2851
	NT2RP2000394	C-NT2RP2000394	2852	2853
	NT2RP2000479	C-NT2RP2000479	2854	2855
	NT2RP2000514	C-NT2RP2000514	2856	2857
	NT2RP2000533	C-NT2RP2000533	2858	2859
35	NT2RP2000649	C-NT2RP2000649	2860	2861
	NT2RP2000663	C-NT2RP2000663	2862	2863
	NT2RP2000694	C-NT2RP2000694	2864	2865
	NT2RP2000903	C-NT2RP2000903	2866	2867
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	NT2RP2001514	C-NT2RP2001514	2872	2873
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	NT2RP2001769	C-NT2RP2001769	2876	2877
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	NT2RP2001915	C-NT2RP2001915	2882	2883
	NT2RP2001956	C-NT2RP2001956	2884	2885
	NT2RP2002063	C-NT2RP2002063	2886	2887
50	NT2RP2002188	C-NT2RP2002188	2888	2889
	NT2RP2002232	C-NT2RP2002232	2890	2891
	NT2RP2002304	C-NT2RP2002304	2892	2893
	NT2RP2002409	C-NT2RP2002409	2894	2895
	NT2RP2002510	C-NT2RP2002510	2896	2897
55	NT2RP2002527	C-NT2RP2002527	2898	2899
	NT2RP2002533	C-NT2RP2002533	2900	2901

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	NT2RP2002564	C-NT2RP2002564	2902	2903
	NT2RP2002674	C-NT2RP2002674	2904	2905
	NT2RP2002721	C-NT2RP2002721	2906	2907
5	NT2RP2002824	C-NT2RP2002824	2908	2909
	NT2RP2002942	C-NT2RP2002942	2910	2911
	NT2RP2002974	C-NT2RP2002974	2912	2913
	NT2RP2002976	C-NT2RP2002976	2914	2915
10	NT2RP2003042	C-NT2RP2003042	2916	2917
	NT2RP2003179	C-NT2RP2003179	2918	2919
	NT2RP2003210	C-NT2RP2003210	2920	2921
	NT2RP2003369	C-NT2RP2003369	2922	2923
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15	NT2RP2003469	C-NT2RP2003469	2926	2927
	NT2RP2003545	C-NT2RP2003545	2928	2929
	NT2RP2003593	C-NT2RP2003593	2930	2931
	NT2RP2003599	C-NT2RP2003599	2932	2933
	NT2RP2003655	C-NT2RP2003655	2934	2935
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	NT2RP2004179	C-NT2RP2004179	2940	2941
	NT2RP2004205	C-NT2RP2004205	2942	2943
	NT2RP2004447	C-NT2RP2004447	2944	2945
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	NT2RP2004524	C-NT2RP2004524	2948	2949
	NT2RP2004556	C-NT2RP2004556	2950	2951
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	NT2RP2004847	C-NT2RP2004847	2962	2963
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	NT2RP2005163	C-NT2RP2005163	2967	2968
	NT2RP2005181	C-NT2RP2005181	2969	2970
	NT2RP2005247	C-NT2RP2005247	2971	2972
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	NT2RP2005463	C-NT2RP2005463	2975	2976
	NT2RP2005514	C-NT2RP2005514	2977	2978
	NT2RP2005541	C-NT2RP2005541	2979	2980
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	NT2RP2005883	C-NT2RP2005883	2985	2986
	NT2RP2005887	C-NT2RP2005887	2987	2988
	NT2RP2005941	C-NT2RP2005941	2989	2990
	NT2RP2005994	C-NT2RP2005994	2991	2992
50	NT2RP2006042	C-NT2RP2006042	2993	2994
	NT2RP2006269	C-NT2RP2006269	2995	2996
	NT2RP2006512	C-NT2RP2006512	2997	2998
	NT2RP3000059	C-NT2RP3000059	2999	3000
	NT2RP3000063	C-NT2RP3000063	3001	3002
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[illegible]

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	NT2RP3004374	C-NT2RP3004374	3117	3118
	NT2RP3004406	C-NT2RP3004406	3119	3120
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	NT2RP3004557	C-NT2RP3004557	3123	3124
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	NT2RP3004647	C-NT2RP3004647	3129	3130
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	NT2RP4001467	C-NT2RP4001467	3137	3138
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	OVARC1000105	C-OVARC1000105	3140	3141
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	OVARC1000208	C-OVARC1000208	3143	
	OVARC1000255	C-OVARC1000255	3144	3145
	OVARC1000275	C-OVARC1000275	3146	3147
	OVARC1000298	C-OVARC1000298	3148	3149
25	OVARC1000410	C-OVARC1000410	3150	3151
	OVARC1000439	C-OVARC1000439	3152	3153
	OVARC1000467	C-OVARC1000467	3154	3155
	OVARC1000529	C-OVARC1000529	3156	3157
	OVARC1000775	C-OVARC1000775	3158	3159
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	OVARC1000811	C-OVARC1000811	3162	3163
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	OVARC1000916	C-OVARC1000916	3166	3167
35	OVARC1000956	C-OVARC1000956	3168	3169
	OVARC1001030	C-OVARC1001030	3170	3171
	OVARC1001049	C-OVARC1001049	3172	3173
	OVARC1001086	C-OVARC1001086	3174	3175
	OVARC1001132	C-OVARC1001132	3176	3177
40	OVARC1001163	C-OVARC1001163	3178	3179
	OVARC1001222	C-OVARC1001222	3180	
	OVARC1001338	C-OVARC1001338	3181	3182
	OVARC1001569	C-OVARC1001569	3183	3184
	OVARC1001596	C-OVARC1001596	3185	3186
45	OVARC1001725	C-OVARC1001725	3187	
	OVARC1001727	C-OVARC1001727	3188	
	OVARC1001807	C-OVARC1001807	3189	3190
	OVARC1001991	C-OVARC1001991	3191	3192
	OVARC1002058	C-OVARC1002058	3193	3194
50	OVARC1002178	C-OVARC1002178	3195	
	PLACE1000033	C-PLACE1000033	3196	3197
	PLACE1000231	C-PLACE1000231	3198	3199
	PLACE1000258	C-PLACE1000258	3200	3201
	PLACE1000442	C-PLACE1000442	3202	3203
55	PLACE1000560	C-PLACE1000560	3204	3205

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	PLACE1000740	C-PLACE1000740	3206	3207
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	PLACE1001016	C-PLACE1001016	3214	3215
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	PLACE1001123	C-PLACE1001123	3221	
	PLACE1001183	C-PLACE1001183	3222	3223
	PLACE1001229	C-PLACE1001229	3224	3225
	PLACE1001231	C-PLACE1001231	3226	3227
15	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
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	PLACE1001401	C-PLACE1001401	3232	3233
	PLACE1001407	C-PLACE1001407	3234	3235
	PLACE1001464	C-PLACE1001464	3236	3237
20	PLACE1001500	C-PLACE1001500	3238	3239
	PLACE1001516	C-PLACE1001516	3240	3241
	PLACE1001536	C-PLACE1001536	3242	3243
	PLACE1001564	C-PLACE1001564	3244	3245
	PLACE1001655	C-PLACE1001655	3246	3247
25	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	nnnn	nnnn
	PLACE1001788	C-PLACE1001788	3250	3251
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	THYRO1000956	C-THYRO1000956	3506	3507
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	NT2RP4001001	C-NT2RP4001001	3942	3943
	NT2RP4001877	C-NT2RP4001877	3944	3945
20	NT2RP4001879	C-NT2RP4001879	3946	3947
	NT2RP4002187	C-NT2RP4002187	3948	3949
	NT2RP4002451	C-NT2RP4002451	3950	3951
	NT2RP4002750	C-NT2RP4002750	3952	3953
	OVARC1000003	C-OVARC1000003	3954	3955
25	OVARC1000313	C-OVARC1000313	3956	3957
	OVARC1000331	C-OVARC1000331	3958	3959
	OVARC1000553	C-OVARC1000553	3960	3961
	OVARC1000873	C-OVARC1000873	3962	3963
	OVARC1000995	C-OVARC1000995	3964	
30	OVARC1001260	C-OVARC1001260	3965	
	OVARC1001336	C-OVARC1001336	3966	3967
	OVARC1001570	C-OVARC1001570	3968	3969
	OVARC1001607	C-OVARC1001607	3970	3971
	OVARC1001833	C-OVARC1001833	3972	3973
35	OVARC1001952	C-OVARC1001952	3974	3975
	PLACE1000986	C-PLACE1000986	3976	
	PLACE1003407	C-PLACE1003407	3977	3978
	PLACE1004078	C-PLACE1004078	3979	3980
	PLACE1004492	C-PLACE1004492	3981	3982
40	PLACE1005539	C-PLACE1005539	3983	3984
	PLACE1005569	C-PLACE1005569	3985	3986
	PLACE1005601	C-PLACE1005601	3987	
	PLACE1005745	C-PLACE1005745	3988	3989
45	PLACE1005815	C-PLACE1005815	3990	3991
	PLACE1005927	C-PLACE1005927	3992	3993
	PLACE1006071	C-PLACE1006071	3994	3995
	PLACE1006073	C-PLACE1006073	3996	3997
	PLACE1006079	C-PLACE1006079	3998	3999
50	PLACE1006786	C-PLACE1006786	4000	
	PLACE1007077	C-PLACE1007077	4001	4002
	PLACE1007971	C-PLACE1007971	4003	
	PLACE1008282	C-PLACE1008282	4004	4005
	PLACE1008359	C-PLACE1008359	4006	4007
55	PLACE1008744	C-PLACE1008744	4008	4009

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	PLACE1010445	C-PLACE1010445	4010	4011
	PLACE1010713	C-PLACE1010713	4012	4013
	nnnnnnnnnnnn	C-nnnnnnnnnnnnn	4014	4015
5	PLACE1011181	C-PLACE1011181	4016	4017
	PLACE1011364	C-PLACE1011364	4018	4019
	PLACE3000181	C-PLACE3000181	4020	4021
	SKNMC1000014	C-SKNMC1000014	4022	4023
10	SKNMC1000082	C-SKNMC1000082	4024	4025
	THYRO1000964	C-THYRO1000964	4026	4027
	THYRO1001242	C-THYRO1001242	4028	4029
	THYRO1001608	C-THYRO1001608	4030	4031
	THYRO1001641	C-THYRO1001641	4032	4033
15	THYRO1001770	C-THYRO1001770	4034	4035
	Y79AA1000030	C-Y79AA1000030	4036	4037
	Y79AA1001212	C-Y79AA1001212	4038	4039
	Y79AA1001426	C-Y79AA1001426	4040	4041
	Y79AA1001427	C-Y79AA1001427	4042	4043
20	Y79AA1001523	C-Y79AA1001523	4044	4045
	Y79AA1001530	C-Y79AA1001530	4046	4047
	Y79AA1001592	C-Y79AA1001592	4048	4049
	Y79AA1001727	C-Y79AA1001727	4050	4051
	Y79AA1001787	C-Y79AA1001787	4052	4053
25	Y79AA1001793	C-Y79AA1001793	4054	4055
	Y79AA1001795	C-Y79AA1001795	4056	4057
	Y79AA1001799	C-Y79AA1001799	4058	4059
	Y79AA1001803	C-Y79AA1001803	4060	4061
30	Y79AA1001863	C-Y79AA1001863	4062	4063
	Y79AA1002058	C-Y79AA1002058	4064	4065
	Y79AA1002121	C-Y79AA1002121	4066	4067
	Y79AA1002213	C-Y79AA1002213	4068	4069
	Y79AA1002373	C-Y79AA1002373	4070	4071
35	Y79AA1002376	C-Y79AA1002376	4072	4073
	Y79AA1002378	C-Y79AA1002378	4074	4075
	Y79AA1002381	C-Y79AA1002381	4076	4077
	BNGH41000087	C-BNGH41000087	4078	4079
40	HEMBA1001886	C-HEMBA1001886	4080	4081
	HEMBA1004067	C-HEMBA1004067	4082	4083
	HEMBA1007226	C-HEMBA1007226	4084	4085
	HEMBB1000309	C-HEMBB1000309	4086	4087
	HEMBB1000567	C-HEMBB1000567	4088	4089
45	MAMMA1000102	C-MAMMA1000102	4090	4091
	MAMMA1001066	C-MAMMA1001066	4092	4093
	MAMMA1001094	C-MAMMA1001094	4094	4095
	MAMMA1001609	C-MAMMA1001609	4096	4097
	MAMMA1001901	C-MAMMA1001901	4098	
50	MAMMA1002091	C-MAMMA1002091	4099	4100
	NT2RM1000462	C-NT2RM1000462	4101	4102
	NT2RM1000542	C-NT2RM1000542	4103	4104
	NT2RM1000789	C-NT2RM1000789	4105	4106
	NT2RM1000855	C-NT2RM1000855	4107	4108
55	NT2RM1000899	C-NT2RM1000899	4109	4110

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	NT2RP2000092	C-NT2RP2000092	4111	4112
	NT2RP2001538	C-NT2RP2001538	4113	4114
	NT2RP2001921	C-NT2RP2001921	4115	4116
5	NT2RP2003138	C-NT2RP2003138	4117	4118
	NT2RP2003302	C-NT2RP2003302	4119	4120
	NT2RP2003950	C-NT2RP2003950	4121	4122
	NT2RP2005535	C-NT2RP2005535	4123	4124
10	NT2RP2005774	C-NT2RP2005774	4125	4126
	NT2RP3000148	C-NT2RP3000148	4127	4128
	NT2RP3000232	C-NT2RP3000232	4129	4130
	NT2RP3000427	C-NT2RP3000427	4131	
15	NT2RP3000652	C-NT2RP3000652	4132	4133
	NT2RP3001650	C-NT2RP3001650	4134	4135
	NT2RP3002409	C-NT2RP3002409	4136	
	NT2RP3002411	C-NT2RP3002411	4137	4138
20	NT2RP3003448	C-NT2RP3003448	4139	
	NT2RP4002715	C-NT2RP4002715	4140	4141
	OVARC1000307	C-OVARC1000307	4142	4143
	PLACE1000907	C-PLACE1000907	4144	4145
25	PLACE1007081	C-PLACE1007081	4146	4147
	PLACE1010011	C-PLACE1010011	4148	4149
	PLACE3000213	C-PLACE3000213	4150	4151
	PLACE4000354	C-PLACE4000354	4152	4153
	PLACE4000455	C-PLACE4000455	4154	
30	THYRO1000776	C-THYRO1000776	4155	4156
	THYRO1001593	C-THYRO1001593	4157	4158
	Y79AA1000750	C-Y79AA1000750	4159	4160
	Y79AA1000888	C-Y79AA1000888	4161	4162
35	Y79AA1002129	C-Y79AA1002129	4163	4164
	Y79AA1002334	C-Y79AA1002334	4165	4166
	MAMMA1002224	C-MAMMA1002224	4167	
40	NT2RP1000271	C-NT2RP1000271	4168	4169
	NT2RP3000481	C-NT2RP3000481	4170	4171
	NT2RP3004481	C-NT2RP3004481	4172	4173
	HEMBA1006658	C-HEMBA1006658	4174	4175
45	NT2RP2006099	C-NT2RP2006099	4176	4177
	NT2RP2006580	C-NT2RP2006580	4178	4179

Homology search result 1

[0287] The result of the homology search in the SwissProt using the representative sequences of the 5'-ends.

Indicated are from the top,
the name of the representative sequence of the cluster,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the organism of which the top hit data is obtained,
the Accession No. of the top hit data.

[0288] Homology search results of the representative sequences of the 5'-end cluster to the data in SwissProt database are shown only for the representative sequences of the cluster from which clones were selected based on the homology search results.

5 [0289] The P-value is the score which is determined by taking into account the statistic probability of occurrence between the two sequences, and generally low score reflects high similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

10 HRIFA000016a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
9.2e-05:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496

15 HRIFA000071a
CIRCUMSPOROZOITE PROTEB PRECURSOR (CS).
5.8e-05:194:29
PLASMODIUM SIMIUM.
Q03110

20 HRIFA000116a
HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.
6.2e-06:83:27
CAENORHABDITIS ELEGANS.
25 P34679

HRIFA000123a
PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).
6.2e-08:89:34
30 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P33154

HRIFA000264a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
35 1.4e-06:231:34
GALLUS GALLUS (CHICKEN).
P02457

40 HRIFA000327a
ATP-BINDING CASSETTE TRANSPORTER 1.
2.0e-16:238:31
MUS MUSCULUS (MOUSE).
P41233

45 HRIFA000415a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-06:120:35
MUS MUSCULUS (MOUSE).
P05142

50 HRIFA000432a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
2.2e-21:86:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
55 Q09818

HRIFA000446a
HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.

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2.5e-09:138:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40085

5 HRIFA000553a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
1.7e-27:117:48
GALLUS GALLUS (CHICKEN).
P05099

10 HRIFA000564a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
2.9e-28:163:38
MUS MUSCULUS (MOUSE).
15 P54116

HRIFA000631a
ZINC FINGER PROTEIN 140.
8.2e-45:155:47
20 HOMO SAPIENS (HUMAN).
P52738

HRIFA000683a
FIBRILLIN 1 PRECURSOR.
25 4.8e-18:77:46
HOMO SAPIENS (HUMAN).
P35555

HRIFA000695a
30 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6" PEPTIDE P-H].
4.0e-06:105:33
HOMO SAPIENS (HUMAN).
P04280

35 HRIFA000776a
FIBRILLIN 2 PRECURSOR.
1.6e-42:214:44
HOMO SAPIENS (HUMAN).
40 P35556

HRIFA000814a
ZINC FINGER PROTEIN 133.
4.4e-16:49:87
45 HOMO SAPIENS (HUMAN).
P52736

HRIFA000845a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
50 6.0e-06:172:34
MUS MUSCULUS (MOUSE).
P11087

HRIFA001099a
55 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-5 (FRAGMENT).
0.92:38:34
HOMO SAPIENS (HUMAN).
P18849

- 5 HRIFA001132a
AGRIN PRECURSOR.
1.3e-26:239:32
GALLUS GALLUS (CHICKEN).
P31696
- 10 HRIFA001138a
CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).
5.9e-114:147:83
HOMO SAPIENS (HUMAN).
P49747
- 15 HRIFA001200a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.035:119:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 20 HRIFA001337a
LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR).
2.4e-17:98:42
CRICETULUS GRISEUS (CHINESE HAMSTER).
P35950
- 25 HRIFA001341a
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L)
(NF68).
1.2e-102:248:87
RATTUS NORVEGICUS (RAT).
30 P19527
- 35 HRIFA001413a
BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
0.0032:33:63
BOS TAURUS (BOVINE).
P19661
- 40 HRIFA001439a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
0.00031:34:61
HOMO SAPIENS (HUMAN).
P20931
- 45 HRIFA001489a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
8.4e-65:105:72
HOMO SAPIENS (HUMAN).
P35414
- 50 HRIFA001558a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
0.0048:80:31
PLASMODIUM LOPHURAE.
P04929
- 55 HRIFA001712a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.5e-19:169:31

THERMOMONOSPORA CURVATA.
P49695

- 5 HRIFA001720a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.4e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923
- 10 HRIFA001866a
EARLY ANTIGEN PROTEIN D (EA-D).
0.10:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191
- 15 HRIFA001942a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1)."
4.7e-12:140:30
20 GALLUS GALLUS (CHICKEN).
P24802
- 25 HRIFA001971a
HYPOTHETICAL 46.3 KD PROTEIN IN PTA1-CDC24 INTERGENIC REGION.
2.5e-10:86:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39727
- 30 HRIFA001972a
LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.10:100:34
MUS MUSCULUS (MOUSE).
P19137
- 35 HRIFA001975a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
6.5e-30:243:33
MUS MUSCULUS (MOUSE).
P21836
- 40 HRIFA001984a
"PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1)."
1.2e-11:140:30
45 GALLUS GALLUS (CHICKEN).
P24802
- 50 HRIFA002063a
GNS1 PROTEIN.
1.3e-05:127:30
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P25358
- 55 HRIFA002102a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
2.9e-07:241:30
HOMO SAPIENS (HUMAN).
Q02817

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- 5 HRIFA002284a
ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
3.8e-05:104:34
RATTUS NORVEGICUS (RAT).
P04474
- 10 HRIFA002309a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
1.5e-08:110:37
THERMOMONOSPORA CURVATA.
P49695
- 15 HRIFA002384a
GAP JUNCTION ALPHA-6 PROTEIN (CONNEXIN 45) (CX45).
1.8e-31:94:42
HOMO SAPIENS (HUMAN).
P36383
- 20 HRIFA002503a
N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-
TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-
FERASE) (GT).
6.1e-92:246:67
MUS MUSCULUS (MOUSE).
25 P15535
- 30 HRIFA002689a
TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6) (DNA BINDING PROTEIN GATA-GT2).
0.38:49:34
RATTUS NORVEGICUS (RAT).
P46153
- 35 HRIFA002694a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.7e-05:93:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602
- 40 HRIFA002743a
BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).
1.2e-23:216:31
HOMO SAPIENS (HUMAN).
P13497
- 45 HRIFA002762a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.1e-09:129:41
MUS MUSCULUS (MOUSE).
P05142
- 50 HRIFA002766a
FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).
1.8e-12:139:34
HOMO SAPIENS (HUMAN).
55 Q06828
- HRIFA002787a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

- 1.6e-10:124:37
HOMO SAPIENS (HUMAN).
P08123
- 5 HRIFA002805a
ZINC FINGER PROTEIN 140.
3.6e-23:43:74
HOMO SAPIENS (HUMAN).
P52738
- 10 HRIFA002891a
"FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)."
2.0e-41:239:39
MUS MUSCULUS (MOUSE).
15 Q08878
- HRIFA002919a
BEM46 PROTEIN (FRAGMENT).
1.0e-12:171:32
20 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069
- HRIFA002980a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
25 ROGLOBULIN RECEPTOR) (A2MR).
8.7e-32:202:37
GALLUS GALLUS (CHICKEN).
P98157
- 30 HRIFA003055a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.4e-08:175:29
MUS MUSCULUS (MOUSE).
P05142
- 35 HRIFA003063a
B-CELL LYMPHOMA 6 PROTEIN HOMOLOG.
2.8e-15:123:34
MUS MUSCULUS (MOUSE).
40 P41183
- HRIFA003093a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-11:142:37
45 MUS MUSCULUS (MOUSE).
P05142
- HRIFA003340a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
50 PHA-0 PROTEIN).
2.3e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 55 HRIFA003357a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
0.0023:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

- P14922
- HRIFA003402a
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
5 3.6e-05:194:27
BOS TAURUS (BOVINE).
P02459
- HRIFA003504a
10 CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
1.4e-08:150:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450
- HRIFA003592a
15 CD9 ANTIGEN.
0.0053:24:70
BOS TAURUS (BOVINE).
P30932
- HRIFA003635a
20 "MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE)."
5.3e-45:239:43
25 DROSOPHILA MELANOGASTER (FRUIT FLY).
P53624
- HRIFA003640a
30 PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
0.00018:28:64
TRYPANOSOMA BRUCEI BRUCEI.
P09791
- HRIFA003883a
35 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (YIN AND YANG 1) (YY-1) (DELTA TRANSCRIPTION FACTOR) (NF-E1) (UCR-MOTIF DNA-BINDING PROTEIN).
1.0:57:35
MUS MUSCULUS (MOUSE).
Q00899
- HRIFA003892a
40 MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
6.5e-08:144:25
BACILLUS SUBTILIS.
45 P39843
- HRIFA003946a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.4e-06:85:37
50 MUS MUSCULUS (MOUSE).
P05142
- HRIFA004006a
55 ZINC FINGER PROTEIN 140.
6.2e-20:83:66
HOMO SAPIENS (HUMAN).
P52738

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- 5 HRIFA004034a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
1.4e-15:192:32
HOMO SAPIENS (HUMAN).
P20749
- 10 HRIFA004112a
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).
7.2e-26:193:37
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450
- 15 HRIFA004162a
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
3.6e-10:117:29
MUS MUSCULUS (MOUSE).
P54116
- 20 HRIFA004401a
LACTOSE OPERON REPRESSOR.
1.1e-07:36:86
ESCHERICHIA COLI.
P03023
- 25 HRIFA004426a
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
5.1e-11:85:41
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P15287
- 30 HRIFA004490a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-19:101:44
MUS MUSCULUS (MOUSE).
35 P23780
- 40 HRIFA004523a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
2.6e-36:180:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 45 HRIFA004663a
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
1.2e-40:112:75
MUS MUSCULUS (MOUSE).
Q00417
- 50 HRIFA004696a
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.1e-62:145:84
CANIS FAMILIARIS (DOG).
P38377
- 55 HRIFA004714a
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
2.3e-50:127:54
CAENORHABDITIS ELEGANS.

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Q09201

- 5 HRIFA004745a
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
5.0e-17:107:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 10 HRIFA004780a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
7.2e-07:142:30
ZEA MAYS (MAIZE).
P14918
- 15 HRIFA004919a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
1.5e-25:156:46
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
P10496
- 20 HRIFA005072a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
8.3e-05:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
25 Q01157
- 30 HRIFA005102a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:188:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 35 HRIFA005184a
CYTOCHROME B5.
3.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 40 HRIFA005214a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
5.9e-05:141:33
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- 45 HRIFA005231a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 50 HRIFA005240a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6.3e-81:194:70
HOMO SAPIENS (HUMAN).
55 Q03923
- HRIFA005255a
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.

- 1.5e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176
- 5 HRIFA005271a
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.2e-55:86:81
HOMO SAPIENS (HUMAN).
Q00325
- 10 HRIFA005296a
INSULIN PROMOTER FACTOR 1 (IPF-1) (ISLET/DUODENUM HOMEODOMAIN-1) (IDX-1) (SOMATOSTATIN
TRANSACTIVATING FACTOR-1) (STF-1) (PANCREAS/DUODENUM HOMEODOMAIN-1) (GLUCOSE SENSITIVE
FACTOR) (GSF).
15 0.82:90:34
HOMO SAPIENS (HUMAN).
P52945
- 20 HRIFA005300a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-07:178:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 25 HRIFA005369a
EBNA-1 NUCLEAR PROTEIN.
2.3e-07:101:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 30 HRIFA005372a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DNA BINDING PROTEIN SUBUNIT B).
1.1e-14:97:38
35 PETROMYZON MARINUS (SEA LAMPREY).
P25210
- 40 HRIFA005392a
SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN)
(HSPG) (SYND2).
1.3e-50:126:84
HOMO SAPIENS (HUMAN).
P34741
- 45 HRIFA005409a
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).
7.1e-66:197:64
50 HOMO SAPIENS (HUMAN).
P30825
- 55 HRIFA005420a
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.5e-33:221:41
MUS MUSCULUS (MOUSE).
P19182

- HRIFA005438a
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)
(FLAVOPROTEIN SUBUNIT OF COMPLEX II).
6.4e-71:175:68
5 HOMO SAPIENS (HUMAN).
P31040
- HRIFA005462a
10 CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.4e-19:137:37
OVIS ARIES (SHEEP).
P08060
- HRIFA005500a
15 EBNA-1 NUCLEAR PROTEIN.
0.00042:54:50
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- HRIFA005540a
20 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.12:47:29
HOMO SAPIENS (HUMAN).
P18850
- HRIFA005644a
25 VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
1.2e-102:233:87
BOS TAURUS (BOVINE).
30 P40682
- HRIFA005702a
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA-ASSOCIATED ANTIGEN MUC18)
35 (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 AN-
TIGEN) (MELANOMA ADHESION MOLECULE).
8.7e-05:174:28
HOMO SAPIENS (HUMAN).
P43121
- HRIFA005720a
40 F-SPONDIN PRECURSOR.
8.9e-12:155:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447
- HRIFA005728a
45 SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.7e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
50 P08458
- HRIFA005732a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
4.4e-26:159:38
55 THERMOMONOSPORA CURVATA.
P49695
- HRIFA005760a

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- FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOS-
YLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).
3.8e-15:53:54
5 HOMO SAPIENS (HUMAN).
P16442
- HRIFA005781a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
10 DROXYSTEROID DEHYDROGENASE).
5.2e-47:228:47
HOMO SAPIENS (HUMAN).
P37058
- HRIFA005944a
PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].
2.5e-06:142:35
15 MUS MUSCULUS (MOUSE).
P28481
- HRIFA006183a
ZINC FINGER PROTEIN 136.
1.3e-42:129:62
20 HOMO SAPIENS (HUMAN).
P52737
- HRIFA006250a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0038:75:37
30 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439
- HRIFA006298a
EBNA-1 NUCLEAR PROTEIN.
35 1.4e-05:80:42
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- HRIFA006448a
40 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.5e-05:183:28
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA006494a
45 AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).
1.2e-18:201:33
HOMO SAPIENS (HUMAN).
Q02246
- HRIFA006510a
50 CORNICHON PROTEIN.
6.0e-53:144:66
DROSOPHILA MELANOGASTER (FRUIT FLY).
P49858
- HRIFA006566a
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-

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- BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).
P25210
- 5
HRIFA006572a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
7.2e-05:158:29
MUS MUSCULUS (MOUSE).
10 P11087
- HRIFA006586a
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.3e-13:219:26
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981
- HRIFA006596a
20 POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
7.2e-22:241:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071
- 25 HRIFA006609a
PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
0.61:28:46
"GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY)."
P01306
30
- HRIFA006633a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
7.8e-07:170:34
HOMO SAPIENS (HUMAN).
35 Q07092
- HRIFA006642a
AMALGAM PROTEIN PRECURSOR.
1.5e-09:185:28
40 DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364
- HRIFA006649a
45 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.7e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923
- HRIFA006667a
50 ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
6.8e-45:180:43
HOMO SAPIENS (HUMAN).
Q03923
- 55 HRIFA006730a
SYG1 PROTEIN.
1.8e-14:164:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40528

HRIFA006798a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.22:149:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA006926a
SYNAPTOTAGMIN IV.
3.6e-19:168:38
RATTUS NORVEGICUS (RAT).
P50232

HRIFA007013a
MIC1 PROTEIN.
1.4e-13:115:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53258

HRIFA007032a
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.00013:92:35
CANIS FAMILIARIS (DOG).
P39881

HRIFA007068a
EBNA-1 NUCLEAR PROTEIN.
7.0e-10:145:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

HRIFA007152a
TRANSCRIPTION FACTOR SOX-4.
0.90:47:44
HOMO SAPIENS (HUMAN).
Q06945

HRIFA007219a
THROMBOSPONDIN 3 PRECURSOR.
1.3e-105:209:88
HOMO SAPIENS (HUMAN).
P49746

HRIFA007228a
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
2.3e-11:174:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

HRIFA007243a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
3.0e-18:163:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

HRIFA007244a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

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- 4.2e-05:81:33
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 5 HRIFA007256a
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
2.3e-77:186:75
HOMO SAPIENS (HUMAN).
P53355
- 10 HRIFA007262a
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.3e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579
- 15 HRIFA007352a
5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).
4.2e-36:146:57
HOMO SAPIENS (HUMAN).
Q15583
- 20 HRIFA007424a
F-SPONDIN PRECURSOR.
8.9e-34:84:89
RATTUS NORVEGICUS (RAT).
P35446
- 25 HRIFA007435a
PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.0e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938
- 30 HRIFA007463a
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
4.8e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53685
- 35 HRIFA007493a
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN
CARRIER PROTEIN).
1.2e-47:171:56
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33296
- 40 HRIFA007512a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
8.0e-07:173:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 45 HRIFA007532a
"CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEIN-
ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE
SUBUNIT)."
1.8e-10:110:37
- 50
- 55

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HOMO SAPIENS (HUMAN).
P20807

5 HRIFA007547a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.068:51:45
BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).
P29836

10 HRIFA007565a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.1e-08:121:37
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA007571a
ORM1 PROTEIN.
5.8e-17:106:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
20 P53224

HRIFA007659a
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
2.5e-47:213:41
25 CAENORHABDITIS ELEGANS.
P49191

HRIFA007722a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
30 7.7e-13:146:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857

HRIFA007728a
35 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
9.1e-05:124:31
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

40 HRIFA007745a
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).
7.0e-15:109:36
TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).
P04058

45 HRIFA007829a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00045:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
50 Q01157

HRIFA007909a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
6.1e-06:173:34
55 BOS TAURUS (BOVINE).
P02453

HRIFA007985a

- 5 T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
0.00079:97:37
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 10 HRIFA008000a
"DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR."
1.6e-37:165:42
ORYCTOLAGUS CUNICULUS (RABBIT).
P13806
- 15 HRIFA008174a
COLLAGEN 1(X) CHAIN PRECURSOR.
4.5e-05:215:28
BOS TAURUS (BOVINE).
P23206
- 20 HRIFA008186a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
DROXYSTEROID DEHYDROGENASE).
2.1e-25:118:46
HOMO SAPIENS (HUMAN).
P37058
- 25 HRIFA008200a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
7.9e-17:139:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
30 P32802
- 35 HRIFA008212a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.035:135:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 40 HRIFA008252a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
0.00015:128:32
MUS MUSCULUS (MOUSE).
P05142
- 45 HRIFA008284a
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
3.9e-18:153:30
HOMO SAPIENS (HUMAN).
P32004
- 50 HRIFA008314a
HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.
2.1e-18:99:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38800
- 55 HRIFA008362a
PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLE-
STEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).

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- 9.1e-42:135:57
GALLUS GALLUS (CHICKEN).
P53760
- 5 HRIFA008426a
HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).
1.3e-08:104:45
GALLUS GALLUS (CHICKEN).
Q90655
- 10 HRIFA008459a
CARBON CATABOLITE DEREPRESSING PROTEIN KINASE (EC 2.7.1.-).
5.5e-15:96:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P06782
- 15 HRIFA008483a
PROBABLE LONG-CHAIN FATTY ACID TRANSPORT PROTEIN.
7.4e-26:154:41
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38225
- HRIFA008547a
ZINC FINGER PROTEIN 136.
25 7.2e-57:228:50
HOMO SAPIENS (HUMAN).
P52737
- HRIFA008596a
30 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.6e-05:97:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 35 HRIFA008611a
NPL1 PROTEIN (SEC63 PROTEIN).
8.1e-15:113:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14906
- 40 HRIFA008661a
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
2.7e-16:184:29
ESCHERICHIA COLI.
45 P37021
- HRIFA008717a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
6.9e-32:198:41
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692
- HRIFA008784a
HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.
55 2.2e-16:93:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38869

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- HRIFA008790a
HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.
4.2e-08:121:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
5 P47111
- HRIFA008976a
ACROSIN PRECURSOR (EC 3.4.21.10).
0.31:20:70
10 HOMO SAPIENS (HUMAN).
P10323
- HRIFA008981a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
15 1.0e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923
- HRIFA008989a
20 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
1.2e-05:134:33
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
25
- HRIFA009071 a
CELLULAR TUMOR ANTIGEN P53 (PHOSPHOPROTEIN P53).
0.14:104:31
HOMO SAPIENS (HUMAN).
30 P04637
- HRIFA009101a
ZINC FINGER PROTEIN 136.
6.5e-47:126:67
35 HOMO SAPIENS (HUMAN).
P52737
- HRIFA009123a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
40 0.010:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA009136a
45 REGULATORY PROTEIN E2.
0.032:100:37
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787
- HRIFA009171a
50 BUTYROPHILIN PRECURSOR (BT).
1.6e-15:168:31
BOS TAURUS (BOVINE).
P18892
55
- HRIFA009220a
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.2e-48:268:41

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09895

- 5 HRIFA009339a
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
0.63:57:35
MUS MUSCULUS (MOUSE).
Q01149
- 10 HRIFA009451a
METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA)
(TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLA-
GENASE INHIBITOR).
1.7e-57:163:73
15 HOMO SAPIENS (HUMAN).
P01033
- 20 HRIFA009482a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
7.7e-25:86:59
MUS MUSCULUS (MOUSE).
P23780
- 25 HRIFA009578a
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
8.8e-10:199:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857
- 30 HRIFA009762a
CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).
0.17:116:32
RATTUS NORVEGICUS (RAT).
P53565
- 35 HRIFA009783a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
6.2e-48:231:48
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
40 Q09782
- 45 HRIFA009825a
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
4.0e-06:70:38
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602
- 50 HRIFA009852a
"NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM
140]."
4.0e-07:198:27
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P16170
- 55 HRIFA009881a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.5e-11:106:35
SORGHUM VULGARE (SORGHUM).

P24152

HRIFA009983a

G-BOX BINDING FACTOR (GBF).

5 3.8e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

HRIFA010005a

10 "M PROTEIN, SEROTYPE 49 PRECURSOR."

1.6e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

15 HRIFA010078a

HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.

4.7e-05:194:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53214

20

HRIFA010085a

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

2.9e-92:243:69

HOMO SAPIENS (HUMAN).

25

Q03923

HRIFA010090a

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

30

6.7e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

HRIFA010130a

35

DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).

5.6e-13:99:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P46971

40 HRIFA010152a

"ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLYL CYCLASE)."

2.3e-05:73:43

CANIS FAMILIARIS (DOG).

45

P30803

HRIFA010176a

HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).

0.066:105:31

50

MUS MUSCULUS (MOUSE).

P35583

HRIFA010301a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

55

1.1e-09:120:34

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

EP 1 130 094 A2

- HRIFA010319a
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
4.8e-23:185:32
5 RATTUS NORVEGICUS (RAT).
Q05754
- HRIFA010361a
10 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.6e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA010394a
15 HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
3.3e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- HRIFA010425a
20 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-09:199:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- HRIFA010460a
25 TRANSCRIPTIONAL ACTIVATOR FE65.
2.3e-27:101:54
RATTUS NORVEGICUS (RAT).
30 P46933
- HRIFA010466a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
5.3e-07:123:34
35 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- HRIFA010490a
40 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
0.0031:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
- HRIFA010736a
45 PROTEIN Q300.
0.018:14:85
MUS MUSCULUS (MOUSE).
Q02722
- HRIFA010790a
50 RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-
PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-
NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
1.6e-82:197:72
55 HOMO SAPIENS (HUMAN).
Q06495
- HRIFA010799a

- PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.7e-05:220:30
GALLUS GALLUS (CHICKEN).
P02457
- 5
- HRIFA010859a
ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOCEPTOR) (SUBTYPE C4).
0.063:134:33
HOMO SAPIENS (HUMAN).
P18825
- 10
- HRIFA010891a
HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.
0.044:28:64
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015
- 15
- HRIFA010975a
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
8.5e-113:144:86
HOMO SAPIENS (HUMAN).
P43405
- 20
- HRIFA010988a
GASTRIN PRECURSOR.
0.084:59:37
HOMO SAPIENS (HUMAN).
P01350
- 25
- HRIFA011016a
PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PRO-
TEIN 2) (CABP2).
3.1e-15:127:37
RATTUS NORVEGICUS (RAT).
P38659
- 30
- HRIFA011105a
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.97:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841
- 35
- HRIFA011128a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0046:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 40
- HRIFA011179a
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).
1.1e-20:127:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244
- 45
- HRIFA011197a
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
5.8e-26:169:40
MUS MUSCULUS (MOUSE).
- 50
- 55

P28843

HRIFA011449a

GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).

1.9e-26:109:53

MUS MUSCULUS (MOUSE).

P24788

HRIFA011484a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.00055:115:33

HOMO SAPIENS (HUMAN).

P21917

HRIFA011512a

POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).

0.00024:139:25

HOMO SAPIENS (HUMAN).

P51531

HRIFA011580a

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI) PHOSVITIN (PV) LIPOVITELLIN II (LVII) YGP40].

4.0e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

HRIFA011659a

VON WILLEBRAND FACTOR PRECURSOR.

9.8e-17:210:25

HOMO SAPIENS (HUMAN).

P04275

HRIFA011820a

ZINC FINGER PROTEIN 136.

1.9e-10:42:73

HOMO SAPIENS (HUMAN).

P52737

HRIFA011926a

TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).

1.0:149:22

PSEUDOMONAS AERUGINOSA.

P15276

HRIFA011947a

ZINC FINGER PROTEIN 136.

1.3e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

HRIFA012069a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.0027:205:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA012151a

EP 1 130 094 A2

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
0.00028:72:37
RATTUS NORVEGICUS (RAT).
Q07008

5

HRIFA012167a
HYPOTHETICAL SYMPORTER IN GLTS-SELC INTERGENIC REGION.
6.4e-09:145:28
ESCHERICHIA COLI.
P31435

10

HRIFA012278a
ZINC FINGER PROTEIN 140.
3.1e-14:88:52
HOMO SAPIENS (HUMAN).
P52738

15

HRIFA012354a
"SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT."
2.1e-05:120:32
RATTUS NORVEGICUS (RAT).
P04775

20

HRIFA012427a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.3e-08:250:28
MUS MUSCULUS (MOUSE).
P11087

25

HRIFA012436a
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
4.7e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941

30

HRIFA012515a
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
3.5e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

35

HRIFA012584a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
4.9e-14:136:29
NEUROSPORA CRASSA.
P23231

40

HRIFA012625a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
9.6e-12:103:40
RATTUS NORVEGICUS (RAT).
P13386

45

HRIFA012692a

50

55

- BLOOM'S SYNDROME PROTEIN.
6.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132
- 5
HRIFA012702a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.9e-07:153:30
ZEA MAYS (MAIZE).
10 P14918
- HRIFA012737a
LEUCOCYTE ANTIGEN CD97 PRECURSOR.
1.6e-09:170:24
15 HOMO SAPIENS (HUMAN).
P48960
- HRIFA012795a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
20 3.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387
- HRIFA012885a
25 HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
2.9e-21:159:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032
- HRIFA012914a
30 ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70
TRANSMEMBRANE PROTEIN P20E].
3.4e-29:134:47
BABOON ENDOGENOUS VIRUS (STRAIN M7).
35 P10269
- HRIFA012969a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
40 1.2e-30:228:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- HRIFA012990a
45 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
7.4e-20:181:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- HRIFA013092a
50 OUTER MEMBRANE PROTEIN H.8 PRECURSOR.
0.0039:51:39
NEISSERIA GONORRHOEAE.
P11910
- 55
HRIFA013103a
N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-
TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-

- FERASE) (GT).
0.25:50:34
MUS MUSCULUS (MOUSE).
P15535
- 5
- HRIFA013135a
CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).
1.6e-05:214:28
CLOSTRIDIUM THERMOCELLUM.
Q06852
- 10
- HRIFA013235a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
1.9e-05:113:40
HOMO SAPIENS (HUMAN).
P02461
- 15
- HRIFA013254a
COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].
3.8e-13:123:41
MUS MUSCULUS (MOUSE).
P01029
- 20
- HRIFA013265a
CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).
7.0e-107:225:86
HOMO SAPIENS (HUMAN).
P07711
- 25
- HRIFA013276a
5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
2.2e-117:270:85
HOMO SAPIENS (HUMAN).
P21589
- 30
- HRIFA013279a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
4.9e-05:127:37
PLASMODIUM VIVAX.
P08677
- 35
- HRIFA013376a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).
8.0e-23:230:31
NEUROSPORA CRASSA.
P23231
- 40
- HRIFA013477a
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
5.8e-87:197:87
HOMO SAPIENS (HUMAN).
P41217
- 45
- HRIFA013586a
ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBI-
TOR) (MA-DBI).
- 50
- 55

- 3.8e-31:93:64
BOS TAURUS (BOVINE).
P07106
- 5 HRIFA013589a
T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).
5.0e-06:95:35
HOMO SAPIENS (HUMAN).
P40200
- 10 HRIFA013620a
"HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT)."
7.1e-08:95:37
- 15 MUS MUSCULUS (MOUSE).
P20490
- HRIFA013726a
SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
20 1.5e-33:99:50
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03497
- HRIFA013744a
25 ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).
7.5e-15:105:38
BOS TAURUS (BOVINE).
P07106
- 30 HRIFA013911a
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
7.8e-37:104:46
HOMO SAPIENS (HUMAN).
35 P43251
- HRIFA013919a
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
1.2e-10:170:32
40 HOMO SAPIENS (HUMAN).
Q02817
- HRIFA013932a
45 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
2.6e-05:168:34
HOMO SAPIENS (HUMAN).
P04280
- 50 HRIFA013980a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
0.00036:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
55 P18480
- HRIFA014006a
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).

EP 1 130 094 A2

- 9.4e-16:185:28
MUS MUSCULUS (MOUSE).
P20937
- 5 HRIFA014024a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0013:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 10 HRIFA014056a
PROTEIN Q300.
5.1e-05:24:70
MUS MUSCULUS (MOUSE).
15 Q02722
- HRIFA014111a
TOLL PROTEIN PRECURSOR.
5.5e-08:203:27
20 DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953
- HRIFA014133a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
25 1.6e-06:143:33
MUS MUSCULUS (MOUSE).
P05142
- HRIFA014185a
30 LEUCOCYTE ANTIGEN CD97 PRECURSOR.
6.0e-14:192:30
HOMO SAPIENS (HUMAN).
P48960
- 35 HRIFA014336a
"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (FRAGMENT)."
2.8e-70:198:58
SUS SCROFA (PIG).
P20305
- 40 HRIFA014396a
CREB-BINDING PROTEIN.
2.6e-07:101:34
MUS MUSCULUS (MOUSE).
45 P45481
- HRIFA014397a
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
5.2e-05:147:30
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655
- HRIFA014465a
55 HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
2.8e-11:166:30
CAENORHABDITIS ELEGANS.
P30638

- 5 HRIFA014500a
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
1.0e-14:149:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862
- 10 HRIFA014561a
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
4.1e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 HRIFA014568a
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
2.4e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 HRIFA014590a
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.18:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 HRIFA014598a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
4.9e-05:124:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 30 HRIFA014620a
ENL PROTEIN.
0.58:170:30
HOMO SAPIENS (HUMAN).
35 Q03111
- 40 HRIFA014621a
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
2.7e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 45 HRIFA014688a
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
6.9e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 50 HRIFA014702a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.4e-05:89:40
MUS MUSCULUS (MOUSE).
P05142
- 55 HRIFA014819a
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
7.8e-26:117:46
HOMO SAPIENS (HUMAN).

P55083

5 HRIFA014868a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
8.9e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

10 HRIFA014951a
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
4.1e-23:132:39
EQUUS CABALLUS (HORSE).
P80010

15 HRIFA014967a
CHLORINE CHANNEL PROTEIN P64.
2.0e-52:142:76
BOS TAURUS (BOVINE).
P35526

20 HRIFA015063a
ZINC FINGER PROTEIN 136.
6.6e-53:229:48
HOMO SAPIENS (HUMAN).
25 P52737

HRIFA015070a
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
9.3e-24:143:41
30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

HRIFA015122a
REGULATORY PROTEIN E2.
35 0.45:129:30
HUMAN PAPILLOMAVIRUS TYPE 5.
P06921

40 HRIFA015219a
FIBRILLIN 1 PRECURSOR (MP340).
9.9e-09:132:32
BOS TAURUS (BOVINE).
P98133

45 HRIFA015246a
PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
2.4e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888

50 HRIFA015351a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.0021:122:30
RATTUS NORVEGICUS (RAT).
55 P03994

HRIFA015423a
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).

- 1.2e-11:148:35
HOMO SAPIENS (HUMAN).
P20749
- 5 HRIFA015453a
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
6.8e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 10 HRIFA015486a
BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING
PROTEIN) (APC INHIBITOR).
2.0e-22:208:27
15 MUS MUSCULUS (MOUSE).
Q01339
- HRIFA015506a
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
20 1.3e-12:73:50
HOMO SAPIENS (HUMAN).
P23508
- HRIFA015536a
25 CHLORINE CHANNEL PROTEIN P64.
1.2e-49:115:79
BOS TAURUS (BOVINE).
P35526
- HRIFA015547a
30 BEM46 PROTEIN (FRAGMENT).
1.4e-33:137:49
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069
- 35 HRIFA015568a
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
2.4e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
40 Q09875
- HRIFA015756a
EBNA-2 NUCLEAR PROTEIN.
2.9e-15:28:75
45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978
- HRIFA015802a
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
50 0.0035:122:30
RATTUS NORVEGICUS (RAT).
P03994
- HRIFA015811a
55 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
6.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

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- 5 HRIFA015902a
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
0.0075:161:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 10 HRIFA015947a
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.035:98:28
MUS MUSCULUS (MOUSE).
P10925
- 15 HRIFA015995a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.
6.2e-08:221:37
HOMO SAPIENS (HUMAN).
P02461
- 20 HRIFA016070a
"COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR."
1.0e-18:179:35
HOMO SAPIENS (HUMAN).
P02745
- 25 HRIFA016214a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.0e-05:96:42
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA016240a
HYPOTHETICAL 65.3 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION.
8.5e-05:103:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
35 P47082
- 40 HRIFA016255a
EBNA-1 NUCLEAR PROTEIN.
4.5e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 45 HRIFA016290a
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
6.7e-21:182:41
HOMO SAPIENS (HUMAN).
P12259
- 50 HRIFA016430a
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
7.1e-50:120:86
HOMO SAPIENS (HUMAN).
P24390
- 55 HRIFA016599a
MEIOTIC RECOMBINATION PROTEIN REC104.
0.57:73:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P33323

HRIFA016639a

"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."

8.0e-06:206:23

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08640

HRIFA016654a

HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).

1.1e-78:181:86

ORYCTOLAGUS CUNICULUS (RABBIT).

P33279

HRIFA016669a

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

1.4e-08:87:36

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

HRIFA016758a

GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).

9.5e-17:158:40

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P43636

HRIFA016963a

FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.

6.2e-08:131:32

LYMNAEA STAGNALIS (GREAT POND SNAIL).

P42565

HRIFA017031a

MYOSIN HEAVY CHAIN KINASE A (EC 2.7.1.129) (MHCK A).

2.6e-11:152:34

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P42527

HRIFA017146a

D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).

0.0014:78:37

HOMO SAPIENS (HUMAN).

P21917

HRIFA017190a

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0026:89:30

HOMO SAPIENS (HUMAN).

Q01543

HRIFA017257a

"GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL)."

2.5e-79:261:57

HOMO SAPIENS (HUMAN).

P06396

HRIFA017295a

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"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."
3.4e-20:66:78
5 HOMO SAPIENS (HUMAN).
Q10469

HRIFA017312a
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
10 2.7e-19:221:33
HOMO SAPIENS (HUMAN).
P04003

HRIFA017456a
15 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN).
0.11:94:35
MUS MUSCULUS (MOUSE).
P19137

HRIFA017457a
20 SYNAPTOTAGMIN II.
7.2e-07:98:35
MUS MUSCULUS (MOUSE).
P46097

HRIFA017643a
25 NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
2.2e-07:81:41
HOMO SAPIENS (HUMAN).
30 P48745

HRIFA017670a
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
4.9e-06:172:27
35 RATTUS NORVEGICUS (RAT).
P19814

HRIFA017703a
40 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
1.9e-16:129:34
THERMOMONOSPORA CURVATA.
P49695

HRIFA017791a
45 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.012:71:38
HOMO SAPIENS (HUMAN).
Q02817

HRIFA017801a
50 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-07:86:39
MUS MUSCULUS (MOUSE).
P05142

HRIFA017818a
55 ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN).
1.0:32:40

STREPTOMYCES LIVIDANS.
P50014

5 HRIFA017836a
"TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H))."
1.3e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

10 HRIFA017855a
ORM1 PROTEIN.
1.7e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

15 HRIFA017921a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
2.0e-09:182:35
20 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393

HRIFA018092a
25 "DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT)."
2.1e-20:119:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898

30 HRIFA018131a
ORM1 PROTEIN.
2.6e-20:137:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224

35 HRIFA018134a
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.1e-11:147:32
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
40 Q05609

HRIFA018238a
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (MOTCH PROTEIN).
8.6e-06:74:44
45 MUS MUSCULUS (MOUSE).
Q01705

HRIFA018262a
50 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
6.4e-10:71:38
THERMOMONOSPORA CURVATA.
P49695

HRIFA018287a
55 HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
1.5e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53214

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- 5 HRIFA018447a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00065:133:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 10 HRIFA018580a
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020
- 15 HRIFA018666a
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE
PHOSPHOHYDROLASE).
1.7e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P16621
- 20 HRIFA018688a
PHLB PROTEIN PRECURSOR.
1.9e-06:110:35
SERRATIA LIQUEFACIENS.
P18954
- 25 HRIFA018754a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE)."
1.8e-06:195:27
30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 35 HRIFA018794a
MSP1 PROTEIN HOMOLOG.
3.2e-06:93:25
CAENORHABDITIS ELEGANS.
P54815
- 40 HRIFA018827a
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.1e-17:180:28
CAENORHABDITIS ELEGANS.
P30638
- 45 HRIFA018870a
HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.
4.7e-09:70:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47088
- 50 HRIFA018904a
MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KI-
NASE) (DMK) (DMPK) (MT-PK).
5.5e-12:142:32
55 HOMO SAPIENS (HUMAN).
Q09013
- HRIFA018931a

- ZINC FINGER PROTEIN 140.
2.9e-10:47:74
HOMO SAPIENS (HUMAN).
P52738
- 5
HRIFA018993a
HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.2e-13:117:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
10 P53073
- HRIFA019105a
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
7.5e-22:203:32
15 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25723
- HRIFA019136a
"MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (PROTEIN KINASE C SUBSTRATE,
20 80 KD PROTEIN, LIGHT CHAIN) (PKCSL) (80K-L PROTEIN)."
1.0e-25:74:81
HOMO SAPIENS (HUMAN).
P29966
- 25 HRIFA019175a
PROTEIN KINASE WIS1 (EC 2.7.1.-).
1.3e-14:84:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P33886
- 30 HRIFA019262a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.5e-55:188:50
HOMO SAPIENS (HUMAN).
35 Q03923
- HRIFA019412a
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.4e-09:121:33
40 CAVIA PORCELLUS (GUINEA PIG).
P25796
- HRIFA019437a
REGULATORY PROTEIN E2.
45 0.26:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783
- HRIFA019466a
50 EBNA-1 NUCLEAR PROTEIN.
2.7e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 55 HRIFA019490a
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TYE4).
1.1e-09:132:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480

5 HRIFA019498a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAL (SHAL2).
5.6e-05:87:36
DROSOPHILA MELANOGASTER (FRUIT FLY).
P17971

10 HRIFA019532a
EBNA-1 NUCLEAR PROTEIN.
1.8e-05:67:49
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

15 HRIFA019651a
ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).
6.1e-05:31:64
PLASMODIUM CHABAUDI.
20 Q02752

HRIFA019867a
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
25 8.2e-34:103:71
RATTUS NORVEGICUS (RAT).
Q06496

30 HRIFA019869a
SERINE/THREONINE-PROTEIN KINASE FUSED (EC 2.7.1.-).
7.2e-29:83:49
DROSOPHILA MELANOGASTER (FRUIT FLY).
P23647

35 HRIFA019958a
REPRESSOR PROTEIN CI (FRAGMENT).
0.99:45:37
BACTERIOPHAGE 434.
40 P16117

HRIFA020144a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-06:176:30
45 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

HRIFA020184a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
50 1.9e-10:102:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

HRIFA020272a
55 MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
5.5e-91:211:85
HOMO SAPIENS (HUMAN).
P20309

- 5 HRIFA020335a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
5.0e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 10 HRIFA020349a
BRITTLE-1 PROTEIN PRECURSOR.
6.0e-30:214:35
ZEA MAYS (MAIZE).
P29518
- 15 HRIFA020453a
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
2.5e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20 HRIFA020693a
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).
3.9e-09:96:35
HOMO SAPIENS (HUMAN).
P43146
- 25 HRIFA020707a
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-
SA-1).
3.4e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
30 Q06084
- 35 HRIFA020748a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
3.2e-09:210:28
NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- 40 HRIFA020862a
MODIFIER 3 PROTEIN (M33).
5.6e-26:76:61
MUS MUSCULUS (MOUSE).
P30658
- 45 HRIFA020883a
PROTEIN Q300.
0.00054:21:66
MUS MUSCULUS (MOUSE).
Q02722
- 50 HRIFA021007a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
0.092:73:36
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
55 P08393
- HRIFA021040a
TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).

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0.98:63:39
HOMO SAPIENS (HUMAN).
P43694

5 HRIFA021061a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.8e-09:162:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

10 HRIFA021213a
OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.
2.0e-38:96:72
CAENORHABDITIS ELEGANS.
15 P46975

HRIFA021224a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
2.8e-06:55:52
20 RATTUS NORVEGICUS (RAT).
Q02975

HRIFA021398a
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
25 2.5e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139

HRIFA021445a
30 PRE-B-CELL LEUKEMIA TRANSCRIPTION FACTOR-1 (HOMEBOX PROTEIN PBX1) (HOMEBOX PROTEIN PRL).
0.38:146:31
HOMO SAPIENS (HUMAN).
P40424

35 HRIFA021494a
EBNA-1 NUCLEAR PROTEIN.
6.8e-07:116:41
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
40 P03211

HRIFA021499a
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.1e-34:159:50
45 GALLUS GALLUS (CHICKEN).
P05099

HRIFA021543a
ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).
50 0.0087:50:40
GALLUS GALLUS (CHICKEN).
Q03352

HRIFA021620a
55 PLATELET FACTOR 4 (PF-4).
0.019:65:27
SUS SCROFA (PIG).
P30034

- 5 HRIFA021637a
 CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
 6.0e-37:147:53
 GALLUS GALLUS (CHICKEN).
 P05099
- 10 HRIFA021651a
 CARG-BINDING FACTOR-A (CBF-A).
 2.6e-11:170:30
 MUS MUSCULUS (MOUSE).
 Q99020
- 15 HRIFA021754a
 CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
 1.2e-37:137:51
 GALLUS GALLUS (CHICKEN).
 P05099
- 20 HRIFA021781a
 DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COM-
 PLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).
 7.1e-19:199:31
 HOMO SAPIENS (HUMAN).
 P18074
- 25 HRIFA021787a
 PROTEIN Q300.
 0.051:13:84
 MUS MUSCULUS (MOUSE).
 Q02722
- 30 HRIFA021794a
 RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
 1.6e-07:90:32
 35 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P54644
- 40 HRIFA021855a
 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
 8.6e-06:163:30
 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 P17437
- 45 HRIFA021906a
 S-ANTIGEN PROTEIN PRECURSOR.
 2.1e-09:226:28
 PLASMODIUM FALCIPARUM (ISOLATE V1).
 P09593
- 50 HRIFA022055a
 BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).
 0.63:118:31
 ACHROMOBACTER LYTICUS.
 P27458
- 55 HRIFA022065a
 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.
 9.7e-24:235:34

- HOMO SAPIENS (HUMAN).
P16279
- 5 HRIFA022139a
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.1e-57:232:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782
- 10 HRIFA022156a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR."
1.4e-07:133:35
TRITICUM AESTIVUM (WHEAT).
P08489
- 15 HRIFA022166a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.5e-28:194:35
HOMO SAPIENS (HUMAN).
20 Q03468
- HRIFA022177a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
2.2e-12:137:32
25 THERMOMONOSPORA CURVATA.
P49695
- HRIFA022182a
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
30 1.2e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793
- HRIFA022203a
35 COLLAGEN ALPHA 1 (III) CHAIN.
1.1e-05:211:33
BOS TAURUS (BOVINE).
P04258
- 40 HRIFA022227a
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
3.2e-31:229:36
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
45 Q10071
- HRIFA022234a
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
1.8e-08:110:30
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620
- HRIFA022249a
ZINC FINGER PROTEIN 133.
55 1.1e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

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- HRIFA022265a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM
KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5.1e-26:188:40
5 RATTUS NORVEGICUS (RAT).
P13234
- HRIFA022328a
SCO1 PROTEIN PRECURSOR.
10 5.4e-25:84:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23833
- HRIFA022335a
15 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
0.21:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
20
- HRIFA022348a
AGAMOUS PROTEIN.
1.0:40:42
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
25 P17839
- HRIFA022411a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
30 0.00059:111:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- HRIFA022423a
35 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
2.5e-15:106:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857
- HRIFA022462a
40 RETINOIC ACID RECEPTOR RXR-BETA.
0.0010:124:33
HOMO SAPIENS (HUMAN).
P28702
45
- HRIFA022493a
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
0.0018:130:34
MUS MUSCULUS (MOUSE).
50 Q01338
- HRIFA022528a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
3.2e-23:230:28
55 ZEA MAYS (MAIZE).
P14918
- HRIFA022546a

- NINAC SHORT PROTEIN (EC 2.7.1.-).
8.5e-42:209:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P10677
- 5
HRIFA022564a
ZINC FINGER PROTEIN 140.
7.9e-23:116:51
HOMO SAPIENS (HUMAN).
10 P52738
- HRIFA022616a
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
15 7.4e-36:172:43
HOMO SAPIENS (HUMAN).
Q07954
- HRIFA022671a
20 PAIRED AMPHIPATHIC HELIX PROTEIN.
2.0e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579
- HRIFA022691a
25 FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
1.4e-44:229:41
PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
P19477
- 30
HRIFA022702a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.1e-08:146:38
GALLUS GALLUS (CHICKEN).
35 P02457
- HRIFA022707a
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
7.0e-40:229:37
40 HOMO SAPIENS (HUMAN).
P16383
- HRIFA022714a
"AMELOGENIN, CLASS I PRECURSOR."
45 0.62:96:31
BOS TAURUS (BOVINE).
P02817
- HRIFA022728a
50 ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
1.7e-06:28:64
SUS SCROFA (PIG).
P08001
- 55
HRIFA022729a
"ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II)."

- 7.7e-29:69:84
HOMO SAPIENS (HUMAN).
Q10469
- 5 HRIFA022737a
TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTEND-
INOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
6.7e-19:170:37
GALLUS GALLUS (CHICKEN).
10 P10039
- HRIFA022776a
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
4.0e-20:199:31
15 MEDICAGO SATIVA (ALFALFA).
P38661
- HRIFA022782a
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
20 3.7e-09:184:36
PLASMODIUM CYNOMOLGI (STRAIN BEROK).
P08672
- HRIFA022865a
25 COLLAGEN ALPHA 1(III) CHAIN.
2.5e-09:169:33
BOS TAURUS (BOVINE).
P04258
- HRIFA022875a
30 BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
9.1e-14:115:33
BOS TAURUS (BOVINE).
P21793
- HRIFA022890a
35 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.8e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
40 P17437
- HRIFA022895a
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.4e-106:283:67
45 HOMO SAPIENS (HUMAN).
Q03923
- HRIFA022985a
50 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-
SA-1).
3.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.
Q06084
- HRIFA023007a
55 MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
1.1e-27:66:54
HOMO SAPIENS (HUMAN).

P22670

HRIFA023048a

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).

2.2e-07:221:33

RATTUS NORVEGICUS (RAT).

P02454

HRIFA023069a

BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).

3.4e-08:149:31

HOMO SAPIENS (HUMAN).

P98160

HRIFA023129a

HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.

4.2e-06:37:51

PLASMODIUM LOPHURAE.

P04929

HRIFA023154a

GLYCOPROTEIN X PRECURSOR.

8.2e-05:140:27

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

HRIFA023212a

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

8.3e-10:249:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

HRIFA023227a

GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).

9.2e-15:180:30

ESCHERICHIA COLI.

P37021

HRIFA023257a

PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.

2.4e-118:229:88

RATTUS NORVEGICUS (RAT).

P38378

HRIFA023304a

PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-ATPASE).

1.3e-23:222:29

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39524

HRIFA023434a

VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).

0.00018:157:30

RATTUS NORVEGICUS (RAT).

P17659

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- 5 HRIFA023464a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 10 HRIFA023489a
HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.
4.4e-09:230:23
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10297
- 15 HRIFA023634a
EBNA-1 NUCLEAR PROTEIN.
1.8e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 20 HRIFA023767a
CYTOCHROME B5.
1.1e-12:92:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 25 HRIFA023894a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.6e-05:80:40
MUS MUSCULUS (MOUSE).
P05142
- 30 HRIFA023923a
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
4.2e-76:128:85
HOMO SAPIENS (HUMAN).
35 P00395
- 40 HRIFA024088a
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.1e-05:118:32
MUS MUSCULUS (MOUSE).
P98084
- 45 HRIFA024132a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
6.5e-40:136:61
HOMO SAPIENS (HUMAN).
P51787
- 50 HRIFA024185a
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.55:128:29
HOMO SAPIENS (HUMAN).
P50548
- 55 HRIFA024197a
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP (CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).

- 7.5e-09:93:34
NEUROSPORA CRASSA.
P23231
- 5 HRIFA024218a
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
6.7e-06:180:36
HOMO SAPIENS (HUMAN).
P02452
- 10 HRIFA024255a
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
4.8e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
15 Q10496
- HRIFA024305a
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.047:47:29
20 HOMO SAPIENS (HUMAN).
P18850
- HRIFA024392a
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
25 6.7e-24:119:43
HOMO SAPIENS (HUMAN).
P51805
- HRIFA024423a
30 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
2.1e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020
- 35 HRIFA024473a
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
3.3e-05:106:41
BOS TAURUS (BOVINE).
P02453
- 40 HRIFA024482a
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.2e-07:99:31
NICOTIANA TABACUM (COMMON TOBACCO).
45 Q03211
- HRIFA024504a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
DROXYSTERIOD DEHYDROGENASE).
50 2.6e-43:205:49
HOMO SAPIENS (HUMAN).
P37058
- HRIFA024543a
55 GLYCOPROTEIN X PRECURSOR.
1.5e-06:257:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

- HRIFA024718a
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
5.3e-45:168:52
MUS MUSCULUS (MOUSE).
5 P23780
- HRIFA024767a
SODIUM CHANNEL PROTEIN (NA⁺ CHANNEL).
7.4e-30:221:31
10 ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
P02719
- HRIFA024884a
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
15 0.0089:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245
- HRIFA024893a
20 REGULATORY PROTEIN E2.
0.0021:167:31
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- HRIFA024937a
25 GNS1 PROTEIN.
1.0e-15:173:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- HRIFA024978a
30 MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.00019:150:32
HOMO SAPIENS (HUMAN).
35 Q02817
- HRIFA024994a
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
5.3e-22:145:46
40 NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- HRIFA025033a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
45 0.50:215:29
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- HRIFA025046a
50 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
1.7e-41:104:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- HRIFA025250a
55 "PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR))."
7.4e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).

P05130

HRIFA025261a
MYOSIN I ALPHA (MMI-ALPHA).
2.3e-64:141:84
MUS MUSCULUS (MOUSE).
P46735

5

HRIFA025290a
EBNA-1 NUCLEAR PROTEIN.
0.016:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10

HRIFA025327a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
2.3e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

15

HRIFA025353a
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.0e-11:75:46
ORYZA SATIVA (RICE).
P29834

20

HRIFA025479a
PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
3.0e-05:112:33
ESCHERICHIA COLI.
P31137

30

HRIFA025488a
PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR (FRAGMENTS).
9.5e-05:104:40
MUS MUSCULUS (MOUSE).
P08121

35

HRIFA025492a
SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
1.8e-53:159:69
HOMO SAPIENS (HUMAN).
Q13627

40

HRIFA025636a
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEXES ASSEMBLY PROTEIN RCA1 (EC 3.4.24.-) (TAT-BIND-
ING HOMOLOG 12).
4.7e-32:81:66
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40341

45

HRIFA025695a
PEREGRIN (BR140 PROTEIN).
3.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

55

HRIFA025703a

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CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
1.8e-08:71:42
MUS MUSCULUS (MOUSE).
P19467

5

HRIFA025706a
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.2e-28:111:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
10 P43636

HRIFA025766a
CYTOCHROME B5.
4.2e-13:133:33
15 ORYCTOLAGUS CUNICULUS (RABBIT).
P00169

HRIFA025771a
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
20 6.7e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288

HRIFA025778a
25 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.5e-05:212:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

30 HRIFA025800a
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
3.7e-18:165:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544

35 HRIFA025904a
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
2.6e-05:211:28
HOMO SAPIENS (HUMAN).
40 P17927

HRIFA025907a
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUPI-5111).
2.1e-38:176:38
45 HOMO SAPIENS (HUMAN).
Q06323

HRIFA025913a
50 DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
2.5e-32:185:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971

HRIFA025936a
55 TRANSCRIPTIONAL ACTIVATOR FE65.
3.4e-09:43:46
RATTUS NORVEGICUS (RAT).
P46933

- 5 HRIFA025966a
SYNAPTOTAGMIN III.
4.5e-05:93:33
RATTUS NORVEGICUS (RAT).
P40748
- 10 HRIFA025978a
"GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR."
3.5e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388
- 15 HRIFA026089a
BUTYROPHILIN PRECURSOR (BT).
1.1e-12:146:29
BOS TAURUS (BOVINE).
P18892
- 20 HRIFA026121a
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
9.7e-06:72:43
HOMO SAPIENS (HUMAN).
P48023
- 25 HRIFA026242a
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
7.4e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566
- 30 HRIFA026265a
DNA BINDING PROTEIN S1FA.
0.67:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551
- 35 HRIFA026303a
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.014:88:32
HOMO SAPIENS (HUMAN).
P10163
- 45 HRIFA026316a
EBNA-2 NUCLEAR PROTEIN.
1.5e-07:82:35
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P12978
- 50 HRIFA026351a
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.019:89:31
HOMO SAPIENS (HUMAN).
Q01543
- 55 HRIFA026364a
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
8.3e-40:167:49
RATTUS NORVEGICUS (RAT).

- P48303
- HRIFA026382a
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
5 6.2e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- HRIFA026465a
10 COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).
8.6e-07:158:35
GALLUS GALLUS (CHICKEN).
P12106
- HRIFA026496a
15 ZINC FINGER PROTEIN 140.
5.9e-24:122:52
HOMO SAPIENS (HUMAN).
P52738
- HRIFA026519a
20 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.3e-08:130:36
MUS MUSCULUS (MOUSE).
25 P05142
- HRIFA026564a
GLYCOPROTEIN X PRECURSOR
1.8e-10:225:25
30 EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- HRIFA026576a
35 "ADP,ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)."
1.7e-09:116:34
HOMO SAPIENS (HUMAN).
P12235
- HRIFA026615a
40 REGULATORY PROTEIN E2.
0.0024:132:31
HUMAN PAPILLOMAVIRUS TYPE 9.
P36780
- HRIFA026618a
45 PROTEIN Q300.
1.2e-05:27:66
MUS MUSCULUS (MOUSE).
50 Q02722
- HRIFA026659a
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-
55 NASE).
2.0e-10:81:45
RATTUS NORVEGICUS (RAT).
Q06226

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- HRIFA026764a
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
3.4e-05:162:25
RATTUS NORVEGICUS (RAT).
5 P10252
- HRIFA026789a
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
8.1e-22:175:38
10 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818
- HRIFA026813a
"PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
15 7.1e-89:256:67
HOMO SAPIENS (HUMAN).
Q15139
- HRIFA026860a
20 MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
2.6e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988
- HRIFA026923a
25 CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.18:119:36
CANIS FAMILIARIS (DOG).
P39881
30
- HRIFA027012a
"MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-
DASE) (ALPHA-MANNOSIDASE 1A)."
1.8e-44:234:41
35 MUS MUSCULUS (MOUSE).
P45700
- HRIFA027045a
HYPOTHETICAL PROTEIN HI0519.
40 2.7e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742
- HRIFA027125a
45 ZINC FINGER PROTEIN 133.
3.9e-33:70:61
HOMO SAPIENS (HUMAN).
P52736
- HRIFA027173a
50 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.15:137:27
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
55
- HRIFA027179a
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
3.6e-30:90:77

HOMO SAPIENS (HUMAN).
Q03468

5 HRIFA027187a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
4.7e-11:44:61
HOMO SAPIENS (HUMAN).
P20931

10 HRIFA027327a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
3.8e-07:184:35
HOMO SAPIENS (HUMAN).
Q03692

15 HRIFA027329a
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
9.1e-08:195:29
DROSOPHILA ERECTA (FRUIT FLY).
20 P13730

HRIFA027355a
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
1.9e-06:33:72
25 HOMO SAPIENS (HUMAN).
P20931

HRIFA027485a
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
30 0.00099:174:36
HOMO SAPIENS (HUMAN).
P12107

HRIFA027536a
35 VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
0.0042:104:35
DROSOPHILA MELANOGASTER (FRUIT FLY).
P13238

40 HRIFA027549a
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00023:101:44
HOMO SAPIENS (HUMAN).
45 P21917

HRIFA027622a
GUANOSINE-DIPHOSPHATASE (EC 3.6.1.42) (GDPASE).
2.2e-23:146:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
50 P32621

HRIFA027625a
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).
1.1e-57:220:54
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P13586

HRIFA027644a

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- COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
7.5e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454
- 5
- HRIFA027656a
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
1.6e-13:149:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160
- 10
- HRIFA027673a
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
6.4e-06:47:57
HOMO SAPIENS (HUMAN).
P29279
- 15
- HRIFA027681a
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.1e-13:158:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458
- 20
- HRIFA027714a
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
7.2e-06:146:30
CAENORHABDITIS ELEGANS.
P46580
- 25
- HRIFA027722a
SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
2.7e-105:242:85
CANIS FAMILIARIS (DOG).
Q00004
- 30
- HRIFA027860a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
8.3e-08:168:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 35
- HRIFA027867a
STANNIÖCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-
EOCALCIN).
1.0:100:27
ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301
- 40
- HRIFA027940a
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).
8.7e-15:149:38
HOMO SAPIENS (HUMAN).
P55103
- 50
- HRIFA028061a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
9.7e-07:157:26
THERMOMONOSPORA CURVATA.
- 55

- P49695
- HRIFA028157a
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).
2.8e-71:201:68
HOMO SAPIENS (HUMAN).
P30825
- HRIFA028187a
EBNA-1 NUCLEAR PROTEIN.
1.5e-09:131:38
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- HRIFA028262a
CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).
7.2e-09:99:33
MUS MUSCULUS (MOUSE).
P53996
- HRIFA028371a
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
1.0e-08:103:33
RATTUS NORVEGICUS (RAT).
Q01177
- HRIFA028402a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
3.2e-33:204:39
THERMOMONOSPORA CURVATA.
P49695
- HRIFA028440a
COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.
1.9e-07:192:36
HOMO SAPIENS (HUMAN).
P53420
- HRIFA028468a
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN (EC 2.7.1.123) (CAM
KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
5.8e-32:178:44
RATTUS NORVEGICUS (RAT).
P13234
- HRIFA028501a
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.6 (RCK2) (KV2).
6.3e-05:161:31
RATTUS NORVEGICUS (RAT).
P17659
- HRIFA028511a
ANKYRIN HOMOLOG PRECURSOR.
3.0e-19:176:34
CHROMATIUM VINOSUM.
Q06527

- 5 HRIFA028576a
ACROSIN PRECURSOR (EC 3.4.21.10).
4.8e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038
- 10 HRIFA028614a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
1.0e-08:82:39
PLASMODIUM LOPHURAE.
P04929
- 15 HRIFA028651a
BAND 3 ANION TRANSPORT PROTEIN.
1.3e-18:156:32
GALLUS GALLUS (CHICKEN).
P15575
- 20 HRIFA028790a
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
5.0e-18:212:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 25 HRIFA028804a
CCAAT-BINDING FACTOR (CBF).
0.98:232:23
MUS MUSCULUS (MOUSE).
P53569
- 30 HRIFA028867a
REGULATORY PROTEIN E2.
0.0057:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787
- 35 HRIFA028911a
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
1.2e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179
- 45 HRIFA028983a
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0051:115:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439
- 50 HRIFA029002a
FIBRINOGEN BETA CHAIN.
3.2e-25:121:45
BOS TAURUS (BOVINE).
P02676
- 55 HRIFA029050a
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.2e-10:134:32
GALLUS GALLUS (CHICKEN).

- P24503
- HRIFA029208a
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
5 1.4e-14:64:59
RATTUS NORVEGICUS (RAT).
Q02975
- HRIFA029209a
10 "ALPHA-MANNOSIDASE II (EC 3.2.1.114) (MANNOsyl-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSI-
DASE) (MAN II) (GOLGI ALPHA-MANNOSIDASE II)."
2.3e-12:114:37
MUS MUSCULUS (MOUSE).
P27046
- HRIFA029256a
15 GAP JUNCTION BETA-2 PROTEIN (CONNEXIN 26) (CX26).
1.8e-35:89:75
HOMO SAPIENS (HUMAN).
20 P29033
- HRIFA029263a
SARCALUMENIN PRECURSOR.
2.1e-16:161:31
25 ORYCTOLAGUS CUNICULUS (RABBIT).
P13666
- HRIFA029278a
30 "SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6" PEPTIDE P-H].
3.5e-10:204:32
HOMO SAPIENS (HUMAN).
P04280
- HRIFA029285a
35 GLYCOPROTEIN 25L PRECURSOR (GP25L).
4.9e-58:197:55
CANIS FAMILIARIS (DOG).
P27869
- HRIFA029317a
40 HIGH AFFINITY SULPHATE TRANSPORTER 2.
2.3e-25:83:50
STYLOSANTHES HAMATA.
45 P53392
- HRIFA029327a
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
9.1e-34:227:37
50 BOS TAURUS (BOVINE).
P22292
- HRIFA029349a
55 CUTICLE COLLAGEN 12 PRECURSOR.
5.1e-09:190:33
CAENORHABDITIS ELEGANS.
P20630

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- 5 HRIFA029393a
PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
9.7e-69:165:84
HOMO SAPIENS (HUMAN).
P35414
- 10 HRIFA029398a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.011:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 15 HRIFA029425a
ALPHA CRYSTALLIN B CHAIN (ALPHA(B)-CRYSTALLIN).
2.0e-08:99:32
BOS TAURUS (BOVINE).
P02510
- 20 HRIFA029434a
"SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CPS) [CONTAINS: BASIC PEPTIDE IB-6" PEPTIDE P-H].
2.6e-05:232:32
HOMO SAPIENS (HUMAN).
P04280
- 25 HRIFA029440a
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.00046:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
30 P17437
- 35 HRIFA029460a
SYNAPTOTAGMIN III.
1.5e-08:102:35
RATTUS NORVEGICUS (RAT).
P40748
- 40 HRIFA029467a
GLYCOPROTEIN X PRECURSOR.
5.2e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 45 HRIFA029508a
PROPERDIN PRECURSOR.
1.9e-06:218:32
HOMO SAPIENS (HUMAN).
P27918
- 50 HRIFA029511a
POTASSIUM CHANNEL PROTEIN EAG.
2.3e-66:139:61
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q02280
- 55 HRIFA029602a
SEX-DETERMINING REGION Y PROTEIN (TESTIS-DETERMINING FACTOR).
1.0:37:37

- SUS SCROFA (PIG).
P36393
- 5 HRIFA029649a
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.30:99:34
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- 10 HRIFA029715a
GROWTH ARREST AND DNA-DAMAGE-INDUCIBLE PROTEIN GADD153 (DNA-DAMAGE INDUCIBLE TRAN-
SCRIPT 3) (DDIT3) (C/EBP-HOMOLOGOUS PROTEIN) (CHOP).
0.54:95:30
HOMO SAPIENS (HUMAN).
15 P35638
- HRIFA029730a
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
3.8e-05:131:29
20 PLASMODIUM LOPHURAE.
P04929
- HRIFA029792a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
25 9.0e-09:178:30
THERMOMONOSPORA CURVATA.
P49695
- HRIFA029802a
30 TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).
7.2e-73:204:69
CANIS FAMILIARIS (DOG).
Q01685
- HRIFA029866a
35 PROTEIN KINASE BYR2 (EC 2.7.1.-) (PROTEIN KINASE STE8) (MAPK KINASE KINASE) (MAPKKK).
1.2e-27:144:45
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P28829
- 40 HRIFA029932a
F-SPONDIN PRECURSOR.
9.1e-24:191:37
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
45 P35447
- HRIFA030025a
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
50 1.0e-11:138:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- HRIFA030045a
55 SARCALUMENIN PRECURSOR.
2.4e-20:151:32
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

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- HRIFA030103a
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.1e-05:215:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
5 P53214
- HRIFA030106a
SCO-SPONDIN (FRAGMENT).
0.53:60:36
10 BOS TAURUS (BOVINE).
P98167
- HRIFA030147a
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
1.8e-10:93:34
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257
- HRIFA030250a
20 ENAMELIN (TUFTELIN).
3.7e-108:250:86
BOS TAURUS (BOVINE).
P27628
- HRIFA030264a
25 SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODI-
UM-GLUCOSE COTRANSPORTER).
3.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
30 P11170
- HRIFA030342a
ESTRADIOL 17 BETA-DEHYDROGENASE 3 (EC 1.1.1.62) (17-BETA-HSD 3) (TESTICULAR 17-BETA-HY-
DROXYSTEROID DEHYDROGENASE).
35 1.5e-42:203:49
HOMO SAPIENS (HUMAN).
P37058
- HRIFA030370a
40 HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
8.0e-12:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- HRIFA030371a
45 "PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU)."
1.6e-68:228:59
HOMO SAPIENS (HUMAN).
Q15139
50
- HRIFA030381a
COLLAGEN 1(X) CHAIN PRECURSOR.
3.0e-05:204:30
GALLUS GALLUS (CHICKEN).
55 P08125
- HRIFA030385a
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

- 0.029:162:31
HOMO SAPIENS (HUMAN).
Q03692
- 5 HRIFA030411a
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).
1.2e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
10 Q09925
- HRIFA030448a
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
2.5e-92:225:77
15 HOMO SAPIENS (HUMAN).
P27448
- HRIFA030456a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
20 9.3e-08:127:35
MUS MUSCULUS (MOUSE).
P05142
- HRIFA030461a
25 CUTICLE COLLAGEN 12 PRECURSOR.
0.046:140:31
CAENORHABDITIS ELEGANS.
P20630
- 30 HRIFA030472a
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0030:98:31
NEUROSPORA CRASSA.
Q06712
- 35 HRIFA030509a
"INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFERON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE)."
2.5e-09:65:43
40 HOMO SAPIENS (HUMAN).
P19525
- HRIFA030511a
T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN.
45 0.00010:99:33
HOMO SAPIENS (HUMAN).
P21145
- HRIFA030545a
50 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
7.6e-21:165:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53974
- 55 HRIFA030566a
"GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)."
2.7e-07:221:30

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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640

5 HRIFA030599a
GLYCOPROTEIN X PRECURSOR.
2.8e-05:236:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

10 HRIFA030629a
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-
UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
3.5e-16:115:38
BOS TAURUS (BOVINE).
15 P05307

HRIFA030642a
SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).
2.5e-12:93:47
20 VOLVOX CARTERI.
P21997

HRIFA030662a
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
25 9.1e-120:279:83
HOMO SAPIENS (HUMAN).
P03886

HRIFA030839a
30 HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135

35 HRIFA031091a
PROTEIN Q300.
0.0042:27:62
MUS MUSCULUS (MOUSE).
Q02722

40 HRIFA031126a
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (RB INTRON ENCODED G-PROTEIN COUPLED
RECEPTOR).
1.3e-06:70:34
45 HOMO SAPIENS (HUMAN).
P43657

HRIFA031249a
50 ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).
5.9e-05:166:31
RATTUS NORVEGICUS (RAT).
P04474

HRIFA031336a
55 CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DNA BINDING PROTEIN SUBUNIT B).
6.6e-15:97:38
PETROMYZON MARINUS (SEA LAMPREY).

P25210

HRIFA031395a
COLD SHOCK PROTEIN CSPB (FRAGMENT).
5 0.95:32:40
BACILLUS GLOBISPORUS.
P41018

HRIFA031397a
10 REGULATORY PROTEIN E2.
0.0077:145:35
HUMAN PAPILLOMAVIRUS TYPE 47.
P22420

HRIFA031438a
15 GLUCOSE REPRESSION MEDIATOR PROTEIN.
1.3e-06:176:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922

HRIFA031869a
20 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY-LIKE) (RHL).
1.7e-18:163:41
RATTUS NORVEGICUS (RAT).
25 Q04666

HRIFA031935a
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
1.8e-06:192:32
30 ZEA MAYS (MAIZE).
P14918

HRIFA031986a
35 SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (AL-
PHA-PAK) (PROTEIN KINASE MUK2).
2.4e-49:222:47
RATTUS NORVEGICUS (RAT).
P35465

HRIFA032009a
40 PROBABLE G PROTEIN-COUPLED RECEPTOR FROM T-CELLS PRECURSOR (GLUCOCORTICOID-IN-
DUCED RECEPTOR).
1.0e-17:118:36
MUS MUSCULUS (MOUSE).
45 P30731

HRIFA032011a
MUSCARINIC ACETYLCHOLINE RECEPTOR M4.
7.8e-35:184:32
50 HOMO SAPIENS (HUMAN).
P08173

HRIFA032070a
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
55 2.1e-18:107:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500

- 5 HRIFA032073a
SECRETOTRANIN III PRECURSOR (SGIII).
9.7e-69:182:76
MUS MUSCULUS (MOUSE).
P47867
- 10 HRIFA032079a
HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.
3.5e-12:96:39
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906
- 15 HRIFA032097a
GLYCOPROTEIN J.
0.023:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480
- 20 HRIFA032161a
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.22:56:42
HOMO SAPIENS (HUMAN).
P49716
- 25 HRIFA032186a
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN) (TAXREB302).
0.86:50:38
HOMO SAPIENS (HUMAN).
Q10586
- 30 HRIFA032224a
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
2.6e-43:196:45
CAENORHABDITIS ELEGANS.
Q03567
- 35 HRIFA032257a
GLUCOSE REPRESSION MEDIATOR PROTEIN.
4.7e-07:204:25
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922
- 40 HRIFA032274a
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
7.8e-60:163:74
MUS MUSCULUS (MOUSE).
Q07231
- 45 HRIFA032275a
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
7.2e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546
- 50 HRIFA032360a
HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME II.
3.0e-05:198:28

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CAENORHABDITIS ELEGANS.
Q09625

5 HRIFA032389a
EBNA-1 NUCLEAR PROTEIN.
1.3e-05:86:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P03211

10 HRIFA032433a
GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).
3.1e-14:54:53
RATTUS NORVEGICUS (RAT).
P30969

15 HRIFA032453a
BUTYROPHILIN PRECURSOR (BT).
5.9e-13:162:32
BOS TAURUS (BOVINE).
P18892

20 HRIFA032478a
GLYCOPROTEIN X PRECURSOR.
3.8e-06:253:28
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
25 P28968

HRIFA032506a
COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR.
1.2e-06:226:34
30 HOMO SAPIENS (HUMAN).
P12111

HRIFA032511a
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
35 8.7e-09:229:34
HOMO SAPIENS (HUMAN).
Q07092

HRIFA032530a
40 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
9.0e-05:159:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

45 HRIFA032587a
SYNAPTOTAGMIN (P65).
3.2e-08:72:52
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P41823

50 HRIFA032605a
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER
PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-
55 ING 1).
8.4e-37:192:41
HOMO SAPIENS (HUMAN).
Q03518

- HRIFA032642a
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.0e-05:127:33
MUS MUSCULUS (MOUSE).
P05142
- HRIFA032696a
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
1.4e-13:200:38
BOS TAURUS (BOVINE).
P02459
- HRIFA032730a
K-GLYPICAN PRECURSOR.
4.8e-67:180:68
MUS MUSCULUS (MOUSE).
P51655
- HRIFA032820a
GLUTAMIC ACID-RICH PROTEIN PRECURSOR.
7.5e-05:192:23
PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA).
P13816
- 25 Homology search result 2
- [0290] Homology of representative sequences of the 5'-end cluster to the data in Swiss-Prot database
[0291] Representative sequence of the 5'-end cluster exhibiting relatively high homology (304 cluster: "exhibiting relatively high homology" means that the P value is 10^{-10} or less)
- HRIFA000327a, HRIFA000432a, HRIFA000553a, HRIFA000564a, HRIFA000631a, HRIFA000683a, HRIFA000776a, HRIFA000814a, HRIFA001132a, HRIFA001138a, HRIFA001337a, HRIFA001341a, HRIFA001489a, HRIFA001712a, HRIFA001720a, HRIFA001942a, HRIFA001975a, HRIFA001984a, HRIFA002384a, HRIFA002503a, HRIFA002743a, HRIFA002766a, HRIFA002805a, HRIFA002891a, HRIFA002919a, HRIFA002980a, HRIFA003063a, HRIFA003093a, HRIFA003635a, HRIFA004006a, HRIFA004034a, HRIFA004112a, HRIFA004426a, HRIFA004490a, HRIFA004523a, HRIFA004663a, HRIFA004696a, HRIFA004714a, HRIFA004745a, HRIFA004919a, HRIFA005184a, HRIFA005231a, HRIFA005240a, HRIFA005271a, HRIFA005372a, HRIFA005392a, HRIFA005409a, HRIFA005420a, HRIFA005438a, HRIFA005462a, HRIFA005644a, HRIFA005720a, HRIFA005732a, HRIFA005760a, HRIFA005781a, HRIFA006183a, HRIFA006494a, HRIFA006510a, HRIFA006566a, HRIFA006586a, HRIFA006596a, HRIFA006649a, HRIFA006667a, HRIFA006730a, HRIFA006926a, HRIFA007013a, HRIFA007219a, HRIFA007228a, HRIFA007243a, HRIFA007352a, HRIFA007424a, HRIFA007435a, HRIFA007463a, HRIFA007493a, HRIFA007571a, HRIFA007659a, HRIFA007722a, HRIFA007745a, HRIFA008000a, HRIFA008200a, HRIFA008284a, HRIFA008314a, HRIFA008362a, HRIFA008459a, HRIFA008483a, HRIFA008547a, HRIFA008611a, HRIFA008661a, HRIFA008717a, HRIFA008784a, HRIFA008981a, HRIFA009101a, HRIFA009171a, HRIFA009220a, HRIFA009451a, HRIFA009482a, HRIFA009783a, HRIFA009881a, HRIFA010085a, HRIFA010090a,
- HRIFA010130a, HRIFA010319a, HRIFA010394a, HRIFA010460a, HRIFA010790a, HRIFA010975a, HRIFA011016a, HRIFA011179a, HRIFA011197a, HRIFA011449a, HRIFA011659a, HRIFA011947a, HRIFA012278a, HRIFA012584a, HRIFA012625a, HRIFA012692a, HRIFA012795a, HRIFA012885a, HRIFA012914a, HRIFA012969a, HRIFA012990a, HRIFA013254a, HRIFA013265a, HRIFA013276a, HRIFA013376a, HRIFA013477a, HRIFA013586a, HRIFA013726a, HRIFA013744a, HRIFA013911a, HRIFA014006a, HRIFA014185a, HRIFA014336a, HRIFA014465a, HRIFA014500a, HRIFA014561a, HRIFA014568a, HRIFA014621a, HRIFA014688a, HRIFA014819a, HRIFA014951a, HRIFA014967a, HRIFA015063a, HRIFA015070a, HRIFA015246a, HRIFA015423a, HRIFA015453a, HRIFA015486a, HRIFA015506a, HRIFA015536a, HRIFA015547a, HRIFA015568a, HRIFA015756a, HRIFA015811a, HRIFA016070a, HRIFA016290a, HRIFA016430a, HRIFA016654a, HRIFA016758a, HRIFA017031a, HRIFA017257a, HRIFA017295a, HRIFA017312a, HRIFA017703a, HRIFA017855a, HRIFA018092a, HRIFA018131a, HRIFA018134a, HRIFA018580a, HRIFA018827a, HRIFA018904a, HRIFA018993a, HRIFA019105a, HRIFA019136a, HRIFA019175a, HRIFA019262a, HRIFA019466a, HRIFA019867a, HRIFA019869a, HRIFA020272a, HRIFA020335a, HRIFA020349a, HRIFA020862a, HRIFA021213a, HRIFA021398a, HRIFA021499a, HRIFA021637a, HRIFA021651a, HRIFA021754a, HRIFA021781a, HRIFA022065a, HRIFA022139a, HRIFA022166a, HRIFA022177a, HRIFA022182a, HRIFA022227a, HRIFA022249a, HRIFA022265a,

HRIFA022328a, HRIFA022423a, HRIFA022528a, HRIFA022546a, HRIFA022564a, HRIFA022616a, HRIFA022671a, HRIFA022691a, HRIFA022707a, HRIFA022729a, HRIFA022737a, HRIFA022776a, HRIFA022875a, HRIFA022895a, HRIFA023007a, HRIFA023227a, HRIFA023257a, HRIFA023304a, HRIFA023464a, HRIFA023767a, HRIFA023923a, HRIFA024132a, HRIFA024255a, HRIFA024392a, HRIFA024423a, HRIFA024504a, HRIFA024718a, HRIFA024767a, HRIFA024937a, HRIFA024994a, HRIFA025046a, HRIFA025250a, HRIFA025261a, HRIFA025353a, HRIFA025492a, HRIFA025636a, HRIFA025695a, HRIFA025706a, HRIFA025766a, HRIFA025800a, HRIFA025907a, HRIFA025913a, HRIFA026089a, HRIFA026364a, HRIFA026496a, HRIFA026789a, HRIFA026813a, HRIFA026860a, HRIFA027012a, HRIFA027045a, HRIFA027125a, HRIFA027179a, HRIFA027187a, HRIFA027622a, HRIFA027625a, HRIFA027656a, HRIFA027681a, HRIFA027722a, HRIFA027940a, HRIFA028157a, HRIFA028402a, HRIFA028468a, HRIFA028511a, HRIFA028651a, HRIFA028790a, HRIFA029002a, HRIFA029208a, HRIFA029209a, HRIFA029256a, HRIFA029263a, HRIFA029285a, HRIFA029317a, HRIFA029327a, HRIFA029393a, HRIFA029511a, HRIFA029802a, HRIFA029866a, HRIFA029932a, HRIFA030025a, HRIFA030045a, HRIFA030250a, HRIFA030342a, HRIFA030370a, HRIFA030371a, HRIFA030411a, HRIFA030448a, HRIFA030545a, HRIFA030629a, HRIFA030642a, HRIFA030662a, HRIFA031336a, HRIFA031869a, HRIFA031986a, HRIFA032009a, HRIFA032011a, HRIFA032070a, HRIFA032073a, HRIFA032079a, HRIFA032224a, HRIFA032274a, HRIFA032275a, HRIFA032433a, HRIFA032453a, HRIFA032605a, HRIFA032696a, HRIFA032730a,

Homology search result 3

[0292] Representative sequence of the 5'-end cluster exhibiting relatively low homology (221 cluster: "exhibiting relatively low homology" means that the P value is higher than 10^{-10} and 10^{-4} or less)
 HRIFA000016a, HRIFA000071a, HRIFA000116a, HRIFA000123a, HRIFA000264a, HRIFA000415a, HRIFA000446a, HRIFA000695a, HRIFA000845a, HRIFA001971a, HRIFA002063a, HRIFA002102a, HRIFA002284a, HRIFA002309a, HRIFA002694a, HRIFA002762a, HRIFA002787a, HRIFA003055a, HRIFA003340a, HRIFA003402a, HRIFA003504a, HRIFA003892a, HRIFA003946a, HRIFA004162a, HRIFA004401a, HRIFA004780a, HRIFA005072a, HRIFA005102a, HRIFA005214a, HRIFA005255a, HRIFA005300a, HRIFA005369a, HRIFA005702a, HRIFA005728a, HRIFA005944a, HRIFA006298a, HRIFA006448a, HRIFA006572a, HRIFA006633a, HRIFA006642a, HRIFA007068a, HRIFA007244a, HRIFA007262a, HRIFA007512a, HRIFA007532a, HRIFA007565a, HRIFA007728a, HRIFA007909a, HRIFA008174a, HRIFA008426a, HRIFA008596a, HRIFA008790a, HRIFA008989a, HRIFA009578a, HRIFA009825a, HRIFA009852a, HRIFA009983a, HRIFA010005a, HRIFA010078a, HRIFA010152a, HRIFA010301a, HRIFA010361a, HRIFA010425a, HRIFA010466a, HRIFA010799a, HRIFA011580a, HRIFA011820a, HRIFA012167a, HRIFA012354a, HRIFA012427a, HRIFA012436a, HRIFA012515a, HRIFA012702a, HRIFA012737a, HRIFA013135a, HRIFA013235a, HRIFA013279a, HRIFA013589a, HRIFA013620a, HRIFA013919a, HRIFA013932a, HRIFA014056a, HRIFA014111a, HRIFA014133a, HRIFA014396a, HRIFA014397a, HRIFA014598a, HRIFA014702a, HRIFA014868a, HRIFA015219a, HRIFA015995a, HRIFA016214a, HRIFA016240a, HRIFA016255a, HRIFA016639a, HRIFA016669a, HRIFA016963a, HRIFA017457a, HRIFA017643a, HRIFA017670a, HRIFA017801a, HRIFA017836a, HRIFA017921a, HRIFA018238a, HRIFA018262a, HRIFA018287a, HRIFA018666a, HRIFA018688a, HRIFA018754a, HRIFA018794a, HRIFA018870a, HRIFA018931a, HRIFA019412a, HRIFA019490a, HRIFA019498a, HRIFA019532a, HRIFA019651a, HRIFA0201440, HRIFA020184a, HRIFA020453a, HRIFA020693a, HRIFA020707a, HRIFA020748a, HRIFA021061a, HRIFA021224a, HRIFA021494a, HRIFA021794a, HRIFA021855a, HRIFA021906a, HRIFA022156a, HRIFA022203a, HRIFA022234a, HRIFA022702a, HRIFA022728a, HRIFA022782a, HRIFA022865a, HRIFA022890a, HRIFA022985a, HRIFA023048a, HRIFA023069a, HRIFA023129a, HRIFA023154a, HRIFA023212a, HRIFA023489a, HRIFA023634a, HRIFA023894a, HRIFA024088a, HRIFA024197a, HRIFA024218a, HRIFA024473a, HRIFA024482a, HRIFA024543a, HRIFA025327a, HRIFA025479a, HRIFA025488a, HRIFA025703a, HRIFA025771a, HRIFA025778a, HRIFA025904a, HRIFA025966a, HRIFA025978a, HRIFA026121a, HRIFA026242a, HRIFA026316a, HRIFA026382a, HRIFA026465a, HRIFA026519a, HRIFA026564a, HRIFA026576a, HRIFA026618a, HRIFA026659a, HRIFA026764a, HRIFA027327a, HRIFA027329a, HRIFA027355a, HRIFA027644a, HRIFA027673a, HRIFA027714a, HRIFA027860a, HRIFA028061a, HRIFA028187a, HRIFA028262a, HRIFA028371a, HRIFA028440a, HRIFA028501a, HRIFA028576a, HRIFA028614a, HRIFA028911a, HRIFA029050a, HRIFA029278a, HRIFA029349a, HRIFA029425a, HRIFA029434a, HRIFA029460a, HRIFA029467a, HRIFA029508a, HRIFA029730a, HRIFA029792a, HRIFA030103a, HRIFA030147a, HRIFA030264a, HRIFA030381a, HRIFA030456a, HRIFA030509a, HRIFA030511a, HRIFA030566a, HRIFA030599a, HRIFA031126a, HRIFA031249a, HRIFA031438a, HRIFA031935a, HRIFA032257a, HRIFA032360a, HRIFA032389a, HRIFA032478a, HRIFA032506a, HRIFA032511a, HRIFA032530a, HRIFA032587a, HRIFA032642a, HRIFA032820a,

Homology search result 4

[0293] Representative sequence of the 5'-end cluster exhibiting low homology (115 cluster: "exhibiting low homology")

means that the P value is higher than 10^{-4} and 1 or less)

HRIFA001099a, HRIFA001200a, HRIFA001413a, HRIFA001439a, HRIFA001558a, HRIFA001866a, HRIFA001972a,
 HRIFA002689a, HRIFA003357a, HRIFA003592a, HRIFA003640a, HRIFA003883a, HRIFA005296a, HRIFA005500a,
 HRIFA005540a, HRIFA006250a, HRIFA006609a, HRIFA006798a, HRIFA007032a, HRIFA007152a, HRIFA007547a,
 5 HRIFA007829a, HRIFA007985a, HRIFA008212a, HRIFA008252a, HRIFA008976a, HRIFA009071a, HRIFA009123a,
 HRIFA009136a, HRIFA009339a, HRIFA009762a, HRIFA010176a, HRIFA010490a, HRIFA010736a, HRIFA010859a,
 HRIFA010891a, HRIFA010988a, HRIFA011105a, HRIFA011128a, HRIFA011484a, HRIFA011512a, HRIFA011926a,
 HRIFA012069a, HRIFA012151a, HRIFA013092a, HRIFA013103a, HRIFA013980a, HRIFA014024a, HRIFA014590a,
 HRIFA014620a, HRIFA015122a, HRIFA015351a, HRIFA015802a, HRIFA015902a, HRIFA015947a, HRIFA016599a,
 10 HRIFA017146a, HRIFA017190a, HRIFA017456a, HRIFA017791a, HRIFA017818a, HRIFA018447a, HRIFA019437a,
 HRIFA019958a, HRIFA020883a, HRIFA021007a, HRIFA021040a, HRIFA021445a, HRIFA021543a, HRIFA021620a,
 HRIFA021787a, HRIFA022055a, HRIFA022335a, HRIFA022348a, HRIFA022411a, HRIFA022462a, HRIFA022493a,
 HRIFA022714a, HRIFA023434a, HRIFA024185a, HRIFA024305a, HRIFA024884a, HRIFA024893a, HRIFA024978a,
 HRIFA025033a, HRIFA025290a, HRIFA026265a, HRIFA026303a, HRIFA026351a, HRIFA026615a, HRIFA026923a,
 15 HRIFA027173a, HRIFA027485a, HRIFA027536a, HRIFA027549a, HRIFA027867a, HRIFA028804a, HRIFA028867a,
 HRIFA028983a, HRIFA029398a,
 HRIFA029440a, HRIFA029602a, HRIFA029649a, HRIFA029715a, HRIFA030106a, HRIFA030385a, HRIFA030461a,
 HRIFA030472a, HRIFA030839a, HRIFA031091a, HRIFA031395a, HRIFA031397a, HRIFA032097a, HRIFA032161a,
 HRIFA032186a,

Homology search result 5

[0294] The result of the homology search in the SwissProt using the clone sequences of the 5'-ends.

Indicated are from the top,
 the name of the clone sequence,
 definition of the top hit data,
 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
 the organism of which the top hit data is obtained,
 30 the Accession No. of the top hit data.

[0295] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
 35 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3).
 1.2e-119:279:83
 HOMO SAPIENS (HUMAN).
 P03886

40 F-BNGH41000087
 PROPERDIN PRECURSOR.
 2.5e-06:218:32
 HOMO SAPIENS (HUMAN).
 P27918

45 F-BNGH41000091
 POTASSIUM CHANNEL PROTEIN EAG.
 3.1e-66:139:61
 DROSOPHILA MELANOGASTER (FRUIT FLY).
 50 Q02280

F-HEMBA1000006
 S-ANTIGEN PROTEIN PRECURSOR.
 3.0e-05:164:31
 55 PLASMODIUM FALCIPARUM (ISOLATE V1).
 P09593

F-HEMBA1000121

EP 1 130 094 A2

- 5 HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.
8.2e-06:83:27
CAENORHABDITIS ELEGANS.
P34679
- 10 F-HEMBA1000128
PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).
8.2e-08:89:34
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P33154
- 15 F-HEMBA1000275
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.9e-06:231:34
GALLUS GALLUS (CHICKEN).
P02457
- 20 F-HEMBA1000300
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
1.4e-13:73:56
HOMO SAPIENS (HUMAN).
P39195
- 25 F-HEMBA1000349
ATP-BINDING CASSETTE TRANSPORTER 1.
2.6e-16:238:31
MUS MUSCULUS (MOUSE).
P41233
- 30 F-HEMBA1000443
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.8e-06:120:35
MUS MUSCULUS (MOUSE).
P05142
- 35 F-HEMBA1000462
PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
2.9e-21:86:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818
- 40 F-HEMBA1000477
HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.
3.3e-09:138:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40085
- 50 F-HEMBA1000590
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
2.2e-27:117:48
GALLUS GALLUS (CHICKEN).
P05099
- 55 F-HEMBA1000634
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).
0.00027:85:43
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-HEMBA1000671
ZINC FINGER PROTEIN 140.
1.1e-44:155:47
HOMO SAPIENS (HUMAN).
P52738

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F-HEMBA1000713
BLADDER CANCER 10 KD PROTEIN.
1.5e-42:81:97
HOMO SAPIENS (HUMAN).
060629

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F-HEMBA1000732
FIBRILLIN 1 PRECURSOR.
6.3e-18:77:46
HOMO SAPIENS (HUMAN).
P35555

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F-HEMBA1000745
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6; PEPTIDE P-H].
5.2e-06:105:33
HOMO SAPIENS (HUMAN).
P04280

25

F-HEMBA1000835
FIBRILLIN 2 PRECURSOR.
2.1e-42:214:44
HOMO SAPIENS (HUMAN).
P35556

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F-HEMBA1000875
ZINC FINGER PROTEIN 133.
5.8e-16:49:87
HOMO SAPIENS (HUMAN).
P52736

35

F-HEMBA1000907
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.2e-05:172:34
MUS MUSCULUS (MOUSE).
P11087

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F-HEMBA1000940
GAP JUNCTION CX43.4 PROTEIN (CONNEXIN 43.4) (CX43.4).
1.4e-20:90:42
BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).
Q92052

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F-HEMBA1000962
WATER-STRESS INDUCIBLE PROTEIN RAB21.
0.089:122:25
ORYZA SATIVA (RICE).
P12253

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F-HEMBA1001184

EP 1 130 094 A2

SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).
 4.9e-33:100:60
 HOMO SAPIENS (HUMAN).
 P55822

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F-HEMBA1001221
 AGRIN PRECURSOR.
 1.7e-26:239:32
 GALLUS GALLUS (CHICKEN).
 P31696

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F-HEMBA1001228
 CARTILAGE OLIGOMERIC MATRIX PROTEIN PRECURSOR (COMP).
 7.7e-114:147:83
 HOMO SAPIENS (HUMAN).
 P49747

15

F-HEMBA1001272
 SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B53).
 5.8e-06:129:33
 HOMO SAPIENS (HUMAN).
 Q15427

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F-HEMBA1001296
 TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6).
 0.0019:115:36
 GALLUS GALLUS (CHICKEN).
 Q98937

25

F-HEMBA1001297
 50S RIBOSOMAL PROTEIN L37E (L35E).
 0.65:40:40
 HALOARCUA MARISMORTUI (HALOBACTERIUM MARISMORTUI).
 P32410

30

F-HEMBA1001390
 SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
 0.00050:89:33
 NEPHILA CLAVIPES (ORB SPIDER).
 P46804

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F-HEMBA1001563
 B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
 0.00041:34:61
 HOMO SAPIENS (HUMAN).
 P20931

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F-HEMBA1001621
 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.
 1.1e-64:105:72
 HOMO SAPIENS (HUMAN).
 P35414

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F-HEMBA1001878
 VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
 1.3e-24:170:35
 PODOSPORA ANSERINA.
 Q00808

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EP 1 130 094 A2

- 5 F-HEMBA1001886
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
1.8e-94:273:64
HOMO SAPIENS (HUMAN).
Q03923
- 10 F-HEMBA1002048
EARLY ANTIGEN PROTEIN D (EA-D).
0.13:93:34
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03191
- 15 F-HEMBA1002131
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1).
6.3e-12:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 20 F-HEMBA1002163
HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.
2.1e-10:204:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q04651
- 25 F-HEMBA1002164
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-
CP).
0.022:62:32
30 GLYCINE MAX (SOYBEAN).
Q42783
- 35 F-HEMBA1002167
ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7).
5.2e-31:247:31
BUNGARUS FASCIATUS (BANDED KRAIT).
Q92035
- 40 F-HEMBA1002178
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HY-
DROXYLASE 1) (LH1).
1.5e-11:140:30
GALLUS GALLUS (CHICKEN).
P24802
- 45 F-HEMBA1002195
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
5.0e-07:52:36
PODOSPORA ANSERINA.
50 Q00808
- 55 F-HEMBA1002227
MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MARCKS) (ACAMP-81).
0.00063:21:100
BOS TAURUS (BOVINE).
P12624
- F-HEMBA1002239

!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!

1.5e-33:101:70

HOMO SAPIENS (HUMAN).

P39192

5

F-HEMBA1002316

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

4.6e-08:186:32

SORGHUM VULGARE (SORGHUM).

10

P24152

F-HEMBA1002420

WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

0.0078:19:68

15

MUS MUSCULUS (MOUSE).

P70315

F-HEMBA1002421

SYNDECAN-2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2).

20

1.1e-52:107:97

HOMO SAPIENS (HUMAN).

P34741

25

F-HEMBA1002524

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

5.0e-05:104:34

RATTUS NORVEGICUS (RAT).

P04474

30

F-HEMBA1002551

HYPOTHETICAL WD-REPEAT PROTEIN SLR0143.

9.9e-09:128:29

SYNECHOCYSTIS SP. (STRAIN PCC 6803).

35

P74442

F-HEMBA1002767

N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).

40

8.0e-92:246:67

MUS MUSCULUS (MOUSE).

P15535

45

F-HEMBA1002985

TRANSCRIPTION FACTOR GATA-6 (GATA BINDING FACTOR-6).

0.060:49:34

MUS MUSCULUS (MOUSE).

Q61169

50

F-HEMBA1002992

HOLOTRICIN 3 PRECURSOR.

0.0035:64:37

HOLOTRICHIA DIOMPHALIA.

55

Q25055

F-HEMBA1003047

BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).

- 1.5e-23:216:31
HOMO SAPIENS (HUMAN).
P13497
- 5 F-HEMBA1003072
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
6.8e-09:129:41
MUS MUSCULUS (MOUSE).
P05142
- 10 F-HEMBA1003101
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
2.2e-10:124:37
HOMO SAPIENS (HUMAN).
15 P08123
- F-HEMBA1003120
ZINC FINGER PROTEIN 140.
4.8e-23:43:74
20 HOMO SAPIENS (HUMAN).
P52738
- F-HEMBA1003230
FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90).
25 2.7e-41:239:39
MUS MUSCULUS (MOUSE).
Q08878
- F-HEMBA1003294
30 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
7.0e-34:84:69
HOMO SAPIENS (HUMAN).
P39194
- F-HEMBA1003315
35 GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).
0.00012:178:32
PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).
40 P10496
- F-HEMBA1003392
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
ROGLOBULIN RECEPTOR) (A2MR).
1.1e-31:202:37
45 GALLUS GALLUS (CHICKEN).
P98157
- F-HEMBA1003399
MVP1 PROTEIN.
50 5.6e-12:67:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40959
- F-HEMBA1003487
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
4.5e-08:175:29
MUS MUSCULUS (MOUSE).
P05142

- 5 F-HEMBA1003497
ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1)
(ZINC FINGER PROTEIN Z13).
9.3e-18:171:33
MUS MUSCULUS (MOUSE).
Q60821
- 10 F-HEMBA1003530
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
9.9e-12:122:35
HOMO SAPIENS (HUMAN).
P81489
- 15 F-HEMBA1003602
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.98:114:33
MUS MUSCULUS (MOUSE).
P05143
- 20 F-HEMBA1003732
TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.35:225:28
PSEUDOMONAS AERUGINOSA.
P15276
- 25 F-HEMBA1003945
HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I.
2.9e-48:268:41
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09895
- 30 F-HEMBA1004007
THYROID TRANSCRIPTION FACTOR 1 (THYROID NUCLEAR FACTOR 1) (TTF-1) (FRAGMENT).
0.90:60:30
CAVIA PORCELLUS (GUINEA PIG).
P97273
- 35 F-HEMBA1004067
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
3.0e-05:200:31
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 40 F-HEMBA1004085
GLUCOSE REPRESSION MEDIATOR PROTEIN.
0.0030:190:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P14922
- 45 F-HEMBA1004110
EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).
1.2e-14:102:36
MUS MUSCULUS (MOUSE).
P42567
- 50 F-HEMBA1004250
CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

EP 1 130 094 A2

1.8e-08:150:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P33450

5 F-HEMBA1004391
TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.
4.5e-09:96:35
MUS MUSCULUS (MOUSE).
P70211

10 F-HEMBA1004444
GLYCOPROTEIN 25L PRECURSOR (GP25L).
4.6e-41:148:52
CANIS FAMILIARIS (DOG).
15 P27869

F-HEMBA1004454
CD9 ANTIGEN.
0.0070:24:70
20 BOS TAURUS (BOVINE).
P30932

F-HEMBA1004505
25 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).
7.0e-45:239:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P53624

30 F-HEMBA1004785
MODIFIER 3 PROTEIN (M33).
7.4e-26:76:61
MUS MUSCULUS (MOUSE).
P30658

35 F-HEMBA1004797
PROTEIN Q300.
0.00071:21:66
MUS MUSCULUS (MOUSE).
40 Q02722

F-HEMBA1004952
EBNA-1 NUCLEAR PROTEIN.
2.4e-05:67:49
45 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

F-HEMBA1004971

50 F-HEMBA1004982
MULTIDRUG RESISTANCE PROTEIN 2 (MULTIDRUG-EFFLUX TRANSPORTER 2).
8.6e-08:144:25
BACILLUS SUBTILIS.
P39843

55 F-HEMBA1005070
HYPOTHETICAL PROTEIN KIAA0310.
1.0e-38:140:68

- HOMO SAPIENS (HUMAN).
O15027
- 5 F-HEMBA1005084
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
2.5e-10:102:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160
- 10 F-HEMBA1005145
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.8e-06:85:37
MUS MUSCULUS (MOUSE).
P05142
- 15 F-HEMBA1005230
ZINC FINGER PROTEIN 140.
8.2e-20:83:66
HOMO SAPIENS (HUMAN).
20 P52738
- F-HEMBA1005246
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).
25 1.5e-09:132:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480
- 30 F-HEMBA1005267
B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN).
1.9e-15:192:32
HOMO SAPIENS (HUMAN).
P20749
- 35 F-HEMBA1005337
ACIDIC PHOSPHOPROTEIN PRECURSOR (50 KD ANTIGEN).
8.0e-05:31:64
PLASMODIUM CHABAUDI.
Q02752
- 40 F-HEMBA1005430
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.34:42:42
DROSOPHILA MELANOGASTER (FRUIT FLY).
45 Q01643
- F-HEMBA1005449
PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PSA-1).
50 4.5e-09:95:33
TRYPANOSOMA BRUCEI BRUCEI.
Q06084
- 55 F-HEMBA1005489
CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110).
7.2e-05:90:36
HOMO SAPIENS (HUMAN).
Q15700

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- 5 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).
3.3e-17:78:51
ORYCTOLAGUS CUNICULUS (RABBIT).
P98139
- 10 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3.
7.2e-91:211:85
HOMO SAPIENS (HUMAN).
P20309
- 15 F-HEMBA1005698
PROTEIN TRANSPORT PROTEIN SEC22 (PROTEIN SLY2).
3.3e-08:132:28
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22214
- 20 F-HEMBA1005913
HYPOTHETICAL 5.8 KD PROTEIN.
0.97:43:30
CLOVER YELLOW MOSAIC VIRUS (CYMV).
P16485
- 25 F-HEMBA1005929
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
6.6e-104:275:72
HOMO SAPIENS (HUMAN).
P27448
- 30 F-HEMBA1005945
BRITTLE-1 PROTEIN PRECURSOR.
7.8e-30:214:35
ZEA MAYS (MAIZE).
35 P29518
- 40 F-HEMBA1006016
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
1.9e-07:34:76
HOMO SAPIENS (HUMAN).
P39188
- 45 F-HEMBA1006171
PROBABLE E5 PROTEIN.
0.98:66:31
HUMAN PAPILLOMAVIRUS TYPE 33.
P06426
- 50 F-HEMBA1006276
ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
4.1e-07:56:57
MUS MUSCULUS (MOUSE).
Q61967
- 55 F-HEMBA1006299
BASIC PROLINE-RICH PEPTIDE P-E (IB-9).
0.11:38:28
HOMO SAPIENS (HUMAN).

- P02811
- F-HEMBA1006311
ZINC FINGER PROTEIN 23 (ZINC FINGER PROTEIN KOX16) (FRAGMENT).
5 0.91:22:45
HOMO SAPIENS (HUMAN).
P17027
- F-HEMBA1006335
10 PERIPHERAL MYELIN PROTEIN 22 (PMP-22) (GROWTH-ARREST-SPECIFIC PROTEIN 3) (GAS3).
0.017:125:27
MUS MUSCULUS (MOUSE).
P16646
- F-HEMBA1006357
15 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.
5.2e-40:136:52
HOMO SAPIENS (HUMAN).
O15127
- F-HEMBA1006430
20 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.
2.7e-38:96:72
CAENORHABDITIS ELEGANS.
25 P46975
- F-HEMBA1006482
SCO1 PROTEIN PRECURSOR.
7.1e-25:84:45
30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23833
- F-HEMBA1006517
HYPOTHETICAL 93.4 KD PROTEIN IN STE3-GIN10 INTERGENIC REGION.
35 0.48:145:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34239
- F-HEMBA1006544
40 TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
7.0e-11:210:37
HOMO SAPIENS (HUMAN).
000268
- F-HEMBA1006572
45 ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).
0.011:50:40
GALLUS GALLUS (CHICKEN).
Q03352
- F-HEMBA1006658
50 SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).
4.6e-44:234:45
CAENORHABDITIS ELEGANS.
55 Q23356
- F-HEMBA1006707
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).

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- 9.3e-34:159:50
GALLUS GALLUS (CHICKEN).
P05099
- 5 F-HEMBA1006724
PLATELET FACTOR 4 (PF-4).
0.025:65:27
SUS SCROFA (PIG).
P30034
- 10 F-HEMBA1006749
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
7.9e-37:147:53
GALLUS GALLUS (CHICKEN).
15 P05099
- F-HEMBA1006770
FLOWERING TIME CONTROL PROTEIN FCA.
3.4e-27:139:39
20 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
004425
- F-HEMBA1006902
CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).
25 1.5e-37:137:51
GALLUS GALLUS (CHICKEN).
P05099
- F-HEMBA1006912
30 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
0.27:121:29
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
35 P08393
- F-HEMBA1006916
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
1.1e-05:163:30
40 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-HEMBA1006960
SMALL PROLINE-RICH PROTEIN 2-1.
1.0:34:35
45 HOMO SAPIENS (HUMAN).
P35326
- F-HEMBA1007013
S-ANTIGEN PROTEIN PRECURSOR.
50 2.8e-09:226:28
PLASMODIUM FALCIPARUM (ISOLATE V1).
P09593
- F-HEMBA1007057
55 PROCYCLIC FORM SPECIFIC POLYPEPTIDE B-ALPHA PRECURSOR (PROCYCLIN) (PARP B-ALPHA) (PS-
SA-1).
4.0e-10:33:72
TRYPANOSOMA BRUCEI BRUCEI.

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- Q06084
- 5 F-HEMBA1007063
AGAMOUS PROTEIN.
1.0:40:42
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P17839
- 10 F-HEMBA1007226
PUTATIVE CUTICLE COLLAGEN C09G5.5.
0.10:105:38
CAENORHABDITIS ELEGANS.
Q09456
- 15 F-HEMBA1007241
HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.
3.3e-15:106:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40857
- 20 F-HEMBA1007291
RETINOIC ACID RECEPTOR RXR-BETA.
0.0013:124:33
HOMO SAPIENS (HUMAN).
25 P28702
- F-HEMBA1007332
ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR).
0.0024:130:34
30 MUS MUSCULUS (MOUSE).
Q01338
- F-HEMBA1000106
CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).
35 9.5e-09:99:33
MUS MUSCULUS (MOUSE).
P53996
- F-HEMBA1000276
40 F-HEMBA1000309
- F-HEMBA1000407
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
45 0.38:99:34
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
P28284
- F-HEMBA1000447
50 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
0.0076:80:31
PLASMODIUM LOPHURAE.
P04929
- 55 F-HEMBA1000542
BETA-2 BUNGAROTOXIN B CHAIN PRECURSOR (BUNGAROTOXIN, B2 CHAIN).
0.017:53:33
BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).

- P00989
- 5 F-HEMBB1000567
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.0e-05:131:29
PLASMODIUM LOPHURAE.
P04929
- 10 F-HEMBB1000642
BASIC PROLINE-RICH PEPTIDE IB-1.
0.0074:66:31
HOMO SAPIENS (HUMAN).
P04281
- 15 F-HEMBB1000668
VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.
7.3e-10:184:32
PODOSPORA ANSERINA.
Q00808
- 20 F-HEMBB1000679
TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN).
9.5e-73:204:69
CANIS FAMILIARIS (DOG).
25 Q01685
- F-HEMBB1000881
F-SPONDIN PRECURSOR.
1.2e-23:191:37
30 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447
- F-HEMBB1000905
TRANSCRIPTIONAL REPRESSOR RCO-1.
35 0.068:105:34
NEUROSPORA CRASSA.
P78706
- 40 F-HEMBB1001026
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
1.3e-11:138:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
45 P32802
- F-HEMBB1001048
SARCALUMENIN PRECURSOR.
3.1e-20:151:32
ORYCTOLAGUS CUNICULUS (RABBIT).
50 P13666
- F-HEMBB1001200
HYPOTHETICAL GENE 51 MEMBRANE PROTEIN.
1.0:66:27
55 ICTALURID HERPESVIRUS 1 (CHANNEL CATFISH VIRUS) (CCV).
Q00135
- F-HEMBB1001407

!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!

2.0e-24:58:60

HOMO SAPIENS (HUMAN).

P39194

5

F-HEMBB1001530

SLS1 PROTEIN PRECURSOR.

0.0012:37:51

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).

10

Q99158

F-HEMBB1001547

HYPOTHETICAL 71.7 KD PROTEIN F52H3.2 IN CHROMOSOME II.

4.1e-49:200:55

15

CAENORHABDITIS ELEGANS.

Q20680

F-HEMBB1001573

PROTEIN Q300.

20

0.0055:27:62

MUS MUSCULUS (MOUSE).

Q02722

F-HEMBB1001847

25

ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP33).

7.8e-05:166:31

RATTUS NORVEGICUS (RAT).

P04474

30

F-HEMBB1001959

CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).

8.8e-15:97:38

PETROMYZON MARINUS (SEA LAMPREY).

35

P25210

F-HEMBB1001978

MICROCIN B17 PROCESSING PROTEIN MCBC.

0.049:100:31

40

ESCHERICHIA COLI.

P23185

F-HEMBB1002039

COLD SHOCK PROTEIN CSPB (FRAGMENT).

45

0.98:32:40

BACILLUS GLOBISPORUS.

P41018

F-HEMBB1002041

50

REGULATORY PROTEIN E2.

0.010:145:35

HUMAN PAPILLOMAVIRUS TYPE 47.

P22420

55

F-HEMBB1002051

FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).

0.0056:89:31

HOMO SAPIENS (HUMAN).

Q01543

F-HEMBB1002120

UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT
(EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).

1.4e-08:154:30

RATTUS NORVEGICUS (RAT).

P56558

F-HEMBB1002162

IMMEDIATE-EARLY PROTEIN IE180.

0.86:130:31

PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).

P11675

F-HEMBB1002228

PTB-ASSOCIATED SPLICING FACTOR (PSF).

0.00092:97:34

HOMO SAPIENS (HUMAN).

P23246

F-HEMBB1002245

PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).

2.5e-55:128:88

RATTUS NORVEGICUS (RAT).

Q62786

F-HEMBB1002302

REGULATORY PROTEIN E2.

0.042:100:37

HUMAN PAPILLOMAVIRUS TYPE 25.

P36787

F-HEMBB1002427

FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOS-
YLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).

5.0e-15:53:54

HOMO SAPIENS (HUMAN).

P16442

F-HEMBB1002465

ACYL-COA DEHYDROGENASE (EC 1.3.99.-).

8.2e-35:162:50

BACILLUS SUBTILIS.

P45857

F-HEMBB1002661

TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).

2.2e-18:159:40

GALLUS GALLUS (CHICKEN).

057337

F-HEMBB1002663

F-HEMBB1002693

GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN

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P30; NUCLEOPROTEIN P10].
0.83:74:28
DUPLAN MURINE LEUKEMIA VIRUS.
P23090

5

F-MAMMA1000046
!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!
2.3e-24:98:67
HOMO SAPIENS (HUMAN).
P39191

10

F-MAMMA1000102
APOLIPOPROTEIN L PRECURSOR (APO-L).
4.3e-22:213:34
HOMO SAPIENS (HUMAN).
O14791

15

F-MAMMA1000106
PSTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP).
1.6e-07:99:31
NICOTIANA TABACUM (COMMON TOBACCO).
Q03211

20

F-MAMMA1000118
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).
0.00059:155:30
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

25

F-MAMMA1000141
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
0.00011:39:66
HOMO SAPIENS (HUMAN).
P39195

30

F-MAMMA1000204
SYNAPTOTAGMIN III (SYTIII).
5.9e-05:93:33
MUS MUSCULUS (MOUSE).
035681

35

F-MAMMA1000226
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DX5 PRECURSOR.
4.6e-06:224:28
TRITICUM AESTIVUM (WHEAT).
P10388

40

F-MAMMA1000403
COLLAGEN ALPHA 1(IX) CHAIN PRECURSOR (FRAGMENTS).
1.1e-06:158:35
GALLUS GALLUS (CHICKEN).
P12106

45

F-MAMMA1000449
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
6.3e-05:137:32
HOMO SAPIENS (HUMAN).
P17600

50

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5 F-MAMMA1000457
NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2).
7.6e-48:151:62
BOS TAURUS (BOVINE).
P07514

10 F-MAMMA1000473
SPERM PROTAMINE P1.
0.024:29:44
DROMICIOPS AUSTRALIS (MONITO DEL MONTE) (DROMICIOPS GLIROIDES). P42132

15 F-MAMMA1000496
HYPOTHETICAL 73.0 KD PROTEIN IN CLA4-MID1 INTERGENIC REGION.
9.8e-09:188:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48566

20 F-MAMMA1000528
DNA BINDING PROTEIN S1FA.
0.77:43:37
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P42551

25 F-MAMMA1000591
SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.018:88:32
HOMO SAPIENS (HUMAN).
P10163

30 F-MAMMA1000614
HYPOTHETICAL 29.3 KD PROTEIN (ORF92).
7.5e-08:148:36
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV). O10341

35 F-MAMMA1000652
!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!
5.3e-36:56:85
HOMO SAPIENS (HUMAN).
P39189

40 F-MAMMA1000681
PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.
7.5e-41:167:51
MUS MUSCULUS (MOUSE).
008530

45 F-MAMMA1000706
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
8.1e-10:135:38
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333

50 F-MAMMA1000788
HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.
2.0e-06:214:32
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P53214

55

5 F-MAMMA1000810
REGULATORY PROTEIN E2.
0.0031:132:31
HUMAN PAPILLOMAVIRUS TYPE 9.
P36780

10 F-MAMMA1000814
PROTEIN Q300.
1.6e-05:27:66
MUS MUSCULUS (MOUSE).
Q02722

15 F-MAMMA1000881
SERINE/THREONINE-PROTEIN KINASE SGK (EC 2.7.1.-) (SERUM/GLUCOCORTICOID-REGULATED KI-
NASE).
2.7e-10:81:45
RATTUS NORVEGICUS (RAT).
Q06226

20 F-MAMMA1000986
INVOLUCRIN.
0.95:125:24
SUS SCROFA (PIG).
P18175

25 F-MAMMA1000994
CUTICLE COLLAGEN 2C (FRAGMENT).
0.00062:97:34
HAEMONCHUS CONTORTUS.
30 P16252

F-MAMMA1001043
MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).
4.5e-05:162:25
35 RATTUS NORVEGICUS (RAT).
P10252

F-MAMMA1001066
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
40 2.6e-06:33:72
HOMO SAPIENS (HUMAN).
P20931

F-MAMMA1001094
45 PUTATIVE GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION C16C9.04C.
1.1e-21:175:38
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09818

50 F-MAMMA1001141
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.13:196:27
HOMO SAPIENS (HUMAN).
P23246

55 F-MAMMA1001150
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
9.4e-89:256:67

- HOMO SAPIENS (HUMAN).
Q15139
- 5 F-MAMMA1001237
MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).
3.5e-19:103:43
MESOCRICETUS AURATUS (GOLDEN HAMSTER).
P53988
- 10 F-MAMMA1001284
AUTOIMMUNE REGULATOR (APECED PROTEIN).
0.027:178:30
HOMO SAPIENS (HUMAN).
043918
- 15 F-MAMMA1001310
HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC RE-
GION.
1.9e-14:151:31
- 20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q04225
- F-MAMMA1001344
MALE SPECIFIC SPERM PROTEIN MST84DC.
25 0.16:35:42
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01644
- F-MAMMA1001418
30 HYPOTHETICAL PROTEIN HI0519.
3.5e-27:181:38
HAEMOPHILUS INFLUENZAE.
P44742
- F-MAMMA1001532
35 ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).
1.1e-34:78:58
MUS MUSCULUS (MOUSE).
Q61967
- 40 F-MAMMA1001609
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
0.20:137:27
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
45 P28284
- F-MAMMA1001615
5E5 ANTIGEN.
2.3e-07:205:34
50 RATTUS NORVEGICUS (RAT).
Q63003
- F-MAMMA1001623
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
55 4.8e-30:90:77
HOMO SAPIENS (HUMAN).
Q03468

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5 F-MAMMA1001634
B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).
6.1e-11:44:61
HOMO SAPIENS (HUMAN).
P20931

10 F-MAMMA1001893
COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR.
0.0013:174:36
HOMO SAPIENS (HUMAN).
P12107

15 F-MAMMA1001901
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
1.3e-21:65:66
HOMO SAPIENS (HUMAN).
P39195

20 F-MAMMA1001957
VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTEIN TU-4) (PROTEIN SV23).
0.0055:104:35
DROSOPHILA MELANOGASTER (FRUIT FLY).
P13238

25 F-MAMMA1001978
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00030:101:44
HOMO SAPIENS (HUMAN).
P21917

30 F-MAMMA1002070
PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).
1.4e-08:103:33
RATTUS NORVEGICUS (RAT).
35 Q01177

40 F-MAMMA1002080
FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR.
8.2e-08:131:32
LYMNAEA STAGNALIS (GREAT POND SNAIL).
P42565

45 F-MAMMA1002087
MALE SPECIFIC SPERM PROTEIN MST84DD.
0.65:24:45
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01645

50 F-MAMMA1002091
APYRASE PRECURSOR (EC 3.6.1.5) (ATP-DIPHOSPHATASE) (ADENOSINE DIPHOSPHATASE) (ADPASE)
(ATP-DIPHOSPHOHYDROLASE).
2.6e-24:155:43
SOLANUM TUBEROSUM (POTATO).
P80595

55 F-MAMMA1002095
CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).
2.3e-58:213:56

YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
043108

5 F-MAMMA1002128
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
9.9e-05:72:40
RATTUS NORVEGICUS (RAT).
P02454

10 F-MAMMA1002142
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
2.1e-13:149:34
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P18160

15 F-MAMMA1002165
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
8.4e-06:47:57
HOMO SAPIENS (HUMAN).
20 P29279

F-MAMMA1002205
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
5.9e-26:56:78
25 HOMO SAPIENS (HUMAN).
P39188

F-MAMMA1002224
!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
30 3.7e-16:62:67
HOMO SAPIENS (HUMAN).
P39194

F-MAMMA1002234
35 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
3.5e-105:242:85
CANIS FAMILIARIS (DOG).
Q00004

40 F-MAMMA1002586
MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSI-
DASE) (ALPHA-MANNOSIDASE 1A).
4.7e-24:203:35
MUS MUSCULUS (MOUSE).
45 P45700

F-MAMMA1002633
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
7.3e-27:49:73
50 HOMO SAPIENS (HUMAN).
P39188

F-MAMMA1003126
55 SARCALUMENIN PRECURSOR.
7.9e-30:156:35
ORYCTOLAGUS CUNICULUS (RABBIT).
P13666

- 5 F-NT2RM1000407
LACTOSE OPERON REPRESSOR.
1.4e-07:36:86
ESCHERICHIA COLI.
P03023
- 10 F-NT2RM1000462
ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).
6.7e-11:85:41
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P15287
- 15 F-NT2RM1000542
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
3.5e-19:104:48
FELIS SILVESTRIUS CATUS (CAT).
O19015
- 20 F-NT2RM1000580
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
3.4e-36:180:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 25 F-NT2RM1000789
T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1) (T-CELL FACTOR 1) (TRANSCRIPTION FACTOR-7).
1.5e-40:112:75
MUS MUSCULUS (MOUSE).
Q00417
- 30 F-NT2RM1000855
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
2.5e-81:152:94
CANIS FAMILIARIS (DOG).
P38377
- 35 F-NT2RM1000858
HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME II.
3.1e-50:127:54
CAENORHABDITIS ELEGANS.
Q09201
- 40 F-NT2RM1000899
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
6.6e-17:107:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 50 F-NT2RM2000241
DOUBLESEX PROTEIN, MALE-SPECIFIC.
0.0021:64:32
DROSOPHILA MELANOGASTER (FRUIT FLY).
P23023
- 55 F-NT2RM2000306
PUTATIVE GTP-BINDING PROTEIN W08E3.3.
1.1e-69:198:69
CAENORHABDITIS ELEGANS.

- P91917
- 5 F-NT2RM2000410
BETA-LYTIC METALLOENDOPEPTIDASE PRECURSOR (EC 3.4.24.32) (BETA-LYTIC PROTEASE).
0.73:118:31
ACHROMOBACTER LYTICUS.
P27458
- 10 F-NT2RM2000423
BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR.
1.3e-23:235:34
HOMO SAPIENS (HUMAN).
P16279
- 15 F-NT2RM2000497
DNA-REPAIR PROTEIN COMPLEMENTING XP-D CELLS (XERODERMA PIGMENTOSUM GROUP D COM-
PLEMENTING PROTEIN) (DNA EXCISION REPAIR PROTEIN ERCC-2).
9.4e-19:199:31
CRICETULUS GRISEUS (CHINESE HAMSTER).
20 Q60452
- F-NT2RM2000514
HYPOTHETICAL PROTEIN HI1558.
7.7e-06:82:34
25 HAEMOPHILUS INFLUENZAE.
P45252
- F-NT2RM2000565
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
30 2.8e-57:232:52
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782
- F-NT2RM2000582
35 PROTEIN Q300.
0.066:13:84
MUS MUSCULUS (MOUSE).
Q02722
- 40 F-NT2RM2000589
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
2.1e-07:90:32
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
45 P54644
- F-NT2RM2000622
GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PRECURSOR.
1.9e-07:133:35
TRITICUM AESTIVUM (WHEAT).
50 P08489
- F-NT2RM2000632
EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).
4.6e-28:194:35
55 HOMO SAPIENS (HUMAN).
Q03468
- F-NT2RM2000773

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MYC-ASSOCIATED ZINC FINGER PROTEIN (MAZI) (PUR-1) (ZF87).
3.4e-24:156:47
HOMO SAPIENS (HUMAN).
P56270

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F-NT2RM2001126
NEURON-SPECIFIC X11 PROTEIN (FRAGMENT).
1.5e-05:118:32
MUS MUSCULUS (MOUSE).
P98084

10

F-NT2RM2001558
MAJOR FIBROUS SHEATH PROTEIN PRECURSOR (FSC1) (P82).
1.9e-24:164:40
MUS MUSCULUS (MOUSE).
Q60662

15

F-NT2RM2001626
HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.
1.6e-09:206:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47179

20

F-NT2RM2001643
HYPOTHETICAL PROTEIN MJ1025.
0.21:203:22
METHANOCOCCUS JANNASCHII.
Q58431

25

F-NT2RM2001738
REGULATORY PROTEIN E2.
0.0076:124:31
HUMAN PAPILLOMAVIRUS TYPE 25.
P36787

30

F-NT2RM2001767
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0068:115:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439

35

F-NT2RM2001792
FIBRINOGEN BETA CHAIN.
4.3e-25:121:45
BOS TAURUS (BOVINE).
P02676

40

F-NT2RM2001818
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
2.4e-06:192:32
ZEA MAYS (MAIZE).
P14918

45

F-NT2RM2001902
SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3)
(P65-PAK).
2.3e-52:250:45
RATTUS NORVEGICUS (RAT).

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Q62829

5 F-NT2RM2001939
PROBABLE G PROTEIN-COUPLEID RECEPTOR GPR19 (GPR-NGA).
4.0e-97:204:92
HOMO SAPIENS (HUMAN).
Q15760

10 F-NT2RM2001941
MUSCARINIC ACETYLCHOLINE RECEPTOR M4.
1.0e-34:184:32
HOMO SAPIENS (HUMAN).
P08173

15 F-NT2RM4000100
EBNA-1 NUCLEAR PROTEIN.
1.7e-05:86:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

20 F-NT2RM4000115
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1).
9.5e-05:116:35
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P36594

25 F-NT2RM4000198
BUTYROPHILIN PRECURSOR (BT).
8.6e-14:162:33
MUS MUSCULUS (MOUSE).
Q62556

30 F-NT2RM4000284
COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).
0.86:95:37
HOMO SAPIENS (HUMAN).
P12110

35 F-NT2RM4000295
COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.
1.1e-08:229:34
HOMO SAPIENS (HUMAN).
Q07092

40 F-NT2RM4000326
SH3 DOMAIN-BINDING PROTEIN 3BP-2.
6.1e-05:187:31
HOMO SAPIENS (HUMAN).
P78314

45 F-NT2RM4000417
SYNAPTOTAGMIN (P65).
4.2e-08:72:52
APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).
P41823

50 F-NT2RM4000444
ANTIGEN PEPTIDE TRANSPORTER 1 (APT1) (PEPTIDE TRANSPORTER TAP1) (PEPTIDE TRANSPORTER

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PSF1) (PEPTIDE SUPPLY FACTOR 1) (PSF-1) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESS-
ING 1).
1.1e-36:192:41
HOMO SAPIENS (HUMAN).
5 Q03518

F-NT2RM4000587
COLLAGEN ALPHA 1(II) CHAIN (FRAGMENTS).
1.8e-13:200:38
10 BOS TAURUS (BOVINE).
P02459

F-NT2RM4000593

15 F-NT2RM4000648
K-GLYPICAN PRECURSOR.
6.4e-67:180:68
MUS MUSCULUS (MOUSE).
P51655

20 F-NT2RM4000761
CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).
2.3e-53:107:81
RATTUS NORVEGICUS (RAT).
25 P05503

F-NT2RM4000965
PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).
4.9e-14:188:34
30 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
060100

F-NT2RM4000997
HISTONE H1C (CLONE XLHW2).
35 0.88:73:26
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P15866

F-NT2RM4001321
40 HOMEBOX PROTEIN HOX-A2...
0.27:77:37
GALLUS GALLUS (CHICKEN).
Q08727

45 F-NT2RM4001325
CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).
3.8e-30:184:39
GALLUS GALLUS (CHICKEN).
Q92179

50 F-NT2RM4001377
HYPOTHETICAL BHLF1 PROTEIN.
5.9e-06:216:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
55 P03181

F-NT2RM4001735
GNS 1 PROTEIN.

- 0.0028:114:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- 5 F-NT2RM4001768
PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).
8.6e-24:205:36
STREPTOMYCES ANTIBIOTICUS.
Q03326
- 10 F-NT2RM4001843
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).
4.6e-33:258:37
XANTHOMONAS MANIHOTIS.
P48982
- 15 F-NT2RM4002352
BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).
1.0e-15:85:45
20 CAENORHABDITIS ELEGANS.
Q06561
- F-NT2RP1000002
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
25 0.00011:24:62
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- F-NT2RP1000050
30 A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
2.5e-07:198:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- F-NT2RP1000181
35 CYTOCHROME B5.
4.4e-11:117:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40312
- 40 F-NT2RP1000239
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).
7.8e-05:141:33
HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).
45 P28284
- F-NT2RP1000261
ORM1 PROTEIN.
2.2e-18:137:35
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- F-NT2RP1000271
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
55 8.3e-81:194:70
HOMO SAPIENS (HUMAN).
Q03923

- 5 F-NT2RP1000300
HYPOTHETICAL 57.1 KD PROTEIN IN MAP2-TEL1 INTERGENIC REGION.
2.0e-07:202:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38176
- 10 F-NT2RP1000325
MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR.
1.6e-55:86:81
HOMO SAPIENS (HUMAN).
Q00325
- 15 F-NT2RP1000448
PROLINE-RICH PEPTIDE P-B.
0.094:32:43
HOMO SAPIENS (HUMAN).
P02814
- 20 F-NT2RP1000465
EBNA-1 NUCLEAR PROTEIN.
3.1e-07:101:39
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 25 F-NT2RP1000468
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DIVA BINDING PROTEIN SUBUNIT B).
1.4e-14:97:38
PETROMYZON MARINUS (SEA LAMPREY).
30 P25210
- F-NT2RP1000551
INTERFERON-RELATED PROTEIN PC4 (TPA INDUCED SEQUENCE 7) (TIS7 PROTEIN).
1.9e-33:221:41
35 MUS MUSCULUS (MOUSE).
P19182
- F-NT2RP1000579
SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR (EC 1.3.5.1) (FP)
40 (FLAVOPROTEIN SUBUNIT OF COMPLEX II).
3.4e-68:247:62
HOMO SAPIENS (HUMAN).
P31040
- 45 F-NT2RP1000613
CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).
1.9e-19:137:37
OVIS ARIES (SHEEP).
50 P08060
- F-NT2RP1000679
EBNA-1 NUCLEAR PROTEIN.
0.00055:54:50
55 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- F-NT2RP1000740
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).

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- 0.071:71:45
HOMO SAPIENS (HUMAN).
000268
- 5 F-NT2RP1000903
SPORE COAT PROTEIN SP96.
0.016:124:26
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P14328
- 10 F-NT2RP1000981
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.1e-08:196:28
HOMO SAPIENS (HUMAN).
15 Q99795
- F-NT2RP1001004
F-SPONDIN PRECURSOR.
1.2e-11:155:31
20 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P35447
- F-NT2RP1001020
SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
25 2.2e-05:126:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458
- F-NT2RP1001031
30 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
5.8e-26:159:38
THERMOMONOSPORA CURVATA.
P49695
- F-NT2RP1001563
35 METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).
0.00036:42:40
BOS TAURUS (BOVINE).
P37359
- 40 F-NT2RP2000092
ZINC FINGER PROTEIN 136.
2.9e-44:129:62
HOMO SAPIENS (HUMAN).
45 P52737
- F-NT2RP2000178
HOMEOTIC GENE REGULATOR (BRAHMA PROTEIN).
0.0050:75:37
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P25439
- F-NT2RP2000240
PUTATIVE CUTICLE COLLAGEN C09G5.5.
55 9.2e-08:137:34
CAENORHABDITIS ELEGANS.
Q09456

- 5 F-NT2RP2000394
PROCYCLIC FORM SPECIFIC POLYPEPTIDE A-BETA PRECURSOR (PROCYCLIN) (PARP A-BETA).
0.00019:28:64
TRYPANOSOMA BRUCEI BRUCEI.
P09791
- 10 F-NT2RP2000447
GOLGIN-95.
6.4e-25:55:67
HOMO SAPIENS (HUMAN).
Q08379
- 15 F-NT2RP2000479
PROBABLE E5B PROTEIN.
1.0:32:37
HUMAN PAPILLOMAVIRUS TYPE 6B.
P06461
- 20 F-NT2RP2000514
AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).
1.5e-18:201:33
HOMO SAPIENS (HUMAN).
Q02246
- 25 F-NT2RP2000533
CORNICHON PROTEIN.
5.6e-52:144:65
DROSOPHILA MELANOGASTER (FRUIT FLY).
P49858
- 30 F-NT2RP2000610
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-
BOX DNA BINDING PROTEIN SUBUNIT B).
8.7e-15:97:38
35 PETROMYZON MARINUS (SEA LAMPREY).
P25210
- 40 F-NT2RP2000616
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
0.028:163:30
MUS MUSCULUS (MOUSE).
P11087
- 45 F-NT2RP2000649
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
9.5e-22:241:32
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071
- 50 F-NT2RP2000663
PANCREATIC HORMONE PRECURSOR (PANCREATIC POLYPEPTIDE) (PP).
0.71:28:46
GALLUS GALLUS (CHICKEN), AND MELEAGRIS GALLOPAVO (COMMON TURKEY).
55 P01306
- F-NT2RP2000694
WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).

- 8.8e-10:90:42
MUS MUSCULUS (MOUSE).
P70315
- 5 F-NT2RP2000712
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
2.3e-50:166:50
HOMO SAPIENS (HUMAN).
Q03923
- 10 F-NT2RP2000739
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
8.9e-45:180:43
HOMO SAPIENS (HUMAN).
15 Q03923
- F-NT2RP2000818
SYG1 PROTEIN.
2.4e-14:164:35
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40528
- F-NT2RP2000903
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
25 0.28:149:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP2001200
30 MIC1 PROTEIN.
1.8e-13:115:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53258
- F-NT2RP2001223
35 CCAAT DISPLACEMENT PROTEIN (HOMEODOMAIN PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.00017:92:35
CANIS FAMILIARIS (DOG).
P39881
- 40 F-NT2RP2001276
NPDC-1 PROTEIN PRECURSOR.
4.9e-35:96:71
MUS MUSCULUS (MOUSE).
45 Q64322
- F-NT2RP2001388
CECROPIN B PRECURSOR.
0.98:31:51
50 DROSOPHILA MELANOGASTER (FRUIT FLY).
P14956
- F-NT2RP2001469
VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.
55 6.0e-07:146:22
PODOSPORA ANSERINA.
Q00808

- 5 F-NT2RP2001480
THROMBOSPONDIN 3 PRECURSOR.
2.1e-100:209:88
HOMO SAPIENS (HUMAN).
P49746
- 10 F-NT2RP2001495
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
3.1e-11:174:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981
- 15 F-NT2RP2001514
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
4.0e-18:163:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- 20 F-NT2RP2001529
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
4.4e-83:186:78
HOMO SAPIENS (HUMAN).
P53355
- 25 F-NT2RP2001538
PAIRED AMPHIPATHIC HELIX PROTEIN.
1.7e-06:152:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579
- 30 F-NT2RP2001562
CLATHRIN LIGHT CHAIN B (BRAIN AND LYMPHOCYTE LCB).
0.0093:124:27
HOMO SAPIENS (HUMAN).
35 P09497
- 40 F-NT2RP2001662
5'-TG-3'INTERACTING FACTOR (HOMEBOX PROTEIN TGIF).
5.6e-36:146:57
HOMO SAPIENS (HUMAN).
Q15583
- 45 F-NT2RP2001755
F-SPONDIN PRECURSOR.
1.2e-33:84:89
RATTUS NORVEGICUS (RAT).
P35446
- 50 F-NT2RP2001769
PROTEIN KINASE CEK1 (EC 2.7.1.-).
1.3e-37:159:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P38938
- 55 F-NT2RP2001817
HST1 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 1).
6.4e-32:85:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

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P53685

F-NT2RP2001878

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

5 1.1e-06:173:28

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-NT2RP2001903

10 CALPAIN P94, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEUTRAL PROTEIN-ASE) (CANP) (P94 PROTEIN) (MUSCLE-SPECIFIC CALCIUM-ACTIVATED NEUTRAL PROTEASE 3 LARGE SUBUNIT).

2.4e-10:110:37

HOMO SAPIENS (HUMAN).

15 P20807

F-NT2RP2001915

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN).

0.0069:74:39

20 HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52).

P28284

F-NT2RP2001921

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).

25 0.016:51:45

BOVINE HERPESVIRUS TYPE 1 (STRAIN K22).

P29836

F-NT2RP2001948

30 COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.

6.7e-08:121:37

HOMO SAPIENS (HUMAN).

Q03692

F-NT2RP2001956

ORM1 PROTEIN.

7.6e-17:106:36

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P53224

40

F-NT2RP2002015

HOMEBOX PROTEIN HOX-A2.

0.12:77:37

GALLUS GALLUS (CHICKEN).

45 Q08727

F-NT2RP2002063

HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.

3.2e-47:213:41

50 CAENORHABDITIS ELEGANS.

P49191

F-NT2RP2002188

ACETYLCHOLINESTERASE PRECURSOR (EC 3.1.1.7) (ACHE).

55 9.2e-15:109:36

TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).

P04058

- 5 F-NT2RP2002232
HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.
2.0e-12:92:50
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09782
- 10 F-NT2RP2002304
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.00059:16:68
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 15 F-NT2RP2002409
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
0.00039:184:33
BOS TAURUS (BOVINE).
P02453
- 20 F-NT2RP2002510
T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).
0.0010:97:37
ORYCTOLAGUS CUNICULUS (RABBIT).
P06333
- 25 F-NT2RP2002527
CYTOCHROME B5.
1.3e-11:77:38
SACCHAROMYCES CEREVISIAE (BAKERS YEAST).
P40312
- 30 F-NT2RP2002533
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL ALPHA-2/DELTA SUBUNITS PRECURSOR.
2.0e-37:165:42
ORYCTOLAGUS CUNICULUS (RABBIT).
35 P13806
- F-NT2RP2002564
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
4.7e-06:81:35
40 NICOTIANA TABACUM (COMMON TOBACCO).
P13983
- F-NT2RP2002674
45 SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HY-
DROLASE) (CEH).
2.4e-25:147:41
HOMO SAPIENS (HUMAN).
P34913
- 50 F-NT2RP2002721
GLUCOSE 6-PHOSPHATE TRANSLOCASE.
0.0073:88:26
HOMO SAPIENS (HUMAN).
043826
- 55 F-NT2RP2002824
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).

- 1.0e-16:139:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- 5 F-NT2RP2002942
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR (N-CAM L1).
5.1e-18:153:30
HOMO SAPIENS (HUMAN).
P32004
- 10 F-NT2RP2002974
HOMEODOMAIN PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT).
3.6e-80:187:84
15 MUS MUSCULUS (MOUSE).
P70178
- F-NT2RP2002976
HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.
20 2.8e-18:99:47
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38800
- F-NT2RP2003042
25 PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).
1.2e-41:135:57
GALLUS GALLUS (CHICKEN).
P53760
- 30 F-NT2RP2003138
5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).
3.3e-09:104:45
MUS MUSCULUS (MOUSE).
35 P70284
- F-NT2RP2003179
CARBON CATABOLITE DEREGULATING PROTEIN KINASE (EC 2.7.1.-).
7.2e-15:96:40
40 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P06782
- F-NT2RP2003210
LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).
45 6.2e-69:235:57
MUS MUSCULUS (MOUSE).
Q60714
- F-NT2RP2003302
50 ZINC FINGER PROTEIN 136.
9.7e-52:140:52
HOMO SAPIENS (HUMAN).
P52737
- 55 F-NT2RP2003369
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).
0.00020:87:32
HOMO SAPIENS (HUMAN).

P10161

F-NT2RP2003383

LONG NEUROTOXIN 2 (TOXINS I AND V).

0.86:38:39

DENDROASPIS VIRIDIS (WESTERN GREEN MAMBA).

P01395

F-NT2RP2003390

NPL1 PROTEIN (SEC63 PROTEIN).

1.1e-14:113:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14906

F-NT2RP2003469

MYO-INOSITOL TRANSPORTER 2.

1.7e-09:148:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P30606

F-NT2RP2003545

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.2e-32:198:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38692

F-NT2RP2003593

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00019:128:32

MUS MUSCULUS (MOUSE).

P05142

F-NT2RP2003599

ATP-DEPENDENT BILE ACID PERMEASE.

0.88:69:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32386

F-NT2RP2003655

HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.

2.9e-16:93:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38869

F-NT2RP2003664

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.

5.6e-08:121:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47111

F-NT2RP2003931

ACROSIN PRECURSOR (EC 3.4.21.10).

0.38:20:70

HOMO SAPIENS (HUMAN).

P10323

F-NT2RP2003940

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

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- 1.3e-84:126:74
HOMO SAPIENS (HUMAN).
Q03923
- 5 F-NT2RP2003950
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (AL-
PHA-0 PROTEIN).
1.5e-05:134:33
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
10 P08393
- F-NT2RP2004069
HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.
4.3e-13:68:54
15 CAENORHABDITIS ELEGANS.
Q09297
- F-NT2RP2004108
ZINC FINGER PROTEIN 136.
20 8.6e-47:126:67
HOMO SAPIENS (HUMAN).
P52737
- F-NT2RP2004141
25 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.013:127:35
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP2004179
30 GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GLYCEROPHOSPHODIESTER
PHOSPHODIESTERASE).
5.9e-10:110:36
ESCHERICHIA COLI.
35 P10908
- F-NT2RP2004205
MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
4.6e-10:99:34
40 HOMO SAPIENS (HUMAN).
Q16653
- F-NT2RP2004447
PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.
45 0.86:48:37
MUS MUSCULUS (MOUSE).
Q01149
- F-NT2RP2004495
50 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
0.031:135:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981
- F-NT2RP2004524
55 HYPOTHETICAL 18.7 KD PROTEIN IN HMS1-ABF2 INTERGENIC REGION.
0.042:96:23
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q04767

F-NT2RP2004556

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

5 0.0082:87:35

HOMO SAPIENS (HUMAN).

P81489

F-NT2RP2004606

10 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

2.2e-57:163:73

HOMO SAPIENS (HUMAN).

15 P01033

F-NT2RP2004648

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

3.2e-25:90:62

20 FELIS SILVESTRIS CATUS (CAT).

O19015

F-NT2RP2004670

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

25 6.6e-14:108:34

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP2004794

30 HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

5.7e-11:140:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

35 F-NT2RP2004837

F-NT2RP2004847

ADULT ENHANCER FACTOR 1 (AEF-1).

7.9e-09:81:37

40 DROSOPHILA MELANOGASTER (FRUIT FLY).

P39413

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN.

45 3.6e-64:130:96

HOMO SAPIENS (HUMAN).

P11169

F-NT2RP2005069

50 CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

0.22:116:32

RATTUS NORVEGICUS (RAT).

P53565

55 F-NT2RP2005163

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

5.3e-06:70:38

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

F-NT2RP2005181

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).

4.2e-54:153:69

HOMO SAPIENS (HUMAN).

P30825

F-NT2RP2005247

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.0e-11:106:35

SORGHUM VULGARE (SORGHUM).

P24152

F-NT2RP2005378

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.11:97:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

F-NT2RP2005391

G-BOX BINDING FACTOR (GBF).

5.1e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

F-NT2RP2005425

M PROTEIN, SEROTYPE 49 PRECURSOR.

2.1e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

F-NT2RP2005463

OVOMUCOID (FRAGMENT).

1.0:21:52

BAMBUSICOLA THORACICA (CHINESE BAMBOO-PARTRIDGE).

P52259

F-NT2RP2005514

MOBC PROTEIN.

1.0:26:53

THIOBACILLUS FERROOXIDANS.

P22899

F-NT2RP2005535

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.8e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

F-NT2RP2005541

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFA-
TASE).

8.8e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

- 5 F-NT2RP2005597
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC
2.4.1.109).
7.4e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 10 F-NT2RP2005632
ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENY-
LYL CYCLASE).
3.0e-05:73:43
CANIS FAMILIARIS (DOG).
P30803
- 15 F-NT2RP2005666
HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.086:105:31
MUS MUSCULUS (MOUSE).
P35583
- 20 F-NT2RP2005774
ZINC FINGER PROTEIN 136.
7.8e-33:128:57
HOMO SAPIENS (HUMAN).
25 P52737
- F-NT2RP2005878
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
6.8e-23:96:48
30 MUS MUSCULUS (MOUSE).
070503
- F-NT2RP2005883
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
35 (DBH).
6.4e-23:185:32
RATTUS NORVEGICUS (RAT).
Q05754
- 40 F-NT2RP2005887
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
1.0:40:30
METHANOCOCCUS JANNASCHII.
Q57650
- 45 F-NT2RP2005941
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
3.5e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
50 P17437
- F-NT2RP2005994
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
4.4e-36:144:47
55 CAENORHABDITIS ELEGANS.
P49191
- F-NT2RP2006004

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- BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG).
0.030:28:50
RATTUS NORVEGICUS (RAT).
5 Q01129
- F-NT2RP2006042
HYPOTHETICAL PROTEIN KIAA0144.
1.2e-22:228:39
10 HOMO SAPIENS (HUMAN).
Q14157
- F-NT2RP2006092
TRANSCRIPTIONAL ACTIVATOR FE65.
15 3.1e-27:101:54
RATTUS NORVEGICUS (RAT).
P46933
- F-NT2RP2006099
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
20 7.0e-07:123:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP2006134
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
25 0.0041:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
30
- F-NT2RP2006269
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
6.3e-17:119:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
35 P46971
- F-NT2RP2006512
GNS1 PROTEIN.
8.6e-14:186:30
40 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- F-NT2RP3000011
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
45 2.9e-12:137:32
THERMOMONOSPORA CURVATA.
P49695
- F-NT2RP3000022
SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
50 1.6e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793
- F-NT2RP3000059
COLLAGEN ALPHA 1(III) CHAIN.
55 1.5e-05:211:33
BOS TAURUS (BOVINE).

P04258

F-NT2RP3000063
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
4.2e-23:230:28
ZEA MAYS (MAIZE).
P14918

F-NT2RP3000125
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
2.3e-08:110:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620

F-NT2RP3000148
ZINC FINGER PROTEIN 133.
1.4e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

F-NT2RP3000169
SMALL PROLINE-RICH PROTEIN 2-1.
0.00092:14:57
HOMO SAPIENS (HUMAN).
P35326

F-NT2RP3000171
24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.
4.6e-10:134:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P28707

F-NT2RP3000172
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
1.8e-33:161:42
RATTUS NORVEGICUS (RAT).
Q63450

F-NT2RP3000201
SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).
4.1e-79:254:64
CAENORHABDITIS ELEGANS.
Q23356

F-NT2RP3000232
ZINC FINGER PROTEIN 184 (FRAGMENT).
8.5e-23:119:45
HOMO SAPIENS (HUMAN).
Q99676

F-NT2RP3000304
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
9.8e-36:172:43
HOMO SAPIENS (HUMAN).
Q07954

F-NT2RP3000378

- PAIRED AMPHIPATHIC HELIX PROTEIN.
2.7e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579
- 5 F-NT2RP3000427
5E5 ANTIGEN.
0.086:204:31
RATTUS NORVEGICUS (RAT).
10 Q63003
- F-NT2RP3000436
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
1.3e-23:106:33
15 CAENORHABDITIS ELEGANS.
Q11067
- F-NT2RP3000444
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
20 0.00052:166:36
HOMO SAPIENS (HUMAN).
000268
- F-NT2RP3000460
25 PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.0e-98:194:100
RATTUS NORVEGICUS (RAT).
P38378
- F-NT2RP3000481
30 NONSENSE-MEDIATED MRNA DECAY PROTEIN 5.
7.4e-19:217:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46970
- F-NT2RP3000616
35 BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
1.2e-13:115:33
BOS TAURUS (BOVINE).
40 P21793
- F-NT2RP3000645
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.3e-10:237:30
45 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP3000652
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
50 3.1e-106:283:67
HOMO SAPIENS (HUMAN).
Q03923
- F-NT2RP3000676
55 ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
7.4e-07:102:32
HOMO SAPIENS (HUMAN).

P12235

F-NT2RP3000677
MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
1.5e-27:66:54
HOMO SAPIENS (HUMAN).
P22670

F-NT2RP3000721
HYPOTHETICAL 62.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION.
1.6e-22:208:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43560

F-NT2RP3000789
ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN) (VENTRAL NEURON-SPECIFIC PROTEIN 1).
1.0e-07:190:26
HOMO SAPIENS (HUMAN).
P51513

F-NT2RP3000818
HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION.
5.9e-05:100:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34248

F-NT2RP3000820
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
0.92:97:26
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P73538

F-NT2RP3000838
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
6.4e-07:231:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

F-NT2RP3000871
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
2.8e-07:221:33
RATTUS NORVEGICUS (RAT).
P02454

F-NT2RP3000907
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
2.2e-41:104:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986

F-NT2RP3000921
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC).
4.5e-08:149:31
HOMO SAPIENS (HUMAN).
P98160

5 F-NT2RP3001012
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.5e-06:37:51
PLASMODIUM LOPHURAE.
P04929

10 F-NT2RP3001044
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDA.
0.10:61:31
STREPTOMYCES COELICOLOR.
P18182

15 F-NT2RP3001061
GLYCOPROTEIN X PRECURSOR.
0.00011:140:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968

20 F-NT2RP3001159
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.1e-09:249:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323

25 F-NT2RP3001170
POU DOMAIN PROTEIN 1 (DJPOU1).
0.020:173:29
DUGESIA JAPONICA (PLANARIAN).
P31370

30 F-NT2RP3001195
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
1.2e-14:180:30
ESCHERICHIA COLI.
P37021

35 F-NT2RP3001240
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
3.1e-118:229:88
RATTUS NORVEGICUS (RAT).
P38378

40 F-NT2RP3001271
EBNA-1 NUCLEAR PROTEIN.
2.3e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

45 F-NT2RP3001322
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-AT-
PASE).
1.7e-23:222:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39524

50 F-NT2RP3001388
SYNAPTOTAGMIN IV.
4.8e-19:168:38

RATTUS NORVEGICUS (RAT).
P50232

5 F-NT2RP3001542
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
2.7e-12:132:37
HOMO SAPIENS (HUMAN).
Q13829

10 F-NT2RP3001560
SYNAPSINS IA AND IB.
0.59:104:35
BOS TAURUS (BOVINE).
P17599

15 F-NT2RP3001592
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
20 P29834

F-NT2RP3001650
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.23:119:36
25 CANIS FAMILIARIS (DOG).
P39881

F-NT2RP3001685
HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).
30 2.2e-48:207:48
PSEUDOMONAS AERUGINOSA.
P28812

F-NT2RP3001738
35 CYTOCHROME B5.
9.5e-13:133:33
ORYCTOLAGUS CUNICULUS (RABBIT).
P00169

40 F-NT2RP3001754
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
7.9e-05:117:29
HOMO SAPIENS (HUMAN).
P17600

45 F-NT2RP3001858
CUTICLE COLLAGEN 2.
0.030:118:35
CAENORHABDITIS ELEGANS.
50 P17656

F-NT2RP3001976
ZINC FINGER PROTEIN 140.
7.8e-24:122:52
55 HOMO SAPIENS (HUMAN).
P52738

F-NT2RP3002015

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5 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
0.018:224:30
GALLUS GALLUS (CHICKEN).
P02457

10 F-NT2RP3002160
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.0058:206:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

15 F-NT2RP3002281
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).
1.3e-14:86:40
HOMO SAPIENS (HUMAN).
P52597

20 F-NT2RP3002286
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
0.65:128:29
HOMO SAPIENS (HUMAN).
P50548

25 F-NT2RP3002311
BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
6.1e-46:172:54
FELIS SILVESTRIUS CATUS (CAT).
O19015

30 F-NT2RP3002324
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.012:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245

35 F-NT2RP3002342
HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.8e-13:219:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39981

40 F-NT2RP3002353
REGULATORY PROTEIN E2.
0.0027:167:31
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422

50 F-NT2RP3002409
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).
9.9e-09:93:34
NEUROSPORA CRASSA.
P23231

55 F-NT2RP3002411
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
5.6e-107:254:80

MUS MUSCULUS (MOUSE).
070503

5 F-NT2RP3002448
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
1.5e-05:163:33
HOMO SAPIENS (HUMAN).
000268

10 F-NT2RP3002571
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
6.4e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10496

15 F-NT2RP3002664
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.062:47:29
HOMO SAPIENS (HUMAN).
20 P18850

F-NT2RP3002721
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
6.2e-140:283:92
25 SUS SCROFA (PIG).
P00889

F-NT2RP3002737
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
30 4.1e-40:136:61
MUS MUSCULUS (MOUSE).
P97414

F-NT2RP3002738
35 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.029:195:28
HOMO SAPIENS (HUMAN).
P10163

40 F-NT2RP3002790
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.7e-08:130:36
MUS MUSCULUS (MOUSE).
P05142

45 F-NT2RP3002836
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
8.9e-24:119:43
HOMO SAPIENS (HUMAN).
50 P51805

F-NT2RP3002887
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-
MENT).
55 2.9e-11:198:34
HOMO SAPIENS (HUMAN).
P02812

- F-NT2RP3002900
 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
 2.8e-18:109:41
 CRICETULUS GRISEUS (CHINESE HAMSTER).
 5 P49020
- F-NT2RP3002958
 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
 6.4e-06:172:27
 10 RATTUS NORVEGICUS (RAT).
 P19814
- F-NT2RP3002983
 COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
 15 4.4e-05:106:41
 BOS TAURUS (BOVINE).
 P02453
- F-NT2RP3003000
 20 SODIUM CHANNEL PROTEIN (NA⁺ CHANNEL).
 9.7e-30:221:31
 ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
 P02719
- 25 F-NT2RP3003076
 ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220].
 0.00033:173:30
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 30 P03200
- F-NT2RP3003354
 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
 2.0e-54:204:51
 35 MUS MUSCULUS (MOUSE).
 035609
- F-NT2RP3003448
 PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
 4.0e-05:112:33
 40 ESCHERICHIA COLI.
 P31137
- F-NT2RP3003469
 45 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
 1.2e-17:70:64
 HOMO SAPIENS (HUMAN).
 P39194
- F-NT2RP3003473
 50 BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
 0.0037:33:63
 BOS TAURUS (BOVINE).
 P19661
- 55 F-NT2RP3003527
 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
 1.8e-53:159:69
 HOMO SAPIENS (HUMAN).

- Q13627
- 5 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
2.3e-114:219:97
HOMO SAPIENS (HUMAN).
P41217
- 10 F-NT2RP3003535
HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3 REGION (ORF57).
0.98:36:30
ASTASIA LONGA (EUGLENOPHYCEAN ALGA).
P34774
- 15 F-NT2RP3003559
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.047:29:48
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643
- 20 F-NT2RP3003614
TRYPSIN INHIBITOR II (BDTI-II).
0.98:23:39
BRYONIA DIOICA (RED BRYONY).
25 P11968
- F-NT2RP3003729
HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.
4.1e-11:204:30
30 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03151
- F-NT2RP3003849
PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).
35 9.7e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).
P05130
- F-NT2RP3003874
40 MYOSIN I ALPHA (MMI-ALPHA).
3.1e-64:141:84
MUS MUSCULUS (MOUSE).
P46735
- 45 F-NT2RP3003939
CELL DIVISION PROTEIN FTSH HOMOLOG 4 (EC 3.4.24.-).
7.1e-34:76:61
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P72991
- 50 F-NT2RP3003963
HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.
0.95:31:38
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
55 Q48251
- F-NT2RP3004000
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).

7.1e-07:187:29
CRICETULUS GRISEUS (CHINESE HAMSTER).
P11414

5 F-NT2RP3004025
EBNA-1 NUCLEAR PROTEIN.
0.022:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-NT2RP3004067
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.0e-07:184:35
HOMO SAPIENS (HUMAN).
15 Q03692-

F-NT2RP3004075
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
2.9e-07:92:40
20 HORDEUM VULGARE (BARLEY).
P17816

F-NT2RP3004083
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
25 0.013:24:45
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
P50682

F-NT2RP3004090
30 SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
1.2e-07:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

35 F-NT2RP3004119
PEREGRIN (BR140 PROTEIN).
4.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

40 F-NT2RP3004130
CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
2.4e-08:71:42
MUS MUSCULUS (MOUSE).
45 P19467

F-NT2RP3004133
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.5e-28:111:44
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

F-NT2RP3004202
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.0e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

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- 5 F-NT2RP3004294
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
8.8e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288
- 10 F-NT2RP3004309
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-05:212:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 15 F-NT2RP3004321
REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP).
2.8e-09:81:40
LEISHMANIA MAJOR.
Q25337
- 20 F-NT2RP3004345
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 25 F-NT2RP3004355
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPV.
0.81:154:26
AZOTOBACTER CHROOCOCCUM MCD 1.
Q43959
- 30 F-NT2RP3004374
HOMEODOMAIN PROTEIN HOX-A2.
0.28:77:37
GALLUS GALLUS (CHICKEN).
Q08727
- 35 F-NT2RP3004406
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
4.9e-18:165:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544
- 40 F-NT2RP3004481
BUTYROPHILIN PRECURSOR (BT).
4.0e-13:152:31
HOMO SAPIENS (HUMAN).
Q13410
- 50 F-NT2RP3004552
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
3.4e-05:211:28
HOMO SAPIENS (HUMAN).
P17927
- 55 F-NT2RP3004557
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111).
1.6e-23:129:35
HOMO SAPIENS (HUMAN).

- Q06323
- 5 F-NT2RP3004625
GLYCOPROTEIN X PRECURSOR.
2.4e-10:225:25
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 10 F-NT2RP3004640
ENAMELIN (TUFTELIN).
2.6e-70:167:85
BOS TAURUS (BOVINE).
P27628
- 15 F-NT2RP3004647
ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
4.6e-10:116:34
HOMO SAPIENS (HUMAN).
20 P12235
- F-NT2RP4000108
NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).
3.4e-107:255:87
25 RATTUS NORVEGICUS (RAT).
P19527
- F-NT2RP4000634
MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).
30 7.9e-142:267:88
MUS MUSCULUS (MOUSE).
Q61083
- F-NT2RP4000962
35 SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).
1.5e-13:158:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08458
- 40 F-NT2RP4001001
- F-NT2RP4001009
POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1)
(PPSEP 1).
45 7.7e-24:235:31
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10071
- F-NT2RP4001467
50 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
1.2e-120:237:97
HOMO SAPIENS (HUMAN).
P21589
- 55 F-NT2RP4001877
GLYCINE-RICH RNA-BINDING PROTEIN.
1.4e-08:89:34
DAUCUS CAROTA (CARROT).

Q03878

F-NT2RP4001879
VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.
0.98:49:34
MYCOBACTERIUM TUBERCULOSIS.
P71934

F-NT2RP4002187
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
4.5e-98:246:78
MUS MUSCULUS (MOUSE).
070503

F-NT2RP4002451
CUTICLE COLLAGEN 2.
0.85:92:35
CAENORHABDITIS ELEGANS.
P17656

F-NT2RP4002715
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.47:31:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245

F-NT2RP4002750
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).
3.3e-63:185:67
HOMO SAPIENS (HUMAN).
P30825

F-OVARC1000003
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-
PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-
NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
2.2e-82:197:72
HOMO SAPIENS (HUMAN).
Q06495

F-OVARC1000090
HOMEBOX PROTEIN HOX-B1 (GHOX-LAB).
0.049:120:32
GALLUS GALLUS (CHICKEN).
P31259

F-OVARC1000105
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN
CARRIER PROTEIN).
8.6e-47:159:58
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33296

F-OVARC1000137
HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.
0.058:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015

5 F-OVARC1000208.
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
2.2e-12:51:74
HOMO SAPIENS (HUMAN).
P39195

10 F-OVARC1000255
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
1.1e-112:144:86
HOMO SAPIENS (HUMAN).
P43405

15 F-OVARC1000275
GASTRIN PRECURSOR.
0.11:59:37
HOMO SAPIENS (HUMAN).
20 P01350

F-OVARC1000298
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.014:74:39
25 MUS MUSCULUS (MOUSE).
P05143

F-OVARC1000307
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
30 1.0:33:54
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

F-OVARC1000313
35 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PRO-
TEIN 2) (CABP2).
4.0e-15:127:37
RATTUS NORVEGICUS (RAT).
P38659

40 F-OVARC1000331
GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).
2.0e-24:64:84
HOMO SAPIENS (HUMAN).
45 P36959

F-OVARC1000410
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREP-A).
1.9e-44:229:41
50 PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
P19477

F-OVARC1000439
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
55 0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

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- 5 F-OVARC1000467
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0061:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 10 F-OVARC1000529
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL 101 W (EC 2.7.1.-).
1.5e-20:127:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244
- 15 F-OVARC1000553
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
7.6e-26:169:40
MUS MUSCULUS (MOUSE).
P28843
- 20 F-OVARC1000775
METALLOTHIONEIN (MT).
0.91:31:38
CARASSIUS AURATUS (GOLDFISH).
P52723
- 25 F-OVARC1000811
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).
2.8e-11:69:43
HOMO SAPIENS (HUMAN).
P00748
- 30 F-OVARC1000853
CUTICLE COLLAGEN 40.
0.00013:130:33
CAENORHABDITIS ELEGANS.
P34804
- 35 F-OVARC1000873
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.00015:53:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643
- 45 F-OVARC1000916
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).
2.5e-26:109:53
MUS MUSCULUS (MOUSE).
P24788
- 50 F-OVARC1000956
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00073:115:33
HOMO SAPIENS (HUMAN).
P21917
- 55 F-OVARC1000995
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).
0.00031:139:25
HOMO SAPIENS (HUMAN).

- P51531
- F-OVARC1001030
5E5 ANTIGEN.
5. 1.9e-09:89:41
RATTUS NORVEGICUS (RAT).
Q63003
- F-OVARC1001049
10 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
1.5e-08:146:38
GALLUS GALLUS (CHICKEN).
P02457
- F-OVARC1001086
15 VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40].
5.3e-08:182:32
GALLUS GALLUS (CHICKEN).
20 P02845
- F-OVARC1001132
GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).
9.2e-40:229:37
25 HOMO SAPIENS (HUMAN).
P16383
- F-OVARC1001163
30 HYPOTHETICAL 49.3 KD PROTEIN C30D 11.06C IN CHROMOSOME I.
8.8e-05:38:44
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09906
- F-OVARC1001222
35 AMELOGENIN, CLASS I PRECURSOR.
0.72:96:31
BOS TAURUS (BOVINE).
P02817
- F-OVARC1001260
40
- F-OVARC1001336
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-
PORTER 2) (NA(+)/PI COTRANSporter 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-
45 NAL NA+-DEPENDENT PHOSPHATE COTRANSporter 2).
1.1e-33:103:71
RATTUS NORVEGICUS (RAT).
Q06496
- F-OVARC1001338
50 SERINE/THREONINE-PROTEIN KINASE UNC-51 (EC 2.7.1.-).
3.8e-30:89:46
CAENORHABDITIS ELEGANS.
Q23023
- F-OVARC1001569
55 ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).
2.2e-06:28:64

SUS SCROFA (PIG).
P08001

5 F-OVARC1001570
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.8e-09:121:33
CAVIA PORCELLUS (GUINEA PIG).
P25796

10 F-OVARC1001596
REGULATORY PROTEIN E2.
0.33:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783

15 F-OVARC1001607
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC
2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANS-
20 FERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).
1.0e-28:69:84
HOMO SAPIENS (HUMAN).
Q10469

25 F-OVARC1001725

F-OVARC1001727

F-OVARC1001807
EARLY RESPONSE PROTEIN NAK1 (TR3 ORPHAN RECEPTOR).
30 2.4e-51:153:75
HOMO SAPIENS (HUMAN).
P22736

F-OVARC1001833
35 CIS-GOLGI MATRIX PROTEIN GM130.
1.2e-55:169:75
RATTUS NORVEGICUS (RAT).
Q62839

40 F-OVARC1001952
EBNA-1 NUCLEAR PROTEIN.
3.5e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

45 F-OVARC1001991
HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).
3.7e-16:141:43
HOMO SAPIENS (HUMAN).
50 Q14681

F-OVARC1002058
LAMININ ALPHA-5 CHAIN (FRAGMENT).
2.8e-22:163:33
55 MUS MUSCULUS (MOUSE).
Q61001

F-OVARC1002178

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TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.12:73:36

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-PLACE1000033

VON WILLEBRAND FACTOR PRECURSOR.

1.7e-19:190:28

CANIS FAMILIARIS (DOG).

Q28295

F-PLACE1000231

DNA-BINDING PROTEIN MNB1A.

0.24:60:33

ZEA MAYS (MAIZE).

P38564

F-PLACE1000258

ZINC FINGER PROTEIN 177.

3.6e-19:55:61

HOMO SAPIENS (HUMAN).

Q13360

F-PLACE1000442

ZINC FINGER PROTEIN 136.

1.7e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

F-PLACE1000560

COLICIN E9 (EC 3.1.21.1).

0.015:47:44

ESCHERICHIA COLI.

P09883

F-PLACE1000740

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).

1.6e-05:75:36

MUS MUSCULUS (MOUSE).

P31695

F-PLACE1000907

ZINC FINGER PROTEIN 141.

2.8e-15:43:88

HOMO SAPIENS (HUMAN).

Q15928

F-PLACE1000912

PROBABLE E4 PROTEIN (E1^E4).

0.19:46:36

HUMAN PAPILLOMAVIRUS TYPE 6B.

P06459

F-PLACE1000914

MALE SPECIFIC SPERM PROTEIN MST87F.

0.054:27:44

DROSOPHILA MELANOGASTER (FRUIT FLY).

P08175

F-PLACE1000927
HYPOTHETICAL PROTEIN HI0044.
3.9e-07:139:30
HAEMOPHILUS INFLUENZAE.
P44477

F-PLACE1000986

F-PLACE1001016
SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT.
2.7e-05:120:32
RATTUS NORVEGICUS (RAT).
P04775

F-PLACE1001100

F-PLACE1001114
PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.5e-07:250:28
MUS MUSCULUS (MOUSE).
P11087

F-PLACE1001123
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
6.2e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941

F-PLACE1001183
NONHISTONE CHROMOSOMAL PROTEIN HMG-17.
0.31:52:34
GALLUS GALLUS (CHICKEN).
P02314

F-PLACE1001229
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).
1.0:38:47
ARTEMIA SAUNA (BRINE SHRIMP).
P19047

F-PLACE1001231
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
4.7e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170

F-PLACE1001340
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
6.5e-14:136:29
NEUROSPORA CRASSA.
P23231

F-PLACE1001401

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HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).
1.3e-11:103:40
RATTUS NORVEGICUS (RAT).
5 P13386

F-PLACE1001407
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
0.013:121:32
10 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
Q05049

F-PLACE1001464
5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
15 1.4e-119:246:89
HOMO SAPIENS (HUMAN).
P21589

F-PLACE1001500
20 BLOOM'S SYNDROME PROTEIN.
8.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132

F-PLACE1001516
25 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
7.4e-07:204:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
30 P08640

F-PLACE1001536

F-PLACE1001564
35 LEUCOCYTE ANTIGEN CD97 PRECURSOR.
2.1e-09:170:24
HOMO SAPIENS (HUMAN).
P48960

F-PLACE1001655
40 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
4.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387

45 F-PLACE1001788
HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I.
6.2e-21:75:58
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
50 Q09695

F-PLACE1001795
HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
3.8e-21:159:40
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032

F-PLACE1001836

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- ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].
4.5e-29:134:47
BABOON ENDOGENOUS VIRUS (STRAIN M7).
5 P10269
- F-PLACE1001918
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
10 1.5e-30:228:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- F-PLACE1001949
15 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).
5.1e-36:210:46
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q12697
- F-PLACE1002080
20 HYPOTHETICAL PROTEIN KIAA0288 (HA6116).
3.5e-26:207:45
HOMO SAPIENS (HUMAN).
P56524
- F-PLACE1002095
25 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (GT).
30 0.32:50:34
MUS MUSCULUS (MOUSE).
P15535
- F-PLACE1002153
35 CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).
0.00021:214:26
CLOSTRIDIUM THERMOCELLUM.
Q06852
- F-PLACE1002329
40 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.
1.1e-35:179:44
MUS MUSCULUS (MOUSE).
Q08509
- F-PLACE1002355
45 COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] (FRAGMENTS).
1.0e-14:183:32
BOS TAURUS (BOVINE).
50 P01030
- F-PLACE1002374
CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).
55 9.2e-107:225:86
HOMO SAPIENS (HUMAN).
P07711
- F-PLACE1002518

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HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.

6.1e-05:59:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38239

5

F-PLACE1002547

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

10

1.0e-22:230:31

NEUROSPORA CRASSA.

P23231

F-PLACE1002726

15

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).

0.61:25:48

ORYCTOLAGUS CUNICULUS (RABBIT).

P02456

20

F-PLACE1002905

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

5.0e-31:93:64

BOS TAURUS (BOVINE).

25

P07106

F-PLACE1002911

T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

6.6e-06:95:35

30

HOMO SAPIENS (HUMAN).

P40200

F-PLACE1002967

35

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT).

9.4e-08:95:37

MUS MUSCULUS (MOUSE).

P20490

40

F-PLACE1003135

SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).

1.9e-33:99:50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03497

45

F-PLACE1003163

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

9.8e-15:105:38

50

BOS TAURUS (BOVINE).

P07106

F-PLACE1003407

CLN5 PROTEIN.

55

4.2e-109:217:89

HOMO SAPIENS (HUMAN).

075503

- 5 F-PLACE1003428
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
1.0e-36:104:46
HOMO SAPIENS (HUMAN).
P43251
- 10 F-PLACE1003438
HYPOTHETICAL 104.4 KD PROTEIN C17A5.16 IN CHROMOSOME 1.
1.1e-10:148:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
013776
- 15 F-PLACE1003460
2-HYDROXY-6-KETONONA-2,4-DIENEDIOIC ACID HYDROLASE (EC 3.7.1.-).
0.00028:134:27
ESCHERICHIA COLI.
P77044
- 20 F-PLACE1003529
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).
0.00047:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480
- 25 F-PLACE1003573
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).
0.022:129:25
MUS MUSCULUS (MOUSE).
30 P20937
- F-PLACE1003598
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (ICP2.9/ER2.6).
0.0017:102:44
35 BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- F-PLACE1003644
PROTEIN Q300.
40 6.7e-05:24:70
MUS MUSCULUS (MOUSE).
Q02722
- F-PLACE1003737
45 TOLL PROTEIN PRECURSOR.
7.3e-08:203:27
DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953
- 50 F-PLACE1003772
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
3.7e-07:141:32
HOMO SAPIENS (HUMAN).
P81489
- 55 F-PLACE1003839
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
1.3e-09:201:31

MUS MUSCULUS (MOUSE).
P05143

5 F-PLACE1003845
PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPI-
MERASE).
5.0e-13:103:33
METHANOCOCCUS JANNASCHII.
Q57664

10 F-PLACE1003852
CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).
2.0e-18:189:29
HOMO SAPIENS (HUMAN).
15 Q14246

F-PLACE1004028
HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION.
0.97:47:31
20 BACILLUS SUBTILIS.
P12049

F-PLACE1004078
ADSEVERIN (SCINDERIN) (SC).
25 5.3e-98:176:90
BOS TAURUS (BOVINE).
Q28046

F-PLACE1004166
30 CREB-BINDING PROTEIN.
9.6e-08:107:34
HOMO SAPIENS (HUMAN).
Q92793

35 F-PLACE1004168
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
6.8e-05:147:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655

40 F-PLACE1004199
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
4.2e-05:65:52
HOMO SAPIENS (HUMAN).
45 P39188

F-PLACE1004279
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.6e-11:166:30
50 CAENORHABDITIS ELEGANS.
P30638

F-PLACE1004282
HISTONE H1C (CLONE XLHW2).
55 0.74:73:26
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P15866

- 5 F-PLACE1004305
RAS-RELATED PROTEIN RAC1.
2.3e-23:161:39
DROSOPHILA MELANOGASTER (FRUIT FLY).
P40792
- 10 F-PLACE1004441
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
5.4e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 F-PLACE1004450
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
3.1e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 F-PLACE1004482
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.23:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 F-PLACE1004492
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
1.2e-05:150:34
BOS TAURUS (BOVINE).
P02453
- 30 F-PLACE1004519
ENL PROTEIN.
0.68:170:30
HOMO SAPIENS (HUMAN).
35 Q03111
- 40 F-PLACE1004520
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
3.5e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 45 F-PLACE1004630
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
9.1e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 50 F-PLACE1004637
MALE SPECIFIC SPERM PROTEIN MST84DA.
0.47:29:44
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01642
- 55 F-PLACE1004648
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
8.4e-05:89:40
MUS MUSCULUS (MOUSE).

- P05142
- 5 F-PLACE1004816
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
1.0e-25:117:46
HOMO SAPIENS (HUMAN).
P55083
- 10 F-PLACE1004887
SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
8.4e-09:195:30
DROSOPHILA ERECTA (FRUIT FLY).
P13730
- 15 F-PLACE1005003
PROSTASIN PRECURSOR (EC 3.4.21.-).
1.2e-24:139:40
HOMO SAPIENS (HUMAN).
Q16651
- 20 F-PLACE1005005
UBIQUITIN-CONJUGATING ENZYME E2 G2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).
2.5e-28:51:84
25 HOMO SAPIENS (HUMAN).
P56554
- 30 F-PLACE1005031
CHLORINE CHANNEL PROTEIN P64.
2.7e-52:142:76
BOS TAURUS (BOVINE).
P35526
- 35 F-PLACE1005239
SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55) (FRAGMENT).
0.27:78:26
ORYCTOLAGUS CUNICULUS (RABBIT).
018776
- 40 F-PLACE1005250
HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.
0.22:35:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53056
- 45 F-PLACE1005383
FIBRILLIN 1 PRECURSOR.
6.7e-09:134:32
MUS MUSCULUS (MOUSE).
50 Q61554
- F-PLACE1005410
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
9.5e-105:204:100
55 RATTUS NORVEGICUS (RAT).
P38378
- F-PLACE1005426

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PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
3.2e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888

5

F-PLACE1005519
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
1.2e-23:143:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692

10

F-PLACE1005539
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
5.5e-05:94:37
BRASSICA NAPUS (RAPE).
P40603

15

F-PLACE1005544
CELL SURFACE A33 ANTIGEN PRECURSOR.
0.00015:132:31
HOMO SAPIENS (HUMAN).
Q99795

20

F-PLACE1005569
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.00092:122:31
EQUUS CABALLUS (HORSE).
Q28381

25

F-PLACE1005601
TOXIN S4C8.
0.34:32:37
DENDROASPIS JAMESONI KAIMOSAË (EASTERN JAMESON'S MAMBA).
P25683

30

F-PLACE1005660
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

35

F-PLACE1005669
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).
0.0078:105:37
HOMO SAPIENS (HUMAN).
Q02388

45

F-PLACE1005682
THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).
2.7e-12:81:41
HOMO SAPIENS (HUMAN).
Q15653

50

F-PLACE1005725
HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.
7.5e-08:142:31
CAENORHABDITIS ELEGANS.
Q11073

55

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- 5 F-PLACE1005736
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
9.0e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 10 F-PLACE1005745
ORM1 PROTEIN.
2.2e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 15 F-PLACE1005768
NEUROTOXINS I AND I'PRECURSOR (AAH I AND AAH I').
0.63:13:69
ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). P01479
- 20 F-PLACE1005815
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
1.8e-12:73:50
HOMO SAPIENS (HUMAN).
P23508
- 25 F-PLACE1005878
CHLORINE CHANNEL PROTEIN P64.
1.6e-49:115:79
BOS TAURUS (BOVINE).
P35526
- 30 F-PLACE1005927
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
3.2e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09875
- 35 F-PLACE1006071
LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
4.1e-08:215:26
MUS MUSCULUS (MOUSE).
P02469
- 40 F-PLACE1006073
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
2.1e-05:137:34
NEPHILA CLAVIPES (ORB SPIDER).
P46804
- 50 F-PLACE1006079
HOMEBOX PROTEIN DLX-3.
1.5e-58:144:83
HOMO SAPIENS (HUMAN).
060479
- 55 F-PLACE1006093
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
3.8e-05:72:40
HOMO SAPIENS (HUMAN).
P17600

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5 F-PLACE1006208
EBNA-2 NUCLEAR PROTEIN.
3.8e-15:28:75
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P12978

10 F-PLACE1006219
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)
(FRAGMENT)
2.0e-09:38:42
KLEBSIELLA PNEUMONIAE.
P45602

15 F-PLACE1006277
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.2e-07:183:29
HOMO SAPIENS (HUMAN).
Q99795

20 F-PLACE1006290
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
8.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

25 F-PLACE1006443
HYPOTHETICAL 60.0 KD PROTEIN IN IMP1-HLJ1 INTERGENIC REGION.
0.0010:155:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03795

30 F-PLACE1006515
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.046:98:28
MUS MUSCULUS (MOUSE).
P10925

35 F-PLACE1006716
30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC
PROTEIN ADIPOQ).
40 3.6e-25:177:35
MUS MUSCULUS (MOUSE).
Q60994

45 F-PLACE1006786
PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (BASIC PROTEIN) (WBP) (FRAGMENT).
1.0:19:42
TRITICUM AESTIVUM (WHEAT).
P26913

50 F-PLACE1006809
SLS1 PROTEIN PRECURSOR.
0.0011:37:51
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
Q99158

55 F-PLACE1006959
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.3e-05:96:41

MUS MUSCULUS (MOUSE).
P05142

5 F-PLACE1007028
EBNA-1 NUCLEAR PROTEIN.
5.9e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-PLACE1007040
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-
MENT).
0.68:138:24
HOMO SAPIENS (HUMAN).
15 P02812

F-PLACE1007077
SERINE/THREONINE-PROTEIN KINASE CLA4 (EC 2.7.1.-).
0.73:177:25
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48562

F-PLACE1007081
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
25 3.0e-20:182:39
BOS TAURUS (BOVINE).
Q28107

F-PLACE1007096
30 HYPOTHETICAL SYMPORTER SLL1374.
2.8e-14:162:30
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P74168

35 F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
9.4e-50:120:86
HOMO SAPIENS (HUMAN).
P24390

40 F-PLACE1007591
MEIOTIC RECOMBINATION PROTEIN REC104.
0.68:73:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
45 P33323

F-PLACE1007626
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.00083:97:34
50 HOMO SAPIENS (HUMAN).
P23246

F-PLACE1007702
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
55 1.9e-08:87:36
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

- F-PLACE1007845
 GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
 1.3e-16:158:40
 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 5 P43636
- F-PLACE1007881
 HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.
 1.2e-11:113:37
 10 CAENORHABDITIS ELEGANS.
 Q19425
- F-PLACE1007971
 METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-III A AND MT-20-III B).
 15 1.0:32:43
 MYTILUS EDULIS (BLUE MUSSEL).
 P80253
- F-PLACE1008282
 20 HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).
 8.1e-87:178:87
 ORYCTOLAGUS CUNICULUS (RABBIT).
 P33279
- F-PLACE1008297
 25 MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
 3.6e-17:187:33
 DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
 P90648
 30
- F-PLACE1008359
 BEM46 PROTEIN (FRAGMENT).
 4.9e-07:103:33
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 35 P54069
- F-PLACE1008469
 D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
 0.0018:78:37
 40 HOMO SAPIENS (HUMAN).
 P21917
- F-PLACE1008549
 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
 45 0.0034:89:30
 HOMO SAPIENS (HUMAN).
 Q01543
- F-PLACE1008657
 50 ADSEVERIN (SCINDERIN) (SC).
 6.7e-127:257:91
 BOS TAURUS (BOVINE).
 Q28046
- F-PLACE1008716
 55 ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).

- 4.5e-20:66:78
HOMO SAPIENS (HUMAN).
Q10469
- 5 F-PLACE1008744
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
3.6e-19:221:33
HOMO SAPIENS (HUMAN).
P04003
- 10 F-PLACE1008984
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).
0.089:61:31
- 15 GLYCINE MAX (SOYBEAN).
Q42783
- F-PLACE1008985
SYNAPTOTAGMIN V.
8.6e-09:123:35
HOMO SAPIENS (HUMAN).
000445
- 20 F-PLACE1009067
HYPOTHETICAL 33.4 KD PROTEIN.
4.3e-09:60:50
HOMO SAPIENS (HUMAN).
Q04323
- 25 F-PLACE1009196
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
0.050:23:34
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
P35303
- 30 F-PLACE1009279
8.6 KD TRANSGLUTAMINASE SUBSTRATE.
1.4e-07:62:35
TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).
P81281
- 35 F-PLACE1009527
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.037:71:38
HOMO SAPIENS (HUMAN).
Q02817
- 40 F-PLACE1009546
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.9e-07:86:39
MUS MUSCULUS (MOUSE).
P05142
- 50 F-PLACE1009600
TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)).
1.7e-08:113:31
PASTEURELLA MULTOCIDA.
P51564
- 55

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- F-PLACE1009735
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE1 10) (VMW110) (AL-
PHA-0 PROTEIN).
2.6e-09:182:35
5 HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- F-PLACE1009982
REGULATORY PROTEIN E2.
10 0.99:94:28
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- F-PLACE1010011
15 DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL
CHOLINEPHOSPHOTRANSFERASE) (CHOPT).
2.8e-20:119:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898
- 20 F-PLACE1010078
ORM1 PROTEIN.
3.4e-20:137:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
25 P53224
- F-PLACE1010081
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.5e-11:147:32
30 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Q05609
- F-PLACE1010251
NEL-LIKE PROTEIN (FRAGMENT).
35 1.8e-10:73:42
HOMO SAPIENS (HUMAN).
Q92832
- F-PLACE1010445
40 HYPOTHETICAL BHLF1 PROTEIN.
0.0042:227:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181
- F-PLACE1010713
45 PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
1.5e-77:177:80
MUS MUSCULUS (MOUSE).
070503
- 50 F-PLACE1010784
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).
1.7e-18:102:40
GALLUS GALLUS (CHICKEN).
55 P32250
- F-PLACE1010827
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).

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- 2.8e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020
- 5 F-PLACE1010968
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE
PHOSPHOHYDROLASE).
2.3e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
10 P16621
- F-PLACE1011045
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
6.0e-14:153:34
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862
- F-PLACE1011116
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
20 GLUCAN GLUCOHYDROLASE).
2.3e-06:195:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 25 F-PLACE1011181
MSP1 PROTEIN HOMOLOG.
4.3e-06:93:25
CAENORHABDITIS ELEGANS.
P54815
- 30 F-PLACE1011236
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
4.1e-17:180:28
CAENORHABDITIS ELEGANS.
35 P30638
- F-PLACE1011364
HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II.
2.1e-24:158:41
40 CAENORHABDITIS ELEGANS.
Q09298
- F-PLACE1011407
ZINC FINGER PROTEIN 140.
45 3.8e-10:47:74
HOMO SAPIENS (HUMAN).
P52738
- F-PLACE1011516
50 HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.6e-13:117:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073
- 55 F-PLACE1011708
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
9.9e-22:203:32
DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

F-PLACE1011824

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3)
(CDC42/RAC EFFECTOR KINASE PAK-B).

1.6e-15:103:36

MUS MUSCULUS (MOUSE).

Q61036

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F-PLACE1011978

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.3e-55:188:50

HOMO SAPIENS (HUMAN).

Q03923

15

F-PLACE2000118

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

2.8e-23:169:43

NICOTIANA TABACUM (COMMON TOBACCO).

20

P13983

F-PLACE2000219

MALE SPECIFIC SPERM PROTEIN MST84DA.

0.11:29:41

25

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01642

F-PLACE3000181

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

30

9.5e-26:193:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

F-PLACE3000213

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

35

2.3e-23:191:34

HOMO SAPIENS (HUMAN).

P17927

40

F-PLACE4000354

E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-
ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).

3.2e-25:150:30

ORYCTOLAGUS CUNICULUS (RABBIT).

45

P27113

F-PLACE4000455

IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).

0.66:52:36

50

HOMO SAPIENS (HUMAN).

P04433

F-SKNMC1000004

OPTOMOTOR-BLIND PROTEIN (LETHAL(1)OPTOMOTOR-BLIND) (L(1)OMB) (BIFID PROTEIN).

55

0.079:88:30

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q24432

F-SKNMC1000014
 SCO-SPONDIN (FRAGMENT).
 0.63:60:36
 BOS TAURUS (BOVINE).
 P98167
 5

F-SKNMC1000082
 PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
 2.4e-10:93:34
 10 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 P53257

F-THYRO1000036
 PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
 0.72:69:36
 15 MUS MUSCULUS (MOUSE).
 P05143

F-THYRO1000061
 COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).
 0.0068:70:38
 BOS TAURUS (BOVINE).
 P25508
 20

F-THYRO1000099
 SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
 0.0063:207:28
 NEPHILA CLAVIPES (ORB SPIDER).
 P46804
 25

F-THYRO1000196
 RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
 1.6e-10:134:32
 GALLUS GALLUS (CHICKEN).
 P24503
 30

F-THYRO1000400
 ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
 3.9e-28:163:38
 35 MUS MUSCULUS (MOUSE).
 P54116

F-THYRO1000580
 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
 3.3e-15:64:62
 45 MUS MUSCULUS (MOUSE).
 Q61751

F-THYRO1000584
 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE)
 (135 KD PROTEIN).
 1.5e-89:197:72
 50 SUS SCROFA (PIG).
 Q28949

F-THYRO1000678
 GAP JUNCTION BETA-6 PROTEIN (CONNEXIN 30) (CX30).
 7.7e-39:89:87
 55

- MUS MUSCULUS (MOUSE).
P70689
- 5 F-THYRO1000776
HIGH AFFINITY SULPHATE TRANSPORTER 2.
3.0e-25:83:50
STYLOSANTHES HAMATA.
P53392
- 10 F-THYRO1000795
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
1.2e-33:227:37
BOS TAURUS (BOVINE).
P22292
- 15 F-THYRO1000846
CUTICLE COLLAGEN 12 PRECURSOR.
6.7e-09:190:33
CAENORHABDITIS ELEGANS.
20 P20630
- F-THYRO1000866
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
0.12:85:31
25 CAENORHABDITIS ELEGANS.
P46580
- F-THYRO1000956
PROBABLE G PROTEIN-COUPLE1) RECEPTOR APJ.
30 1.3e-68:165:84
HOMO SAPIENS (HUMAN).
P35414
- F-THYRO1000964
35 TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.015:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 40 F-THYRO1000999
CRYPTDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).
0.28:40:45
MUS MUSCULUS (MOUSE).
45 P50715
- F-THYRO1001063
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6; PEPTIDE P-H].
3.5e-05:232:32
50 HOMO SAPIENS (HUMAN).
P04280
- F-THYRO1001071
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
55 0.00061:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

- 5 F-THYRO1001102
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.25:94:38
HOMO SAPIENS (HUMAN).
000268
- 10 F-THYRO1001113
SYNAPTOTAGMIN III (SYTIII).
2.0e-08:102:35
MUS MUSCULUS (MOUSE).
035681
- 15 F-THYRO1001128
GLYCOPROTEIN X PRECURSOR.
6.8e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 20 F-THYRO1001205
NEUROGRANIN (NG) (PROTEIN KINASE C SUBSTRATE 7.5 KD PROTEIN) (RC3).
0.91:33:42
RATTUS NORVEGICUS (RAT).
Q04940
- 25 F-THYRO1001237
HYPOTHETICAL PROTEIN IN NIFH2 3 REGION (FRAGMENT).
4.0e-07:68:38
METHANOCOCCUS THERMOLITHOTROPHICUS.
P05410
- 30 F-THYRO1001242
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
1.0:104:35
HOMO SAPIENS (HUMAN).
P17600
- 35 F-THYRO1001266
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODI-
UM-GLUCOSE COTRANSPORTER).
4.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- 40 F-THYRO1001327
HYPOTHETICAL 23.7 KD PROTEIN IN CYR1-OST1 INTERGENIC REGION.
1.7e-06:141:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P41544
- 45 F-THYRO1001456
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
1.1e-11:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- 50 F-THYRO1001457
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
2.1e-68:228:59

HOMO SAPIENS (HUMAN).
Q15139

5 F-THYRO1001471
COLLAGEN 1(X) CHAIN PRECURSOR.
3.9e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125

10 F-THYRO1001478
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
0.038:162:31
HOMO SAPIENS (HUMAN).
Q03692

15 F-THYRO1001495
!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
4.8e-19:50:82
HOMO SAPIENS (HUMAN).
20 P39193

F-THYRO1001523
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!
5.0e-13:66:62
25 HOMO SAPIENS (HUMAN).
P39195

F-THYRO1001529
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT
30 2).
1.6e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09925

35 F-THYRO1001593
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
3.3e-92:225:77
HOMO SAPIENS (HUMAN).
P27448

40 F-THYRO1001608
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.2e-07:127:35
MUS MUSCULUS (MOUSE).
45 P05142

F-THYRO1001641
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0039:98:31
50 NEUROSPORA CRASSA.
Q06712

F-THYRO1001700
INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFER-
55 ON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE).
3.3e-09:65:43
HOMO SAPIENS (HUMAN).
P19525

- 5 F-THYRO1001702
MYELOID UPREGULATED PROTEIN.
7.8e-62:161:78
MUS MUSCULUS (MOUSE).
035682
- 10 F-THYRO1001725
PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).
0.00061:82:41
RATTUS NORVEGICUS (RAT).
P20468
- 15 F-THYRO1001770
PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
1.0e-20:165:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53974
- 20 F-THYRO1001803
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
3.6e-07:221:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 25 F-Y79AA1000030
TRANSCRIPTIONAL ACTIVATOR FE65.
4.5e-09:43:46
RATTUS NORVEGICUS (RAT).
30 P46933
- F-Y79AA1000127
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
1.3e-05:72:43
35 HOMO SAPIENS (HUMAN).
P48023
- F-Y79AA1000207
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-
EOCALCIN).
1.0:100:27
40 ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301
- 45 F-Y79AA1000226
HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV.
2.6e-07:188:28
CAENORHABDITIS ELEGANS.
P49049
- 50 F-Y79AA1000270
VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
1.6e-102:233:87
BOS TAURUS (BOVINE).
55 P40682
- F-Y79AA1000426
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).

- 1.1e-14:149:38
HOMO SAPIENS (HUMAN).
P55103
- 5 F-Y79AA1000521
MALE SPECIFIC SPERM PROTEIN MST84DD.
0.00079:60:36
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01645
- 10 F-Y79AA1000750
EBNA-1 NUCLEAR PROTEIN.
2.0e-09:131:38
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 15 F-Y79AA1000776
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER)
(SPRP).
0.080:44:40
SUS SCROFA (PIG).
P35323
- 20 F-Y79AA1000777
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
4.2e-33:204:39
THERMOMONOSPORA CURVATA.
P49695
- 25 F-Y79AA1000876
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-
UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
4.6e-16:115:38
BOS TAURUS (BOVINE).
P05307
- 30 F-Y79AA1000888
TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE
SYNTHASE I) (URACIL HYDROLYASE).
2.0e-09:159:35
TREPONEMA PALLIDUM.
083802
- 35 F-Y79AA1000959
HOMEODOMAIN PROTEIN HOX-B3 (HOX-2.7) (MH-23).
8.8e-08:72:38
MUS MUSCULUS (MOUSE).
P09026
- 45 F-Y79AA1000967
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
1.1e-37:202:42
RATTUS NORVEGICUS (RAT).
Q63450
- 50 F-Y79AA1001013
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS : PEPTIDE P-D] (FRAGMENT).
0.038:128:28
- 55

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HOMO SAPIENS (HUMAN).
P10162

5 F-Y79AA1001056
HYPOTHETICAL 7.1 KD PROTEIN IN TK-VS INTERGENIC REGION.
0.41:42:30
BACTERIOPHAGE T4.
P13307

10 F-Y79AA1001062
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
9.9e-13:132:38
HOMO SAPIENS (HUMAN).
Q13829

15 F-Y79AA1001090
ANKYRIN HOMOLOG-PRECURSOR.
4.0e-19:176:34
CHROMATIUM VINOSUM.
20 Q06527

F-Y79AA1001212
HYPOTHETICAL PROTEIN MJ0110.
0.095:55:34
25 METHANOCOCCUS JANNASCHII.
Q57574

F-Y79AA1001264
HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.
30 3.3e-53:177:55
CAENORHABDITIS ELEGANS.
Q10005

F-Y79AA1001272
35 ACROSIN PRECURSOR (EC 3.4.21.10).
6.3e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038

40 F-Y79AA1001328
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
1.3e-08:118:39
RATTUS NORVEGICUS (RAT).
P97677

45 F-Y79AA1001426
BAND 3 ANION TRANSPORT PROTEIN.
1.7e-18:156:32
GALLUS GALLUS (CHICKEN).
50 P15575

F-Y79AA1001427
INDUCIBLE NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR).
1.1e-49:131:51
55 GLYCINE MAX (SOYBEAN).
P39870

F-Y79AA1001430

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- 5 RING CANAL PROTEIN (KELCH PROTEIN).
2.5e-24:157:40
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q04652
- 10 F-Y79AA1001523
TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).
6.2e-15:141:39
HOMO SAPIENS (HUMAN).
Q13263
- 15 F-Y79AA1001530
TUBULIN BETA-5 CHAIN.
8.0e-76:204:76
HOMO SAPIENS (HUMAN).
P04350
- 20 F-Y79AA1001592
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.42:104:33
HOMO SAPIENS (HUMAN).
P23246
- 25 F-Y79AA1001727
AMALGAM PROTEIN PRECURSOR.
1.9e-09:185:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364
- 30 F-Y79AA1001787
PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).
7.6e-43:210:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
35 Q12697
- 40 F-Y79AA1001793
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
0.077:44:40
SUS SCROFA (PIG).
P35323
- 45 F-Y79AA1001795
HYPOTHETICAL BHLF1 PROTEIN.
0.00014:210:31
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181
- 50 F-Y79AA1001799
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
2.8e-18:107:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 55 F-Y79AA1001803
SECRETOGRANIN III PRECURSOR (SGIII).
1.3e-68:182:76

- MUS MUSCULUS (MOUSE).
P47867
- 5 F-Y79AA1001863
GLYCOPROTEIN J.
0.030:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480
- 10 F-Y79AA1002022
WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).
9.8e-08:127:37
HOMO SAPIENS (HUMAN).
P42768
- 15 F-Y79AA1002058
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.28:56:42
20 HOMO SAPIENS (HUMAN).
P49716
- F-Y79AA1002121
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).
25 0.71:57:36
MUS MUSCULUS (MOUSE).
Q60925
- F-Y79AA1002129
30 TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.98:158:24
PSEUDOMONAS AERUGINOSA.
P15276
- 35 F-Y79AA1002213
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
4.7e-39:218:41
CAENORHABDITIS ELEGANS.
Q03567
- 40 F-Y79AA1002334
HYPOTHETICAL PROTEIN MJ1345.
1.8e-08:164:26
METHANOCOCCUS JANNASCHII.
45 Q58741
- F-Y79AA1002373
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
50 0.083:44:40
SUS SCROFA (PIG).
P35323
- F-Y79AA1002376
55 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC (DH IC-2).
3.0e-91:214:83
RATTUS NORVEGICUS (RAT).
Q62871

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F-Y79AA1002378
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
1.0e-59:163:74
MUS MUSCULUS (MOUSE).
Q07231

F-Y79AA1002381
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
9.5e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546

Homology search result 6

[0296] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 5'-ends. except EST and STS sequences

Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0297] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
H.sapiens mitochondrial DNA, complete genome.
6.0e-188:913:97
X93334

F-BNGH41000087
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
7.1e-32:176:99
AL034418

F-BNGH41000091
Homo sapiens potassium channel h-eag.
1.6e-79:687:76
AJ001366

F-HEMBA1000006
S.erythraea second and third ORF's of eryA gene, complete cds.
0.95:243:64
M63677

F-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
5.9e-70:450:89
AL031291

F-HEMBA1000128
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence.
1.0:274:59
Z98549

F-HEMBA1000275

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Herpes simplex virus type 2 (strain HG52), complete genome.

0.036:625:55

Z86099

5 F-HEMBA1000300

Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.

1.4e-40:343:80

AC005702

10 F-HEMBA1000349

Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.

7.5e-65:451:72

AC005922

15 F-HEMBA1000443

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.

8.1e-77:216:95

Z93241

20

F-HEMBA1000462

Caenorhabditis elegans cosmid C49H3.

3.7e-06:98:82

U42436

25

F-HEMBA1000477

Mus musculus BALB/c putative growth factor GDF7 (Gdf7) gene, partial cds.

9.1e-05:190:65

U08339

30

F-HEMBA1000590

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

35

3.0e-102:209:99

AL021578

F-HEMBA1000634

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.

40

2.0e-95:460:99

AC004480

F-HEMBA1000671

Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.

45

1.5e-28:259:69

AC006116

F-HEMBA1000713

Homo sapiens 10kD protein (BC10) mRNA, complete cds.

50

6.5e-126:442:97

AF053470

F-HEMBA1000732

Homo sapiens clone IMAGE Consortium 302831 latent transforming growth factor-beta binding protein 4 mRNA, partial cds.

55

1.7e-45:258:94

AF054502

- 5 F-HEMBA1000745
Streptomyces coelicolor cosmid 3F9.
3.5e-06:360:61
AL023862
- 10 F-HEMBA1000835
Homo sapiens fibrillin mRNA, complete cds.
1.3e-07:151:69
L13923
- 15 F-HEMBA1000875
Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds.
2.6e-28:249:81
U28322
- 20 F-HEMBA1000907
Spermatozopsis similis mRNA for 95 kD basal apparatus-protein.
3.4e-09:599:60
AJ001438
- 25 F-HEMBA1000940
Homo sapiens connexin46.6 (Cx46.6) gene, complete cds.
1.7e-16:307:66
AF014643
- 30 F-HEMBA1000962
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
0.00040:497:59
AC004228
- 35 F-HEMBA1001184
Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds.
8.8e-23:404:67
AF042081
- 40 F-HEMBA1001221
Human transmembrane protein mRNA, complete cds.
2.4e-42:858:63
U19878
- 45 F-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
1.9e-82:470:91
L32137
- 50 F-HEMBA1001272
Human Ig gamma-2 heavy chain switch region.
0.032:549:60
U39934
- 55 F-HEMBA1001296
H.sapiens mRNA for PQ-rich protein.
6.9e-07:73:98
Z50194
- F-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.

- 9.3e-14:143:81
AF017789
- F-HEMBA1001390
5 Mus musculus polymerase I-transcript release factor mRNA, complete cds.
2.5e-56:464:81
AF036249
- F-HEMBA1001563
10 Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.
3.1e-06:210:68
15 AL022165
- F-HEMBA1001621
Human G protein-coupled receptor APJ gene, complete cds.
2.0e-98:516:95
20 U03642
- F-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
1.0e-170:810:98
25 AF090988
- F-HEMBA1001886
Human repressor transcriptional factor (ZNF85) mRNA, complete cds.
3.3e-114:849:80
30 U35376
- F-HEMBA1002048
HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=22 Row=B, genomic survey sequence.
3.8e-11:244:66
35 AQ103440
- F-HEMBA1002131
Homo sapiens mRNA for KIAA0584 protein, partial cds.
3.5e-44:709:66
40 AB011156
- F-HEMBA1002163
Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
2.3e-28:373:71
45 AC002489
- F-HEMBA1002164
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
50 QUENCE.
1.3e-127:493:99
AL031427
- F-HEMBA1002167
55 Rattus norvegicus neuroligin I mRNA, complete cds.
8. 1e-155:850:91
U22952

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5 F-HEMBA1002178
Homo sapiens mRNA for KIAA0584 protein, partial cds.
2.6e-46:794:65
AB011156

10 F-HEMBA1002195
Human lysosomal alpha-mannosidase (manB) gene, 5' flanking region and exon 1.
7.7e-35:255:86
U60885

15 F-HEMBA1002227
Homo sapiens mRNA for 80K-L protein, complete cds.
3.8e-137:382:95
D10522

20 F-HEMBA1002239
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.
4.5e-43:452:74
AC003049

25 F-HEMBA1002316
Homo sapiens DNA sequence from PAC 29C18 on chromosome 22.
3.0e-22:609:67
Z97192

30 F-HEMBA1002420
Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
4.2e-142:322:98
AC005632

35 F-HEMBA1002421
Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.
1.3e-165:778:98
J04621

40 F-HEMBA1002524
Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.
1.3e-153:313:96
AC004209

45 F-HEMBA1002551
Human potential CENP-C binding target sequence, 0.7 kb clone, partial sequence 2.
6.1e-16:108:97
U57994

50 F-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.
1.4e-168:798:98
AF038660

55 F-HEMBA1002985
HS_3165_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3165 Col=16 Row=E, genomic survey sequence.
1.7e-08:127:76
AQ142051

F-HEMBA1002992
RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67815, genomic survey sequence.

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- 2.7e-11:119:86
AQ201833
- F-HEMBA1003047
5 Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
4.5e-187:873:99
AF034611
- F-HEMBA1003072
10 Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.
4.1e-50:515:73
U68380
- F-HEMBA1003101
15 Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
5.3e-139:671:98
AF049891
- F-HEMBA1003120
20 Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
3.3e-44:213:73
AC006116
- F-HEMBA1003230
25 Homo sapiens UP50 mRNA, complete cds.
5.5e-183:856:98
AF093118
- F-HEMBA1003294
30 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SE-
QUENCE.
4.2e-38:558:69
AL031121
- F-HEMBA1003315
35 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.
1.2e-61:737:68
AB013390
- F-HEMBA1003392
40 Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.9e-183:851:99
AF074264
- F-HEMBA1003399
45 Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.
8.7e-16:215:74
AC005282
- F-HEMBA1003487
50 H.sapiens DNA sequence.
0.0075:158:67
Z22340
- F-HEMBA1003497
55 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27O5, WORKING DRAFT SEQUENCE.
1.1e-109:538:98
AL033529

- 5 F-HEMBA1003530
S.scrofa mRNA for BM88 antigen.
2.8e-47:644:69
X82027
- 10 F-HEMBA1003602
Human (lambda) DNA for immunoglobulin light chain.
2.5e-94:551:91
D86997
- 15 F-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
6.1e-151:777:96
AC006011
- 20 F-HEMBA1003945
Homo sapiens clone 638 unknown mRNA, complete sequence.
1.8e-76:310:93
AF091085
- 25 F-HEMBA1004007
F-HEMBA1004067
Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.
8.7e-133:718:94
AL031864
- 30 F-HEMBA1004085
Homo sapiens, clone hRPK.2_A_1, complete sequence.
2.7e-58:256:80
AC006197
- 35 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds.
3.8e-159:779:96
AF064243
- 40 F-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
1.2e-183:863:99
AC005752
- 45 F-HEMBA1004391
H.sapiens gene for neural cell adhesion molecule L1.
0.51:426:59
Z29373
- 50 F-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
3.3e-147:463:93
AC004938
- 55 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds.
0.00036:230:62
AF065389

- 5 F-HEMBA1004505
D.melanogaster mRNA for alpha 1,2 mannosidase.
5.5e-17:663:58
X82640
- 10 F-HEMBA1004785
Gallus gallus mRNA for chromobox protein (CHCB3), complete cds.
6.6e-19:322:68
AB005619
- 15 F-HEMBA1004797
Haemonchus contortus GT microsatellite DNA sequence.
3.0e-08:175:71
U84474
- 20 F-HEMBA1004952
Mus musculus recombinant quaking gene sequence.
4.8e-15:398:65
U44942
- F-HEMBA1004971
F-HEMBA1004982
- 25 F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
2.5e-65:370:93
AB002308
- 30 F-HEMBA1005084
Mouse transcriptional control element.
0.0024:189:63
M17284
- 35 F-HEMBA1005145
Pseudorabies virus glycoprotein gp50 gene, complete cds.
0.00022:395:60
AF092447
- 40 F-HEMBA1005230
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
2.8e-102:302:94
AC006116
- 45 F-HEMBA1005246
Homo sapiens CAGH44 mRNA, partial cds.
5.0e-29:429:66
U80741
- 50 F-HEMBA1005267
Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.
1.0e-43:320:87
AF042089
- 55 F-HEMBA1005337
Plasmodium falciparum MAL3P6, complete sequence.
4.1e-08:84:89

Z98551

F-HEMBA1005430

5 F-HEMBA1005449
T.aestivum mRNA for a proline-rich protein.
0.00097:385:61
X52472

10 F-HEMBA1005489
Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.
15 7.8e-16:405:62
U52111

F-HEMBA1005522
O.cuniculus rACNG mRNA for aorta CNG channel.
20 5.9e-47:344:85
X59668

F-HEMBA1005545
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.
25 5.1e-173:810:98
U29589

F-HEMBA1005698

30 F-HEMBA1005913
HS_2249_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2249
Col=1 Row=J, genomic survey sequence.
0.17:215:61
AQ072649

35 F-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
7.0e-107:285:93
AC005581

40 F-HEMBA1005945
Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.
1.8e-46:670:65
AF004161

45 F-HEMBA1006016
CIT-HSP-2334L16.TF CIT-HSP Homo Sapiens genomic clone 2334L16, genomic survey sequence.
2.1e-13:246:69
AQ038406

50 F-HEMBA1006171

F-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
55 1.4e-144:416:93
AC005261

F-HEMBA1006299

F-HEMBA1006311

F-HEMBA1006335

Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.

5 9.6e-61:370:91

AL023582

F-HEMBA1006357

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

10 2.3e-26:389:67

AF005038

F-HEMBA1006430

Caenorhabditis elegans cosmid T12A2.

15 4.6e-23:283:72

U13019

F-HEMBA1006482

Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.

20 1.9e-144:575:98

AF026852

F-HEMBA1006517

25 F-HEMBA1006544

Homo sapiens suppressor of white-apricot homolog 2 (SWAP2) gene, exons 12 and 13.

2.3e-151:732:97

AF042809

30 F-HEMBA1006572

HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058

Col=22 Row=B, genomic survey sequence.

1.9e-45:245:96

AQ103440

35

F-HEMBA1006658

Homo sapiens mRNA for KIAA0687 protein, partial cds.

3.6e-127:646:95

AB014587

40

F-HEMBA1006707

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

45 1.7e-118:397:98

AL021578

F-HEMBA1006724

H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.

50 1.4e-53:282:97

Z55440

F-HEMBA1006749

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

55

3.9e-116:457:98

AL021578

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- 5 F-HEMBA1006770
Xenopus laevis elav-type ribonucleoprotein (etr-1) mRNA, complete cds.
1.6e-53:280:81
U16800
- 10 F-HEMBA1006902
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
4.9e-122:462:98
AL021578
- 15 F-HEMBA1006912
F-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds.
1.6e-118:651:92
L76687
- 20 F-HEMBA1006960
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.
0.20:298:60
AL033526
- 25 F-HEMBA1007013
Rattus norvegicus repeat element associated with the Rasgrf1 gene.
8.0e-07:531:59
AF056927
- 30 F-HEMBA1007057
Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs, complete sequence.
0.27:277:64
35 Z98885
- F-HEMBA1007063
F-HEMBA1007226
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.
0.00033:488:63
AL031658
- 45 F-HEMBA1007241
Caenorhabditis elegans cosmid T15B7.
0.068:304:59
AF022985
- 50 F-HEMBA1007291
Homo sapiens chromosome 19; fosmid 37502, complete sequence.
6.2e-123:587:98
AC004755
- 55 F-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
1.3e-30:172:97
U56430

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- 5 F-HEMBB1000106
Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.
0.033:332:61
AL030995
- 10 F-HEMBB1000276
Dictyostelium discoideum gene encoding a novel glycoprotein.
0.00070:440:60
AJ005262
- 15 F-HEMBB1000309
Homo sapiens zinc finger protein (MBLL) mRNA, complete cds.
7.6e-34:180:100
AF061261
- 20 F-HEMBB1000407
Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. 0.16:228:64
AC000384
- 25 F-HEMBB1000447
Homo sapiens JWA protein mRNA, complete cds.
1.4e-158:750:98
AF070523
- 30 F-HEMBB1000542
Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.
4.3e-141:874:89
Z99496
- 35 F-HEMBB1000567
Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF.
9.7e-122:572:99
X07868
- 40 F-HEMBB1000642
- 45 F-HEMBB1000668
Caenorhabditis elegans cosmid K06A5.
0.00041:174:64
AF039038
- 50 F-HEMBB1000679
C.familiaris mRNA for TRAM-protein.
6.1e-100:756:80
X63678
- 55 F-HEMBB1000881
Danio rerio mRNA for MINDIN2, complete cds.
6.2e-40:581:66
AB006085
- F-HEMBB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.9e-91:209:94
AC005089

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- 5 F-HEM BB1001026
Human p76 mRNA, complete cds.
1.9e-06:410:61
U81006
- 10 F-HEM BB1001048
Human Hpast (HPAST) mRNA, complete cds.
6.8e-55:524:75
AF001434
- 15 F-HEM BB1001200
Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9
unordered pieces.
4.4e-12:794:59
AC004157
- 20 F-HEM BB1001407
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1
ordered pieces.
2.7e-43:281:91
AC004150
- 25 F-HEM BB1001530
HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens
genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.
2.1e-14:95:97
AQ131814
- 30 F-HEM BB1001547
S.cerevisiae chromosome VII reading frame ORF YGL236c.
1.1e-19:550:61
Z72758
- 35 F-HEM BB1001573
Homo sapiens 12p13.3 PAC RPCI5-951N9 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
2.7e-07:467:60
AC004672
- 40 F-HEM BB1001847
H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.
1.1e-14:94:100
Z64565
- 45 F-HEM BB1001959
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.2e-82:492:90
AL034405
- 50 F-HEM BB1001978
Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.
7.0e-23:239:76
AC005386
- 55 F-HEM BB1002039
Human DNA sequence from cosmid 315B17, between markers DXS366 and DXS87 on chromosome X contains
ESTs.

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- 3.5e-49:605:71
Z73967
- 5 F-HEM BB1002041
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
3.5e-09:501:60
X83546
- 10 F-HEM BB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
3.1e-95:454:99
AF049703
- 15 F-HEM BB1002120
- F-HEM BB1002162
Homo sapiens genethonin 1 mRNA, complete cds.
7.0e-67:328:99
AF062534
- 20 F-HEM BB1002228
Homo sapiens unknown mRNA, complete cds.
1.6e-39:208:98
AF047439
- 25 F-HEM BB1002245
Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds.
3.7e-68:424:87
U26595
- 30 F-HEM BB1002302
RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.
2.7e-15:101:98
B88081
- 35 F-HEM BB1002427
Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
2.9e-123:249:90
AC002319
- 40 F-HEM BB1002465
Mouse short chain acyl-CoA dehydrogenase mRNA, complete cds.
7.9e-18:545:61
L11163
- 45 F-HEM BB1002661
Drosophila melanogaster; Chromosome 2R; Region 44A1-44A2; P1 clone DS07435, WORKING DRAFT SE-
QUENCE, 2 unordered pieces.
1.9e-07:187:67
AC005445
- 50 F-HEM BB1002663
- F-HEM BB1002693
Homo sapiens full length insert cDNA, clone ZD85G07.
2.1e-20:136:93
AF086462
- 55

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F-MAMMA1000046
 CIT-HSP-2166017.TF CIT-HSP Homo sapiens genomic clone 2166O17, genomic survey sequence.
 2.0e-60:345:92
 B92334
 5

F-MAMMA1000102
 Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.
 3.0e-161:766:98
 Z79996
 10

F-MAMMA1000106
 Rat gene for alpha 1B adrenergic receptor, promoter region and partial cds.
 0.0025:247:64
 D32045
 15

F-MAMMA1000118
 Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.
 6.1e-06:545:60
 U73207
 20

F-MAMMA1000141
 Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.
 1.5e-10:151:78
 AC004024
 25

F-MAMMA1000204
 Homo Sapiens mRNA for LGMD2B protein.
 2.1e-166:781:98
 AJ007670
 30

F-MAMMA1000226
 *** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B331O8; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.
 2.9e-35:188:100
 AC004064
 35

F-MAMMA1000403
 Human vascular addressin MAdCAM-1 mRNA, complete cds.
 0.00043:538:59
 U82483
 40

F-MAMMA1000449
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.
 0.090:514:60
 Z97651
 45

F-MAMMA1000457
 H.sapiens mRNA for NADH-cytochrome b5 reductase.
 5.5e-36:469:68
 Y09501
 50

F-MAMMA1000473
 Caenorhabditis elegans cosmid B0491, complete sequence.
 0.0052:187:64
 Z49907
 55

F-MAMMA1000496

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- Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
1.2e-81:318:92
AC004997
- 5 F-MAMMA1000528
P.falciparum complete gene map of plastid-like DNA (IR-B).
0.016:343:58
X95276
- 10 F-MAMMA1000591
Mus musculus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T3 mRNA, complete cds.
1.2e-24:493:63
U70538
- 15 F-MAMMA1000614
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 21 unordered pieces.
7.5e-13:615:60
AC004670
- 20 F-MAMMA1000652
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.
1.6e-59:451:82
AC004638
- 25 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6.
1.2e-32:636:65
AJ000479
- 30 F-MAMMA1000706
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0110D16; HTGS phase 1,
WORKING DRAFT SEQUENCE, 7 unordered pieces.
6.8e-06:428:62
AC004578
- 35 F-MAMMA1000788
HS_3080_A2_B03_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080
Col=6 Row=C, genomic survey sequence.
4.9e-35:204:94
AQ128409
- 40 F-MAMMA1000810
Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.
5.8e-06:246:65
AL022098
- 45 F-MAMMA1000814
Anadara trapezia (alpha 3.15L) hemoglobin alpha-chain (HBA) gene, exons 2 and 3, intron 2, including hypervar-
iable microsatellite polymorphic repeat regions.
1.0e-12:176:75
L25098
- 50 F-MAMMA1000881
Rattus norvegicus serum and glucocorticoid-regulated kinase (sgk) mRNA, complete cds.
2.8e-07:283:63
L01624
- 55

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- 5 F-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
1.8e-166:306:99
AF001550
- 10 F-MAMMA1000994
Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.
0.75:260:61
AL021897
- 15 F-MAMMA1001043
H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2).
0.038:376:60
Z37976
- 20 F-MAMMA1001066
Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence.
4.4e-15:162:72
AD001527
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence.
6.2e-181:844:99
AF091094
- 30 F-MAMMA1001141
Cams familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.
1.3e-10:602:59
U73207
- 35 F-MAMMA1001150
M.musculus (Balb/c) mRNA for serine/threonine protein kinase.
7.7e-57:447:67
Z34524
- 40 F-MAMMA1001237
Rattus norvegicus monocarboxylate transporter MCT3 mRNA, complete cds.
1.5e-08:306:65
AF059258
- 45 F-MAMMA1001284
HS_3076_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3076
Col=15 Row=K, genomic survey sequence.
5.2e-53:307:93
AQ120674
- 50 F-MAMMA1001310
1(2)09851 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3'
end of P element, genomic survey sequence.
0.00072:209:66
AQ025672
- 55 F-MAMMA1001344
Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1)
gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds;
and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete
sequence.
5.2e-05:164:67

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AF026198

F-MAMMA1001418

Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds.

6.0e-35:622:63

U62966

F-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

5.2e-46:538:74

AC004865

F-MAMMA1001609

Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. 0.00031:592:57

AC005886

F-MAMMA1001615

H.sapiens CpG island DNA genomic MseI fragment, clone 71h9, reverse read cpq71h9.rt1a.

1.2e-25:146:99

Z62710

F-MAMMA1001623

Homo sapiens 12q24.2 BAC RPCI11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

3.9e-69:471:85

AC006065

F-MAMMA1001634

Human DNA sequence from PAC 93C23 on chromosome X. Contains steroid 5-alpha-reductase pseudogene, ESTs and STS.

2.2e-22:228:79

AL008713

F-MAMMA1001893

HS_3067_B2_H09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=18 Row=P, genomic survey sequence.

2.5e-29:188:93

AQ138065

F-MAMMA1001901

Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS, complete sequence.

2.0e-23:287:71

Z95118

F-MAMMA1001957

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.5e-14:192:66

AC004573

F-MAMMA1001978

Human immunoglobulin S(u) like sequence.

0.60:150:66

X15517

F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-116:250:93

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AC002073

F-MAMMA1002080

Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.

1.1e-59:493:78

AC004807

F-MAMMA1002087

HS-1047-B2-A09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830

Col=18 Row=B, genomic survey sequence.

2.1e-31:174:98

B38457

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.

1.6e-156:743:98

AF039916

F-MAMMA1002095

Rat alternatively spliced mRNA.

4.9e-126:691:91

M93017

F-MAMMA1002128

Mus musculus C2C12 unknown mRNA, partial cds.

5.0e-41:353:77

U31629

F-MAMMA1002142

F-MAMMA1002165

Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.

1.2e-34:219:90

AF100780

F-MAMMA1002205

Homo Sapiens Chromosome X clone bWXD691, complete sequence.

8.1e-33:535:67

AC004386

F-MAMMA1002224

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.

1.2e-31:274:82

Z86090

F-MAMMA1002234

Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).

9.8e-145:736:91

X53744

F-MAMMA1002586

Drosophila melanogaster cosmid clone 86E4.

0.0071:306:58

AL021086

F-MAMMA1002633

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.

- 3.9e-33:297:79
AL031680
- 5 F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds.
1.7e-82:801:74
AF001434
- 10 F-NT2RM1000407
Cloning vector pUC-GM-INT, complete sequence.
9.4e-141:673:98
AF025392
- 15 F-NT2RM1000462
, complete sequence.
1.5e-86:232:82
AC005300
- 20 F-NT2RM1000542
Mouse beta-galactosidase (BGAL) gene, complete cds.
4.4e-17:468:62
M57734
- 25 F-NT2RM1000580
Caenorhabditis elegans cosmid F09E5.
1.6e-08:352:61
U37429
- 30 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4.
1.1e-94:299:92
Y11306
- 35 F-NT2RM1000855
Canis familiaris sec61 homologue mRNA, complete cds.
6.6e-110:671:87
M96629
- 40 F-NT2RM1000858
tricarboxylate carrier.[rats, liver, mRNA Partial, 2986 nt].
2.0e-65:716:70
S70011
- 45 F-NT2RM1000899
S.pombe chromosome I cosmid c8C9.
0.0010:300:59
Z99168
- 50 F-NT2RM2000241
Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.
0.99:201:65
AC005844
- 55 F-NT2RM2000306
Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseu-
dogenes CYP2D7P, CYP2D8P, CYP2D6(D),TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA
repeat, STS, GSS.
1.1e-142:595:97

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AL021878

- 5 F-NT2RM2000410
S.gregaria Abd-B gene.
0.076:172:66
X69161
- 10 F-NT2RM2000423
Arthrobacter sp. beta-galactosidase gene, complete cds.
4.2e-06:606:57
U78028
- 15 F-NT2RM2000497
Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.
1.2e-55:285:81
AC005969
- 20 F-NT2RM2000514
F-NT2RM2000565
Caenorhabditis elegans cosmid F28C5, complete sequence.
4.2e-18:539:62
Z68315
- 25 F-NT2RM2000582
P.zebra microsatellite locus DNA, 429bp.
0.00015:160:69
X99784
- 30 F-NT2RM2000589
Bos taurus myosin X, complete cds.
3.4e-139:817:88
U55042
- 35 F-NT2RM2000622
H.sapiens MFH-1 gene.
0.0010:466:57
Y08223
- 40 F-NT2RM2000632
Homo sapiens mRNA for TBP-associated factor 170 (TAFII170).
0.0052:331:59
AJ001017
- 45 F-NT2RM2000773
Oryctolagus cuniculus serum amyloid A-activating factor SAF-8 mRNA, partial cds.
2.9e-91:496:93
AF076786
- 50 F-NT2RM2001126
Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.
1.6e-161:663:99
AF093419
- 55 F-NT2RM2001558
Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.
1.2e-164:770:98
AF093408

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F-NT2RM2001626
 F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.
 4.5e-46:606:68
 Z88651
 5

F-NT2RM2001643
 HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT775
 Col=18 Row=J, genomic survey sequence.
 2.5e-06:181:66
 B41504
 10

F-NT2RM2001738
 S.capreolus ard2 gene and orf2, orf4 and orf5.
 0.41:273:63
 Y11036
 15

F-NT2RM2001767
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.
 8.0e-18:130:92
 AL034380
 20

F-NT2RM2001792
 Homo sapiens mRNA for serum lectin P35, complete cds.
 2.5e-12:244:67
 D49353
 25

F-NT2RM2001818

F-NT2RM2001902
 Drosophila melanogaster mRNA for p21 activated kinase related protein.
 7.2e-74:683:75
 AJ011578
 30

F-NT2RM2001939
 Human G protein-coupled receptor GPR-NGA gene, complete cds.
 1.4e-140:702:96
 U55312
 35

F-NT2RM2001941
 Human gene for muscarinic acetylcholine receptor HM1.
 6.3e-20:488:62
 X15263
 40

F-NT2RM4000100
 Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.
 7.7e-25:162:74
 AC004827
 45

F-NT2RM4000115
 50

F-NT2RM4000198

F-NT2RM4000284
 Human IgG Fc receptor hFcRn mRNA, complete cds.
 7.3e-37:194:98
 U12255
 55

F-NT2RM4000295

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Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds.
1.6e-05:642:59
AF047717

5 F-NT2RM4000326
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.
1.0e-127:340:92
AJ003147

10 F-NT2RM4000417
Oncorhynchus kisutch microsatellite OKi20 DNA.
0.44:144:66
AF055444

15 F-NT2RM4000444
S.salar mRNA for transport-associated protein Tap2A.
1.7e-27:577:62
Z83328

20 F-NT2RM4000587
Homo sapiens chromosome 19, cosmid R28058, complete sequence.
7.7e-16:388:64
AC005615

25 F-NT2RM4000593

F-NT2RM4000648
M.musculus mRNA for K-glypican.
30 1.4e-50:610:70
X83577

F-NT2RM4000761
Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
35 4.8e-167:787:98
M10546

F-NT2RM4000965
S.scrofa mRNA for calcium release channel (CRC).
40 0.044:356:60
X62880

F-NT2RM4000997

45 F-NT2RM4001321
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

50 F-NT2RM4001325
Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds.
6.6e-12:384:64
AB012192

55 F-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
9.7e-155:719:99

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AB014538

F-NT2RM4001735

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 483K16, WORKING DRAFT SE-
QUENCE.

1.3e-162:679:96

AL034374

F-NT2RM4001768

Human HepG2 partial cDNA, clone hmd3a07m5.

2.7e-52:271:98

D17020

F-NT2RM4001843

F-NT2RM4002352

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.

1.4e-155:761:97

AB009462

F-NT2RP1000002

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.7e-06:252:65

M21096

F-NT2RP1000050

Human HepG2 partial cDNA, clone hmd3g02m5.

7.1e-18:115:97

D17047

F-NT2RP1000181

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.

4.2e-139:427:98

AC004228

F-NT2RP1000239

Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.

1.4e-90:524:91

U92989

F-NT2RP1000261

Homo sapiens hPMS1 gene, promoter region and exon 1.

2.5e-14:132:85

AB006462

F-NT2RP1000271

Homo sapiens DNA-binding protein mRNA, complete cds.

4.3e-139:678:97

AF038951

F-NT2RP1000300

Homo sapiens, complete sequence.

0.012:146:69

AC005854

F-NT2RP1000325

H.sapiens gene for phosphate carrier.

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- 4.2e-110:438:98
X77337
- 5 F-NT2RP1000448
Streptomyces coelicolor cosmid 1A6.
0.79:209:61
AL023496
- 10 F-NT2RP1000465
Mus musculus nuclear protein NIP45 mRNA, complete cds.
2.2e-29:489:68
U76759
- 15 F-NT2RP1000468
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.6e-49:306:91
AL034405
- 20 F-NT2RP1000551
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.
7.5e-139:742:93
U09585
- 25 F-NT2RP1000579
Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.
3.6e-140:798:91
L21936
- 30 F-NT2RP1000613
Sequence 1 from patent US 5589579.
8.1e-10:468:58
I32995
- 35 F-NT2RP1000679
Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.
1.3e-112:448:89
AC003688
- 40 F-NT2RP1000740
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
9.3e-14:211:73
Z60772
- 45 F-NT2RP1000903
HS_2256_B1_E10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2256
Col=19 Row=J, genomic survey sequence.
9.0e-21:197:84
AQ084622
- 50 F-NT2RP1000981
F-NT2RP1001004
Danio rerio mRNA for MINDIN2, complete cds.
4.1e-22:472:63
AB006085
- 55 F-NT2RP1001020
Mus musculus clone OST66, genomic survey sequence.

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1.5e-47:352:81
AF046696

5 F-NT2RP1001031
CIT-HSP-2330P23.TR CIT-HSP Homo sapiens genomic clone 2330P23, genomic survey sequence.
8.0e-26:145:99
AQ035969

10 F-NT2RP1001563
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. 0.096:405:59
AC004971

15 F-NT2RP2000092
Human zinc finger protein ZNF136.
1.8e-54:652:70
U09367

20 F-NT2RP2000178
Streptomyces coelicolor cosmid 3F9.
0.92:217:64
AL023862

25 F-NT2RP2000240
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
2.9e-96:534:90
AF001550

30 F-NT2RP2000394
Gallus gallus p52 pro-apototic protein mRNA, complete cds.
2.9e-19:380:65
AF029071

35 F-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
1.3e-109:289:98
AC005630

40 F-NT2RP2000479
Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudo-
gene, ESTs and STSs.
0.0039:219:63
AL008627

45 F-NT2RP2000514
Homo sapiens roundabout 2 (robo2) mRNA, partial cds.
3.7e-89:461:95
AF040991

50 F-NT2RP2000533
Mus musculus cornichon mRNA, complete cds.
1.4e-113:677:89
AF022811

55 F-NT2RP2000610
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
4.3e-25:177:89
AL034405

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F-NT2RP2000616
 RPC111-75J11.TK MCI11 Homo sapiens genomic clone R-75J11, genomic survey sequence.
 8.4e-34:135:91
 AQ268877

5

F-NT2RP2000649
 Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.
 1.2e-165:802:97
 AF064867

10

F-NT2RP2000663
 Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.
 1.6e-106:365:97
 Z73913

15

F-NT2RP2000694
 Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
 4.2e-112:561:96
 AJ012159

20

F-NT2RP2000712
 HS_3071_A2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
 Plate=3071 Col=10 Row=G, genomic survey sequence.
 7.6e-78:389:97
 AQ166085

25

F-NT2RP2000739
 Human mRNA for KIAA0326 gene, partial cds.
 6.4e-24:574:62
 AB002324

30

F-NT2RP2000818
 Drosophila melanogaster, chromosome 2R, region 38A5-38B4, BAC clone BACR48M05, complete sequence.
 0.00047:304:61
 AC005719

35

F-NT2RP2000903
 Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
 2.6e-110:541:97
 AJ012159

40

F-NT2RP2001200
 Homo sapiens mRNA for KIAA0676 protein, partial cds.
 3.3e-1 10:540:96
 AB014576

45

F-NT2RP2001223
 HS-1054-B2-C02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776
 Col=4 Row=F, genomic survey sequence.
 7.2e-10:128:77
 B41982

50

F-NT2RP2001276
 Mouse regulatory protein (npdc-1) mRNA, complete cds.
 1.2e-38:296:81
 L03814

55

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5 F-NT2RP2001388
RPCI11-30G23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30G23, genomic survey sequence.
0.32:53:94
B87787

10 F-NT2RP2001469
M.musculus tex292 mRNA (5'region).
4.2e-10:120:83
X80434

15 F-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
9.0e-140:686:96
L38969

20 F-NT2RP2001495
Human transporter protein (g17) mRNA, complete cds.
1.9e-35:581:64
U49082

25 F-NT2RP2001514
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
3.7e-22:475:62
AC005115

30 F-NT2RP2001529
Homo sapiens mRNA for ZIP-kinase, complete cds.
4.6e-152:757:96
AB007144

35 F-NT2RP2001538
Sequence 11 from patent US 5624818.
1.4e-88:528:88
I41141

40 F-NT2RP2001562
Homo sapiens GLE1 (GLE1) mRNA, complete cds.
2.3e-117:572:97
AF058922

45 F-NT2RP2001662
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
6.1e-107:365:91
AL031662

50 F-NT2RP2001755
Sequence 9 from patent US 5750502.
1.5e-53:518:75
AR007441

55 F-NT2RP2001769
A.sativa Aspk11 mRNA.
4.7e-17:537:60
X79992

F-NT2RP2001817
Candida albicans SIR2 (SIR2) gene, complete cds.
4.6e-10:285:61

AF045774

F-NT2RP2001878

Mus musculus repeat element upstream of the Rasgrf1/Cdc25Mm gene.

5 5.0e-06:554:60

AF021791

F-NT2RP2001903

M.musculus mRNA for m-calpain.

10 3.1e-06:337:60

Y10139

F-NT2RP2001915

Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.

15 6.8e-28:488:65

AC005670

F-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

20 1.1e-77:148:99

AC005538

F-NT2RP2001948

Sequence 2 from patent US 5541311.

25 0.59:284:57

I24091

F-NT2RP2001956

Feline c-sis proto-oncogene, segment 4.

30 0.99:101:69

M25356

F-NT2RP2002015

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775

35 Col=18 Row=J, genomic survey sequence.

3.0e-06:181:65

B41504

F-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

40 1.3e-108:418:94

AC004050

F-NT2RP2002188

Rattus norvegicus neuroligin 3 mRNA, complete cds.

45 1.0e-125:700:90

U41663

F-NT2RP2002232

50

F-NT2RP2002304

Human FMR1 gene, 5' end.

0.12:93:67

L19476

55

F-NT2RP2002409

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partial cds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1 (rpoE1), and response regulator homolog (frzS) genes, complete cds; and unknown

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- genes.
9.0e-10:553:59
AF049107
- 5 F-NT2RP2002510
Mus musculus (129SV) DNA, unmapped BAC 10817, complete sequence.
4.2e-27:573:62
AC004093
- 10 F-NT2RP2002527
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.
3.2e-110:439:99
AC004228
- 15 F-NT2RP2002533
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds.
6.4e-141:726:95
AF040709
- 20 F-NT2RP2002564
Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.
2.6e-112:403:98
AC004941
- 25 F-NT2RP2002674
HS_3122_B2_A02_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122 Col=4 Row=B, genomic survey sequence.
4.8e-13:86:100
AQ182907
- 30 F-NT2RP2002721
- 35 F-NT2RP2002824
Arabidopsis thaliana BAC T19D16 genomic sequence.
1.3e-12:135:69
U95973
- 40 F-NT2RP2002942
Homo sapiens mRNA for KIAA0806 protein, complete cds.
6.1e-145:758:94
AB018349
- 45 F-NT2RP2002974
Mus musculus mRNA for Six5, partial cds.
8.0e-84:588:82
D83146
- 50 F-NT2RP2002976
H.sapiens gene for phospholipase C beta 3, exon 14.
0.93:210:61
Z37557
- 55 F-NT2RP2003042
G.gallus mRNA for lecithin-cholesterol acyltransferase.
9.1e-26:462:65
X91011

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5 F-NT2RP2003138
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
3.9e-142:702:96
AL031662

10 F-NT2RP2003179
Homo sapiens mRNA for KIAA0537 protein, complete cds.
3.3e-42:587:70
AB011109

15 F-NT2RP2003210
Mus musculus fatty acid transport protein 4 mRNA, partial cds.
2.6e-112:726:85
AF072759

20 F-NT2RP2003302
Human zinc finger protein ZNF136.
5.5e-63:691:69
U09367

25 F-NT2RP2003369
Homo sapiens chromosome 7q22 sequence, complete sequence.
2.0e-49:249:95
AF053356

30 F-NT2RP2003383
Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds.
1.5e-159:817:95
AF016005

35 F-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds.
7.0e-115:554:98
AF100141

40 F-NT2RP2003469
Genomic sequence from Human 9q34, complete sequence.
5.6e-38:210:97
AC001644

45 F-NT2RP2003545
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.
2.2e-48:579:71
AF024636

50 F-NT2RP2003593
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SE-
QUENCE.
1.8e-90:326:99
AL021396

55 F-NT2RP2003599

F-NT2RP2003655
M.musculus tex261 mRNA.
5.3e-77:513:85
X81058

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5	F-NT2RP2003664 Homo sapiens mRNA for leptin receptor gene-related protein. 1.7e-132:630:98 Y12670
10	F-NT2RP2003931 Homo sapiens chromosome 19, overlapping cosmids R27918 and R33775, complete sequence. 1.3e-114:411:97 AC004447
15	F-NT2RP2003940 Human ZNF43 mRNA. 1.4e-97:693:82 X59244
20	F-NT2RP2003950 Sequence 1 from patent US 5648238. 6.9e-13:143:79 I55887
25	F-NT2RP2004069 F-NT2RP2004108 Human zinc finger protein ZNF136. 1.5e-67:548:78 U09367
30	F-NT2RP2004141 Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon. 8.0e-10:487:62 U87960
35	F-NT2RP2004179 Homo sapiens chromosome 11 from 11p15.5 region, complete sequence. 0.56:600:57 AF015416
40	F-NT2RP2004205 Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence. 0.32:431:55 AC005356
45	F-NT2RP2004447 Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces. 2.0e-23:252:79 AC000353
50	F-NT2RP2004495 Human transporter protein (g17) mRNA, complete cds. 3.6e-25:497:61 U49082
55	F-NT2RP2004524 Genomic sequence from Human 9q34, complete sequence. 5.9e-60:203:98 AC001644
	F-NT2RP2004556

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HS_3022_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022
Col=21 Row=A, genomic survey sequence.

1.3e-51:419:79

AQ119143

5

F-NT2RP2004606

cDNA encoding NIC(Natural Inhibitor of Collagenase).

1.2e-113:617:92

E00985

10

F-NT2RP2004648

Felis catus lysosomal beta-galactosidase (Bgal) mRNA, complete cds.

1.5e-15:403:64

AF006749

15

F-NT2RP2004670

Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.

1.1e-73:493:85

L22557

20

F-NT2RP2004794

Mus musculus mRNA for B-IND1 protein.

5.6e-12:109:86

Z97207

25

F-NT2RP2004837

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.8e-39:352:78

AC006030

30

F-NT2RP2004847

CIT-HSP-2357D24.TR CIT-HSP Homo sapiens genomic clone 2357D24, genomic survey sequence.

2.5e-35:196:96

AQ074738

35

F-NT2RP2005027

Human glucose transporter-like protein-III (GLUT3), complete cds.

2.2e-145:713:96

M20681

40

F-NT2RP2005069

Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.

9.4e-51:200:90

U35245

45

F-NT2RP2005163

Mouse DNA fragment that hybridizes to HSV-1 Smal A fragment.

1.4e-08:231:67

M11041

50

F-NT2RP2005181

Mus musculus cationic amino acid trmsporter (CAT3) mRNA, complete cds.

1.6e-96:575:85

U70859

55

F-NT2RP2005247

Mus musculus ret finger protein mRNA, complete cds.

1.8e-13:310:66

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L46855

F-NT2RP2005378

RPCI11-21D23.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21D23, genomic survey sequence.

5 3.0e-12:131:80

B85846

F-NT2RP2005391

S.muris mRNA for microneme antigen.

10 2.5e-10:345:61

Z26947

F-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

15 1.0e-116:566:97

AB018346

F-NT2RP2005463

20 F-NT2RP2005514

F-NT2RP2005535

Homo sapiens DNA-binding protein mRNA, complete cds.

25 2.3e-125:726:90

AF038951

F-NT2RP2005541

CIT-HSP-2386E2.TF.1 CIT-HSP Homo sapiens genomic clone 2386E2, genomic survey sequence.

30 6.2e-20:152:88

AQ240341

F-NT2RP2005597

D.melanogaster mRNA for rotated abdomen protein.

35 0.088:270:57

X95956

F-NT2RP2005632

Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.

40 2.0e-07:207:67

U47276

F-NT2RP2005666

Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.

45 1.0:328:57

AC005849

F-NT2RP2005774

Human zinc finger protein ZNF136.

50 4.0e-44:451:74

U09367

F-NT2RP2005878

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

55 5.1e-16:382:63

AF064635

F-NT2RP2005883

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-

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GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
1.5e-30:191:95
AL023578

5 F-NT2RP2005887

Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
1.8e-50:394:79
AC006030

10 F-NT2RP2005941

Human DNA sequence from cosmid CFAT5, chromosome region 11p13 contains PAX6 exons 1-4, EST and CpG Islands.
9.5e-93:468:96
Z95332

15

F-NT2RP2005994

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
1.6e-139:692:96
AC004050

20

F-NT2RP2006004

CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.
6.6e-39:206:98
AQ080257

25

F-NT2RP2006042

Human mRNA for KIAA0144 gene, complete cds.
1.7e-10:220:69
D63478

30

F-NT2RP2006092

Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
3.6e-121:562:82
AC005214

35

F-NT2RP2006099

Human Chromosome 11 pac pDJ392a17, complete sequence.
8.7e-76:383:92
AC000385

40

F-NT2RP2006134

Homo sapiens Chromosome 22q11.2 Cosmid Clone 91c In DGCR Region, complete sequence. 0.055:125:71
AC000091

45

F-NT2RP2006269

D.melanogaster mRNA for rotated abdomen protein.
5.4e-05:357:58
X95956

50

F-NT2RP2006512

Sequence 1 from Patent EP 0285405.
3.7e-102:659:85
I05465

55

F-NT2RP3000011

RPCI11-43E12.TJ RPCI11 Homo sapiens genomic clone R-43E12, genomic survey sequence.
1.8e-10:113:84
AQ195722

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- F-NT2RP3000022
Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.
5 6.7e-116:284:99
AL031178
- F-NT2RP3000059
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
10 0.0031:511:59
X83546
- F-NT2RP3000063
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
15 0.20:544:57
AC004755
- F-NT2RP3000125
HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.
20 1.0e-21:161:88
AQ101452
- F-NT2RP3000148
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
25 5.2e-40:257:77
AC002310
- F-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
30 3.4e-106:501:99
AF093239
- F-NT2RP3000171
Mus musculus mRNA for B-IND1 protein.
35 1.8e-97:571:89
Z97207
- F-NT2RP3000172
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
40 2.0e-123:702:86
L22557
- F-NT2RP3000201
Homo sapiens mRNA for KIAA0687 protein, partial cds.
45 9.2e-170:792:98
AB014587
- F-NT2RP3000232
HS_3238_B2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=8 Row=H, genomic survey sequence.
50 9.2e-24:174:88
AQ219879
- F-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
55 3.3e-171:797:98
AF074264

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5 F-NT2RP3000378
Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.
5.8e-137:774:89
L38621

10 F-NT2RP3000427
Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.
1.5e-18:390:65
M21096

15 F-NT2RP3000436
cDNA encoding a human novel protein disulfide isomerase like enzyme, EP52.
4.5e-05:353:59
E13330

20 F-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.
9.7e-75:203:97
AL022315

25 F-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.
7.1e-131:643:88
M96629

30 F-NT2RP3000481
Homo sapiens RanBP7/importin 7 mRNA, complete cds.
1.7e-162:770:98
AF098799

35 F-NT2RP3000616
Homo sapiens KIAA0405 mRNA, complete cds.
4.7e-31:579:62
AB007865

40 F-NT2RP3000645
Human chromosome 12p13 sequence, complete sequence.
5.9e-07:484:61
U47924

45 F-NT2RP3000652
Human ZNF43 mRNA.
4.4e-131:853:84
X59244

50 F-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
2.7e-86:420:98
AB007915

55 F-NT2RP3000677
Human estrogen receptor-related protein (variant ER from breast cancer) mRNA, complete cds.
2.9e-21:125:100
M69296

F-NT2RP3000721
HS_2221_A2_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221
Col=2 Row=E, genomic survey sequence.

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0.94:254:60
AQ253443

- 5 F-NT2RP3000789
Mus musculus coding region determinant binding protein mRNA, complete cds.
5.4e-139:827:87
AF061569
- 10 F-NT2RP3000818
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
3.0e-28:218:86
Z97201
- 15 F-NT2RP3000820
Mus musculus WSB-1 mRNA, complete cds.
1.1e-77:477:87
AF033186
- 20 F-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.6e-77:682:79
AB014538
- 25 F-NT2RP3000871
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds.
5.8e-07:350:60
AF043431
- 30 F-NT2RP3000907
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
1.7e-13:330:62
AC005115
- 35 F-NT2RP3000921
cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell.
6.8e-68:812:69
E12950
- 40 F-NT2RP3001012
cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).
2.4e-129:692:92
E12829
- 45 F-NT2RP3001044
Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
3.7e-60:393:79
AC006030
- 50 F-NT2RP3001061
F.rubripes GSS sequence, clone 154E17aC12, genomic survey sequence.
1.8e-07:239:62
AL018519
- 55 F-NT2RP3001159
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
4.4e-24:156:72

AC004770

F-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

5 2.3e-181:859:98

AB018327

F-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

10 3.8e-53:253:92

AC001644

F-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

15 1.4e-133:740:87

M96629

P-NT2RP3001271

Homo sapiens chromosome 19, cosmid F20237, complete sequence.

20 0.082:370:60

AC005775

F-NT2RP3001322

Homo sapiens mRNA for KIAA0566 protein, partial cds.

25 1.9e-38:728:63

AB011138

F-NT2RP3001388

Rattus norvegicus synaptotagmin XI mRNA, complete cds.

30 1.2e-103:701:83

AF000423

F-NT2RP3001542

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

35 8.6e-17:293:65

U73643

F-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

40 7.8e-135:742:91

D67067

F-NT2RP3001592

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

45 7.2e-12:188:71

U22398

F-NT2RP3001650

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

50 1.9e-26:374:72

AC005281

F-NT2RP3001685

Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.

55 4.6e-73:284:98

AC004550

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F-NT2RP3001738
 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
 1.8e-21:186:67
 5 AC004770

F-NT2RP3001754
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
 5.0e-21:131:96
 10 AL034380

F-NT2RP3001858
 Homo sapiens mRNA for KIAA0584 protein, partial cds.
 5.9e-39:770:63
 15 AB011156

F-NT2RP3001976
 M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
 2.0e-37:536:70
 20 Z30174

F-NT2RP3002015
 Homo sapiens huntingtin gene, partial exon.
 0.024:175:65
 25 L49359

F-NT2RP3002160
 Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
 1.6e-95:249:91
 30 AC002319

F-NT2RP3002281
 Homo sapiens mRNA for KIAA0765 protein, partial cds.
 1.6e-149:713:98
 35 AB018308

F-NT2RP3002286
 Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
 2.0e-136:756:92
 40 U57368

F-NT2RP3002311
 Mouse beta-galactosidase (BGAL) gene, complete cds.
 1.0e-29:624:63
 45 M57734

F-NT2RP3002324
 Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.
 5.7e-122:655:93
 50 Z69890

F-NT2RP3002342
 Human transporter protein (g17) mRNA, complete cds.
 9.8e-36:565:65
 55 U49082

F-NT2RP3002353

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- Streptomyces phaeochromogenes plasmid pJV1, complete sequence.
0.15:466:60
U23762
- 5 F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-189:897:98
AB018262
- 10 F-NT2RP3002411
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
7.8e-122:796:84
AF064635
- 15 F-NT2RP3002448
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
4.0e-11:403:64
X83546
- 20 F-NT2RP3002571
Bos taurus mRNA for lyncein.
8.7e-114:652:90
Y17923
- 25 F-NT2RP3002664
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
6.1e-14:211:72
Z60772
- 30 F-NT2RP3002721
Homo sapiens citrate synthase mRNA, complete cds.
7.5e-179:873:96
AF047042
- 35 F-NT2RP3002737
Homo sapiens mRNA for HNSPC, complete cds.
1.4e-42:409:75
D82346
- 40 F-NT2RP3002738
Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.
8.9e-122:812:83
D29766
- 45 F-NT2RP3002790
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
2.2e-15:626:62
U22398
- 50 F-NT2RP3002836
Homo sapiens mRNA for KIAA0463 protein, partial cds.
6.8e-152:717:99
AB007932
- 55 F-NT2RP3002887
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
2.0e-05:491:59
X83546

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F-NT2RP3002900
 Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.
 7.3e-13:327:66
 U26264
 5

F-NT2RP3002958
 Mus musculus IgK chain (6S) intron with insertion/deletion mutations.
 5.6e-22:403:66
 L12153
 10

F-NT2RP3002983
 Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.
 1.2e-118:339:99
 AP000047
 15

F-NT2RP3003000
 Homo sapiens T-type calcium channel:alpha-1 subunit mRNA, complete cds.
 7.9e-88:555:88
 AF051946
 20

F-NT2RP3003076
 Streptomyces coelicolor cosmid 2A11.
 0.15:505:59
 AL031184
 25

F-NT2RP3003354
 Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.
 1.2e-34:625:64
 AF005038
 30

F-NT2RP3003448
 CIT-HSP-721P7.TV CIT-HSP Homo sapiens genomic clone 721P7, genomic survey sequence.
 1.2e-16:126:89
 B50017
 35

F-NT2RP3003469
 Homo sapiens chromosome 19, cosmid F23990, complete sequence.
 2.0e-18:126:94
 AC005262
 40

F-NT2RP3003473
 Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence.
 7. 1e-68:474:71
 AC005181
 45

F-NT2RP3003527
 Homo sapiens mRNA for protein kinase Dyrk1B.
 1.4e-160:769:98
 Y17999
 50

F-NT2RP3003532
 Mus musculus cell surface molecule OX-2 mRNA, complete cds.
 1.3e-96:712:80
 AF004023
 55

F-NT2RP3003535
 Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence, complete sequence. 0.027:155:65
 AC004313

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- 5 F-NT2RP3003559
H.sapiens CpG island DNA genomic MseI fragment, clone 171h5, reverse read cpg171h5.rt1a.
3.9e-50:261:97
Z59762
- 10 F-NT2RP3003614
Mus musculus semaphorin VIa mRNA, complete cds.
1.7e-131:811:86
AF030430
- 15 F-NT2RP3003729
Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-ordered pieces.
1.4e-97:259:91
AC006171
- F-NT2RP3003849
- 20 F-NT2RP3003874
M.musculus mRNA for myosin I heavy chain.
2.9e-151:863:89
X69987
- 25 F-NT2RP3003939
T24C19TF TAMU Arabidopsis thaliana genomic clone T24C19, genomic survey sequence.
1.4e-19:293:68
B29025
- 30 F-NT2RP3003963
CIT-HSP-2050C19.TF CIT-HSP Homo sapiens genomic clone 2050C19, genomic survey sequence.
1.3e-16:111:95
B80539
- 35 F-NT2RP3004000
Homo sapiens klotho gene, exon 1.
0.042:430:60
AB009666
- 40 F-NT2RP3004025
Human DNA sequence from Fosmid 49D8 on chromosome 22, complete sequence.
0.062:197:65
Z82186
- 45 F-NT2RP3004067
Human mRNA for KIAA0375 gene, complete cds.
1.7e-33:556:66
AB002373
- 50 F-NT2RP3004075
jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.
1.5e-12:438:61
B13419
- 55 F-NT2RP3004083
- F-NT2RP3004090
Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

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1.4e-06:469:60
L01060

5 F-NT2RP30041 19
Human mRNA for KIAA0215 gene, complete cds.
1.3e-72:640:75
D86969

10 F-NT2RP3004130
F-NT2RP3004133
Pseudomonas aeruginosa phage phi CTX DNA, complete genome.
0.0018:421:60
Y13918

15 F-NT2RP3004202
F-NT2RP3004294
Xenopus laevis ER1 mRNA, complete cds.
20 5.0e-77:335:78
AF015454

25 F-NT2RP3004309
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete se-
quence.
9.6e-25:231:65
AC004770

30 F-NT2RP3004321
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
3.7e-80:279:95
AF015416

35 F-NT2RP3004345
Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
7.2e-12:188:71
U22398

40 F-NT2RP3004355
HS_3212_A1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3212 Col=15 Row=E, genomic survey sequence.
0.061:266:65
AQ176625

45 F-NT2RP3004374
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

50 F-NT2RP3004406
CIT-HSP-2340N18.TF CIT-HSP Homo sapiens genomic clone 2340N18, genomic survey sequence.
9.9e-74:359:99
AQ058326

55 F-NT2RP3004481
Mus musculus bassoon gene, exon 6 to 11.
0.0060:528:59

Y17038

F-NT2RP3004552

Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.

5 7.6e-40:731:64

D64009

F-NT2RP3004557

Human Ki nuclear autoantigen mRNA, complete cds.

10 8.1e-120:626:94

U11292

F-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

15 9.8e-151:710:98

AF082516

F-NT2RP3004640

Bos taurus tuftelin mRNA, complete cds.

20 8.2e-104:565:87

AF105228

F-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds.

25 2.1e-109:524:98

AB007915

F-NT2RP4000108

Human gene for neurofilament subunit NF-L.

30 7.0e-158:862:93

X05608

F-NT2RP4000634

Sequence 11 from patent US 5753446.

35 2.9e-155:828:92

AR008281

F-NT2RP4000962

Mus musculus clone OST66, genomic survey sequence.

40 6.0e-48:352:81

AF046696

F-NT2RP4001001

Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.

45 4.8e-47:360:84

AC005915

F-NT2RP4001009

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

50 5.9e-175:828:98

AF064867

F-NT2RP4001467

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

55 3.3e-159:742:98

X55740

F-NT2RP4001877

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1.7e-27:401:69
AC005637

5 F-NT2RP4001879

F-NT2RP4002187
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.
4.2e-115:777:83
AF064635

10 F-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
6.1e-86:452:96
Z98200

15 F-NT2RP4002715
Homo sapiens clone NH0523H20, complete sequence.
3.6e-59:410:77
AC005041

20 F-NT2RP4002750
Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.
3.4e-105:586:87
U70859

25 F-OVARC1000003
B.taurus mRNA for sodium dependent phosphate transporter.
9.0e-125:823:83
X81699

30 F-OVARC1000090
RPCI11-25E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-25E14, genomic survey sequence.
1.9e-06:151:74
B86784

35 F-OVARC1000105
S.cerevisiae UBC6 gene.
4.6e-25:525:64
X73234

40 F-OVARC1000137
Human SNARE protein Ykt6 (YKT6) mRNA, complete cds.
1.2e-33:184:98
U95735

45 F-OVARC1000208
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.
1.7e-79:362:91
AC002544

50 F-OVARC1000255
Porcine protein-tyrosine kinase (syk) mRNA, complete cds.
4.9e-116:424:88
M73237

55 F-OVARC1000275
Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..
333303.

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0.32:314:61
AJ011930

5 F-OVARC1000298
Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.5e-121:306:98
AC005632

10 F-OVARC1000307
Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].
0.017:162:67
X94677

15 F-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds.
1.7e-119:585:97
AB011145

20 F-OVARC1000331
Sequence 2 from patent US 5756332.
1.9e-48:290:91
AR009648

25 F-OVARC1000410
Homo sapiens mRNA for angiopoietin-like factor.
4.6e-26:538:62
Y16132

30 F-OVARC1000439
F-OVARC1000467
HS_3008_A2_D12_MR CIT Approved Human Genomic Sperm Library D, Homo sapiens genomic clone
Plate=3008 Col=24 Row=G, genomic survey sequence.
2.0e-11:132:82
35 AQ116995

F-OVARC1000529
HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092
Col=22 Row=F, genomic survey sequence.
40 8.2e-12:115:84
AQ127947

F-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894, complete sequence.
45 6.5e-92:221:96
AC005594

F-OVARC1000775
Human chromosome 3p21.1 gene sequence.
50 6.9e-69:380:95
L13435

F-OVARC1000811
Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
55 6.7e-77:500:86
AC004235

F-OVARC1000853

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HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234
Col=9 Row=K, genomic survey sequence.

4.6e-05:111:71

AQ191345

5

F-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

8.2e-42:234:96

10

AL034418

F-OVARC1000916

Sequence 3 from patent US 5674748.

2.0e-55:422:84

15

I68139

F-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

1.2e-107:540:97

20

Z69708

F-OVARC1000995

H.sapiens genomic DNA (chromosome 3; clone NL1106D).

4.3e-28:166:95

25

X87478

F-OVARC1001030

Human mRNA for KIAA0339 gene, complete cds.

2.1e-10:334:64

30

AB002337

F-OVARC1001049

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.

5.4e-12:420:62

35

AC004670

F-OVARC1001086

Homo sapiens cyclin T2a mRNA, complete cds.

1.9e-164:761:99

40

AF048731

F-OVARC1001132

Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.

1.5e-89:328:75

45

AP000038

F-OVARC1001163

Caenorhabditis elegans cosmid F40E10, complete sequence.

3.8e-26:337:71

50

Z69792

F-OVARC1001222

CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.

1.2e-08:171:70

55

B57734

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- F-OVARC1001260
- F-OVARC1001336
B.taurus mRNA for sodium dependent phosphate transporter.
5 5.4e-83:622:80
X81699
- F-OVARC1001338
HS_2181_B2_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181
10 Col=22 Row=J, genomic survey sequence.
2.3e-17:144:86
AQ022764
- F-OVARC1001569
15 Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.
2.9e-06:241:63
AF100904
- F-OVARC1001570
20 Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.
1.6e-10:235:64
AJ011929
- F-OVARC1001596
25 Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
2.2e-45:498:73
AC005951
- F-OVARC1001607
30 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
1.7e-38:323:80
U15128
- F-OVARC1001725
35 Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
3.5e-172:821:98
AF064800
- F-OVARC1001727
40 Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
2.2e-132:633:98
AL031132
- F-OVARC1001807
45 Human TR3 orphan receptor mRNA, complete cds.
7.1e-90:566:87
L13740
- F-OVARC 1001833
50 Rattus norvegicus cis-Golgi matrix protein GM130 mRNA, complete cds.
5.2e-46:364:79
U35022
- F-OVARC1001952
55 Homo sapiens FGFR-4 gene.
1.7e-14:392:62
Y13901

5 F-OVARC1001991
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.
2.3e-06:298:64
U73643

10 F-OVARC1002058
, complete sequence.
1.3e-108:617:92
AC005500

15 F-OVARC1002178
Herpes simplex virus type 2 (strain HG52), complete genome.
0.43:234:63
Z86099

20 F-PLACE1000033
Mus musculus otogelin mRNA, complete cds.
5.9e-18:579:59
U96411

25 F-PLACE1000231
Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.
1.1e-18:273:68
AF037272

30 F-PLACE1000258
Human KRAB zinc finger protein (ZNP177) mRNA, complete cds.
1.2e-13:241:70
U37263

35 F-PLACE1000442
Human zinc finger protein ZNF136.
2.3e-87:774:76
U09367

40 F-PLACE1000560
Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
4.1e-107:318:96
AC005368

45 F-PLACE1000740
Rat notch 2 mRNA.
1.1e-37:399:74
M93661

50 F-PLACE1000907
RPC11-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.
3.5e-21:147:92
AQ269030

55 F-PLACE1000912

F-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.8e-74:206:93
AC002093

F-PLACE1000927

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- Cowpox virus strain GRI-90 DNA (49 kb fragment).
6.8e-75:683:74
Y15035
- 5 F-PLACE1000986
RPCI11-75H23.TK RPCI11 Homo sapiens genomic clone R-75H23, genomic survey sequence.
1.0:316:57
AQ268409
- 10 F-PLACE1001016
Human dihydropyridine-sensitive L-type calcium channel alpha-1 subunit (CACNL1A3) mRNA, complete cds.
0.28:432:59
L33798
- 15 F-PLACE1001100
RPCI11-32N5.TK RPCI-11 Homo sapiens genomic clone RPCI-11-32N5, genomic survey sequence.
0.48:145:64
AQ047336
- 20 F-PLACE1001114
Lysobacter enzymogenes beta-lactamase gene sequence.
0.033:349:60
M97392
- 25 F-PLACE1001123
F.rubripes GSS sequence, clone 084A20aC12, genomic survey sequence.
9.7e-05:138:64
AL015804
- 30 F-PLACE1001183
Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.
0.15:576:59
AC005091
- 35 F-PLACE1001229
F.rubripes GSS sequence, clone 144D13aC10, genomic survey sequence.
2.2e-21:271:70
AL017986
- 40 F-PLACE1001231
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
6.4e-102:677:84
AF026554
- 45 F-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds.
1.3e-130:636:97
AB018262
- 50 F-PLACE1001401
CIT-HSP-2323H22.TR CIT-HSP Homo sapiens genomic clone 2323H22, genomic survey sequence.
6.4e-13:165:76
AQ028562
- 55 F-PLACE1001407
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
2.4e-28:228:85
AL023582

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5 F-PLACE1001464
Human placental cDNA coding for 5 nucleotidase (EC 3.1.3.5).
5.0e-151:742:96
X55740

10 F-PLACE1001500
CIT-HSP-2368L16.TR CIT-HSP Homo sapiens genomic clone 2368L16, genomic survey sequence.
1.1e-25:150:97
AQ078655

15 F-PLACE1001516
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.
1.2e-139:676:98
AC002425

20 F-PLACE1001536
Human Chromosome X clone bWXd173, WORKING DRAFT SEQUENCE, 2 ordered pieces.
1.7e-142:513:97
AC004387

25 F-PLACE1001564
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
QUENCE.
2.9e-104:373:89
AL033377

30 F-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.
1.3e-123:585:98
AF043472

35 F-PLACE1001788
Homo sapiens mRNA for HYA22, complete cds.
9.9e-21:234:75
D88153

40 F-PLACE1001795
Drosophila melanogaster; Chromosome 3L; Region 83F1-83F2; P1 clone DS07437, WORKING DRAFT SE-
QUENCE, 3 unordered pieces.
1.4e-05:218:64
AC005985

45 F-PLACE1001836
Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence.
4.9e-79:577:82
AC004022

50 F-PLACE1001918
Arabidopsis thaliana BAC T19D16 genomic sequence.
3.7e-24:417:63
U95973

55 F-PLACE1001949
S.cerevisiae chromosome XV reading frame ORF YOR291w.
3.6e-16:255:70
Z75199

F-PLACE1002080

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- Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.
7.5e-129:622:98
AF039691
- 5 F-PLACE1002095
Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.
2.3e-48:551:71
AC004219
- 10 F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
8.3e-161:764:98
AF095791
- 15 F-PLACE1002329
Sequence 12 from Patent WO 9000403.
6.9e-05:380:63
I09634
- 20 F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds.
2.8e-17:190:77
AF055917
- 25 F-PLACE1002374
Human mRNA for pro-cathepsin L(major excreted protein MEP).
6.2e-162:716:94
X12451
- 30 F-PLACE 1002518
HS_3091_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3091
Col=15 Row=K, genomic survey sequence.
3.2e-74:316:94
AQ123005
- 35 F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.6e-171:819:98
AB018262
- 40 F-PLACE1002726
CIT-HSP-2369G10.TR CIT-HSP Homo sapiens genomic clone 2369G10, genomic survey sequence.
4.8e-18:135:88
AQ075115
- 45 F-PLACE1002905
Drosophila melanogaster DNA sequence (P1 DS00906 (D99)), complete sequence.
3.7e-06:235:66
AC004154
- 50 F-PLACE1002911
Bovine herpesvirus 1 complete genome.
0.93:264:63
AJ004801
- 55 F-PLACE1002967
Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds.
0.0041:302:60

L35848

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

4.7e-49:450:75

AF024636

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-152:722:98

AF069301

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

6.3e-141:682:97

AF068227

F-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2, ESTs, GSSs,, complete sequence.

1.2e-116:286:100

AL032821

F-PLACE1003438

Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.

0.13:468:60

AF092918

F-PLACE1003460

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

5.8e-05:111:71

AQ191345

F-PLACE1003529

Homo sapiens clone DJ0981O07, complete sequence.

5.8e-134:457:97

AC006017

F-PLACE1003573

Sequence 2 from patent US 5792648.

0.93:186:62

AR022348

F-PLACE1003598

Mus musculus mismatch repair protein (MSH6) gene, exon 1.

3.3e-07:311:63

AF031085

F-PLACE1003644

Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.

1.8e-06:138:74

AC001234

F-PLACE1003737

Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.

1.4e-165:791:98

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AC005859

F-PLACE1003772

Human p300/CBP-associated factor (P/CAF) mRNA, complete cds.

5 2.2e-07:448:61

U57317

F-PLACE1003839

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.

10 2.0e-106:525:97

AC004131

F-PLACE1003845

Caenorhabditis elegans cosmid D2096.

15 9.8e-26:386:69

U40800

F-PLACE1003852

Homo sapiens mRNA for KIAA0758 protein, partial cds.

20 7.4e-171:814:98

AB018301

F-PLACE1004028

F-PLACE1004078

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

2.0e-116:274:98

AC005281

30 F-PLACE1004166

HS_3223_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223

Col=17 Row=O, genomic survey sequence.

0.77:304:58

AQ193346

35

F-PLACE1004168

F-PLACE1004199

CIT-HSP-2328F14.TR CIT-HSP Homo sapiens genomic clone 2328F14, genomic survey sequence.

40 9.4e-16:186:76

AQ042262

F-PLACE1004279

Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.

45 1.2e-18:456:62

AF057039

F-PLACE1004282

F-PLACE1004305

Homo sapiens mRNA for KIAA0740 protein, complete cds.

2.7e-121:612:96

AB018283

55

F-PLACE1004441

Human G protein-coupled receptor (GPR1) gene, complete cds.

2.4e-104:537:95

U13666

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F-PLACE1004450
 Pleuronectes americanus aminopeptidase N (ampN) mRNA, complete cds.
 3.1e-20:601:60
 AF012465
 5

F-PLACE1004482
 HS_3032_B1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
 Plate=3032 Col=5 Row=F, genomic survey sequence.
 1.1e-86:423:98
 10 AQ129106

F-PLACE1004492
 Human DNA sequence from PAC 434P1 on chromosome 22. Contains inward rectifier potassium channel 4, (po-
 tassium channel, inwardly rectifying, subfamily J, member 4) (hippocampal inward rectifier) (HIR) (HRK1) (HIRK2)
 15 (KIR2.3), ESTs similar to lumen protein retaining receptor 2 (KDEL receptor 2), DEAD-box protein P72, ESTs, CpG
 islands.
 0.17:180:67
 Z97056

F-PLACE1004519
 Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene,
 VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete
 sequence.
 1.1e-75:432:84
 20 AL021808

F-PLACE1004520
 Human pregnancy-specific beta-1-glycoprotein mRNA PSG95, complete cds.
 4.1e-109:606:92
 25 M34715

F-PLACE1004630
 Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds.
 6.2e-138:749:92
 35 AB008375

F-PLACE1004637
 HS-1061-B1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 783
 Col=19 Row=J, genomic survey sequence.
 0.013:92:75
 40 B45487

F-PLACE1004648

F-PLACE1004816
 Homo sapiens mRNA for Hakata antigen, complete cds.
 3.8e-98:590:90
 45 D88587

F-PLACE1004887
 Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.
 1.2e-06:469:60
 50 L01060

F-PLACE1005003
 Human SNC19 mRNA sequence.
 4.8e-20:472:63
 55 U20428

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- 5 F-PLACE1005005
Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.
7.8e-143:650:97
AJ011930
- 10 F-PLACE1005031
Bovine chlorine channel protein (p64) mRNA, complete cds.
7.1e-62:463:83
L16547
- 15 F-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-31.
2.2e-14:115:85
AJ223349
- 20 F-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
3.3e-40:370:77
U50734
- 25 F-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.7e-126:633:96
AF093118
- 30 F-PLACE1005410
Rattus rattus sec61 homologue mRNA, complete cds.
1.9e-115:771:85
M96630
- 35 F-PLACE1005426
Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.
7.2e-113:391:96
AC005392
- 40 F-PLACE1005519
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.
1.0e-53:521:74
AF024636
- 45 F-PLACE1005539
c-erbB=proto-oncogene {exon 1, promoter} [chickens, Genomic, 700 nt].
3.6e-05:434:62
S66408
- 50 F-PLACE1005544
Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.
3.3e-56:575:74
U89915
- 55 F-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
1.1e-118:381:96
AL034397
- F-PLACE1005601
Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

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3.9e-143:697:98
AC002073

5 F-PLACE1005660

F-PLACE1005669
Fruit fly (*D.melanogaster*) Glued mRNA, complete cds.
3.4e-14:275:66
J02932

10 F-PLACE1005682
Mus musculus Ankhzn mRNA, complete cds.
0.75:347:57
AB011370

15 F-PLACE1005725
Homo sapiens huntingtin (HD) gene, exon 1.
1.4e-06:425:62
L27350

20 F-PLACE1005736

F-PLACE1005745
HS_3039_B1_F12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039
Col=23 Row=L, genomic survey sequence.
1.0:283:59
AQ155068

25 F-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
1.5e-141:719:96
Z82185

30 F-PLACE1005815
Sequence 1 from patent US 5571905.
0.088:199:62
I28535

35 F-PLACE1005878
Bovine chlorine channel protein (p64) mRNA, complete cds.
2.5e-54:394:84
L16547

40 F-PLACE1005927
HS_3138_B2_B03_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138
Col=6 Row=D, genomic survey sequence.
8.0e-32:162:95
AQ183333

45 F-PLACE1006071
1.6e-180:877:96
AF028816

50 F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
1.7e-94:464:98
AB009598

55

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F-PLACE1006079
 Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.
 5.2e-107:423:96
 AF028233

5
 F-PLACE1006093
 jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.
 0.00018:316:60
 B13419

10
 F-PLACE1006208
 Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
 1.4e-12:421:64
 L14320

15
 F-PLACE1006219
 Caenorhabditis elegans cosmid D2096.
 6.4e-25:386:69
 U40800

20
 F-PLACE1006277
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
 7.2e-135:381:97
 AL034397

25
 F-PLACE1006290
 Caenorhabditis elegans cosmid F09E5.
 1.4e-08:354:61
 U37429

30
 F-PLACE1006443
 Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
 2.9e-80:168:95
 AC002093

35
 F-PLACE1006515
 Homo sapiens mRNA for KIAA0576 protein, partial cds.
 4.2e-140:655:99
 AB011148

40
 F-PLACE1006716
 Human DNA sequence from PAC 151B14 on chromosome 22q12-qter contains somatostatin receptor subtype 3 (SSTR3), tRNA, ESTs, CpG island and STS.
 2.2e-51:621:70
 Z86000

45
 F-PLACE1006786
 CITBI-E1-2502A9.TR CITBI-E1 Homo sapiens genomic clone 2502A9, genomic survey sequence.
 0.43:237:64
 AQ264473

50
 F-PLACE1006809
 HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.
 2.1e-14:95:97
 AQ131814

55

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5 F-PLACE1006959
HS_3247_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247
Col=5 Row=J, genomic survey sequence.
1.1e-09:199:70
AQ220414

10 F-PLACE1007028
Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene,
complete sequence.
2.0e-24:658:62
AC005950

15 F-PLACE1007040
Mus musculus neuronal intermediate filament protein (alpha-internexin) gene, complete cds.
8.8e-09:585:62
L27220

20 F-PLACE1007077

20 F-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
2.3e-42:228:97
AQ016433

25 F-PLACE1007096

30 F-PLACE1007296
Human mRNA for a presumptive KDEL receptor.
1.3e-71:542:83
X55885

35 F-PLACE1007591
Homo sapiens full length insert cDNA clone YP44A02.
1.1e-18:141:90
AF085890

40 F-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
7.8e-104:516:97
AF047439

45 F-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
7.5e-50:439:77
AC002348

50 F-PLACE1007845
Caenorhabditis elegans cosmid F09E5.
4.4e-08:355:62
U37429

55 F-PLACE1007881
CITBI-E1-2517N6.TF CITBI-E1 Homo sapiens genomic clone 2517N6, genomic survey sequence.
1.4e-14:104:95
AQ279407

F-PLACE1007971
HS_3237_B2_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237

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- Col=18 Row=L, genomic survey sequence.
1.2e-12:169:76
AQ206052
- 5 F-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
4.5e-101:192:100
AC005995
- 10 F-PLACE1008297
Mycoplasma genitalium random genomic clone hg1, partial cds.
0.099:193:60
U02109
- 15 F-PLACE1008359
Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate CL16-1 (Chr.16).
0.53:185:65
AJ001218
- 20 F-PLACE1008469
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.2e-93:213:98
AC002093
- 25 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
5.7e-144:693:98
AF049703
- 30 F-PLACE1008657
Bovine mRNA for adseverin, complete cds.
5.6e-140:782:90
D26549
- 35 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
1.1e-133:648:97
U15128
- 40 F-PLACE1008744
Sequence 1 from patent US 5691147.
8.4e-91:475:95
I76197
- 45 F-PLACE1008984
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
4.2e-103:493:99
AL031427
- 50 F-PLACE1008985
Mus musculus synaptotagmin VIII mRNA, partial cds.
1.1e-23:289:72
U20107
- 55 F-PLACE1009067
H.sapiens CpG island DNA genomic Mse1 fragment, clone 52e12, forward read cpg52e12.ft1a.
1.2e-28:164:96

Z61442

F-PLACE1009196

5 F-PLACE1009279
H.sapiens mRNA for serine protease.
6.0e-10:327:64
Y07921

10 F-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds.
2.0e-19:125:96
U82613

15 F-PLACE1009546
S.lividans mercury resistance operon.
0.56:358:59
X65467

20 F-PLACE1009600
Mouse mRNA for tetracycline transporter-like protein, complete cds.
2.1e-128:718:91
D88315

25 F-PLACE1009735
Homo sapiens clone NH0523H20, complete sequence.
2.9e-128:613:99
AC005041

30 F-PLACE1009982

F-PLACE1010011
, complete sequence.
2.1e-26:234:83
35 AC005409

F-PLACE1010078
Saccharomyces cerevisiae chromosome XII cosmid 8300.
0.066:273:58
40 U19028

F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
7.0e-150:733:97
45 AF027706

F-PLACE1010251
Sequence 1 from patent US 5665588.
0.0012:309:62
50 I64695

F-PLACE1010445
Herpes simplex virus type 2 (strain HG52), complete genome.
9.4e-07:511:58
55 Z86099

F-PLACE1010713
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

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- 2.1e-89:612:83
AF064635
- 5 F-PLACE1010784
Sequence 1 from patent US 5686597.
2.5e-103:505:98
I73723
- 10 F-PLACE1010827
Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.
7.3e-13:327:66
U26264
- 15 F-PLACE1010968
O.cuniculus mRNA for titin.
0.44:165:64
X64696
- 20 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.8e-127:595:99
AF094516
- 25 F-PLACE1011116
HS_2033_A2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033
Col=10 Row=I, genomic survey sequence.
8.3e-29:192:92
AQ229784
- 30 F-PLACE1011181
H.sapiens CpG island DNA genomic Mse1 fragment, clone 99f2, reverse read cpg99f2.rt1a.
4.8e-35:200:95
Z64239
- 35 F-PLACE1011236
Mus musculus mRNA for RST, complete cds.
4.5e-54:717:66
AB005451
- 40 F-PLACE1011364
Homo sapiens protein kinase/endoribonulcease (IRE1) mRNA, complete cds.
0.13:502:57
AF059198
- 45 F-PLACE1011407
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
7.2e-15:313:68
Z30174
- 50 F-PLACE1011516
Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SE-
QUENCE, 4 unordered pieces.
1.8e-16:317:66
AC005720
- 55 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
1.8e-143:722:96

AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds.

5 5.0e-100:561:92

U26424

F-PLACE 101 1978

Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.

10 9.6e-76:722:74

M27877

F-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

15

5.2e-112:568:95

AL022578

20

F-PLACE2000219

Homo sapiens Down Syndrome critical region, partial sequence.

0.0059:144:71

AF015262

25

F-PLACE3000181

Sequence 102 from patent US 5643781.

4.1e-127:745:90

I51041

30

F-PLACE3000213

F-PLACE4000354

HS_3071_A2_B06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071

35

Col=12 Row=C, genomic survey sequence.

4.4e-12:335:64

AQ137396

F-PLACE4000455

Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.

40

9.5e-118:563:98

M63896

F-SKNMC1000004

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

45

2.9e-141:292:98

AC005632

F-SKNMC1000014

CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.

50

0.89:136:67

AQ075724

F-SKNMC1000082

H.sapiens CpG island DNA genomic MseI fragment, clone 26g3, reverse read cpg26g3.rt1b.

55

5.6e-06:60:98

265216

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	F-THYRO1000036
	F-THYRO1000061
5	Homo sapiens chromosome 19, cosmid R28991, complete sequence. 2.4e-105:425:94 AC004623
	F-THYRO1000099
10	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon. 0.35:609:57 U87960
	F-THYRO1000196
15	Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds. 5.1e-125:475:98 AF016272
	F-THYRO1000400
20	Mycobacterium tuberculosis sequence from clone y423. 1.0:264:59 AD000014
	F-THYRO1000580
25	HS_3216_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=17 Row=O, genomic survey sequence. 2.8e-25:157:96 AQ184086
	F-THYRO1000584
30	Boar mRNA for 135kDa protein, complete cds. 2.0e-104:787:80 D28521
	F-THYRO1000678
35	M.musculus Cx30 gene. 6.9e-41:285:85 Z70023
	F-THYRO1000776
40	Drosophila melanogaster DNA sequence (P1 DS08948 (D168)), complete sequence. 2.7e-10:389:59 AC004288
	F-THYRO1000795
45	Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier. 1.2e-107:736:83 AJ223355
	F-THYRO1000846
50	CITBI-E1-2505H6.TR CITBI-E1 Homo sapiens genomic clone 2505H6, genomic survey sequence. 0.00025:351:61 AQ260270
	F-THYRO1000866
55	Homo sapiens SKB1Hs mRNA, complete cds. 3.3e-91:529:89 AF015913

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- 5 F-THYRO1000956
Human G protein-coupled receptor APJ gene, complete cds.
3.8e-148:724:97
U03642
- 10 F-THYRO1000964
Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
5.0e-37:714:64
AF091624
- 15 F-THYRO1000999
CITBI-E1-2508B3.TF CITBI-E1 Homo sapiens genomic clone 2508B3, genomic survey sequence.
1.2e-06:280:62
AQ261426
- 20 F-THYRO1001063
H.sapiens (xs174) mRNA, 300bp.
1.6e-41:298:85
Z36825
- 25 F-THYRO1001071
Human mRNA for KIAA0154 gene, partial cds.
7.4e-16:197:73
D63876
- 30 F-THYRO1001102
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
3.5e-10:128:83
AC004997
- 35 F-THYRO1001113
Homo sapiens mRNA for LGMD2B protein.
8.8e-52:684:68
AJ007670
- 40 F-THYRO1001128
Homo sapiens chromosome 9q34, clone 63G10, complete sequence.
1.2e-141:227:97
AC002096
- 45 F-THYRO1001205
- F-THYRO1001237
Mus musculus interleukin-2 (II-2) gene, 5'end.
0.77:78:74
L07576
- 50 F-THYRO1001242
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
5.1e-127:721:90
D67067
- 55 F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds.
2.7e-41:806:62
U66088
- F-THYRO1001327

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Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
3.1e-117:374:96
5 AL021578

F-THYRO1001456

F-THYRO1001457
10 M.musculus (Balb/c) mRNA for serine/threonine protein kinase.
1.8e-57:491:69
Z34524

F-THYRO1001471
15 Sequence 52 from Patent WO9712992.
0.00019:546:58
A62364

F-THYRO1001478
20

F-THYRO1001495
Homo sapiens clone DJ1163L11, complete sequence.
4.4e-20:222:76
AC005230

25 F-THYRO1001523
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F17, WORKING DRAFT SEQUENCE.
8.8e-21:538:62
30 Z83845

F-THYRO1001529
M.musculus mRNA for serine palmitoyltransferase subunit B.
5.8e-32:448:66
35 X95642

F-THYRO1001593
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
5.8e-91:213:98
40 AC005581

F-THYRO1001608
Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.
45 0.0028:335:65
AE000662

F-THYRO1001641
Leishmania major chromosome 3 clone L6290 strain Friedlin, WORKING DRAFT SEQUENCE, 2 ordered pieces.
50 0.92:378:61
AC005928

F-THYRO1001700
HS_3220_A1_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=15 Row=C, genomic survey sequence.
55 1.0e-49:265:96
AQ184388

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F-THYRO1001702
 Mus musculus mRNA for myeloid associated differentiation protein.
 1.4e-70:502:82
 AJ001616

5
 F-THYRO1001725
 F.rubripes GSS sequence, clone 133B16aE1, genomic survey sequence.
 3.8e-06:249:65
 AL004967

10
 F-THYRO1001770
 S.cerevisiae chromosome II reading frame ORF YBR059c.
 1.5e-07:320:62
 Z35928

15
 F-THYRO1001803
 Homo sapiens chromosome 10 clone CRI-JC2019 map 10q22.1-10q22.2, WORKING DRAFT SEQUENCE, 1
 ordered pieces.
 1.2e-38:234:94
 AC006108

20
 F-Y79AA1000030
 Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
 9.9e-92:389:98
 AC005214

25
 F-Y79AA1000127
 Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
 9.2e-131:359:100
 AP000034

30
 F-Y79AA1000207
 Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
 2.2e-151:302:98
 AC005562

35
 F-Y79AA1000226
 Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.
 1.1e-50:549:67
 AC004573

40
 F-Y79AA1000270
 Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.
 6.4e-111:771:83
 U10039

45
 F-Y79AA1000426
 Mus musculus activin beta E subunit mRNA, complete cds.
 2.4e-87:703:76
 U96386

50
 F-Y79AA1000521
 Homo sapiens LERK-6 (EPLG6) gene, exon 1.
 0.0092:148:68
 U92893

55
 F-Y79AA1000750
 Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

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9.0e-07:143:74
AC002544

F-Y79AA1000776

5

F-Y79AA1000777
Podospora anserina beta transducin-like protein (het-e1) gene, complete cds.
6.6e-17:760:59
L28125

10

F-Y79AA1000876
Homo sapiens long form transcription factor C-MAF (c-maf) mRNA, complete cds.
3.3e-10:323:66
AF055377

15

F-Y79AA1000888
Streptomyces coelicolor cosmid 8A6.
3.1e-06:665:59
AL031013

20

F-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.6e-52:277:96
AF093420

25

F-Y79AA1000967
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
2.9e-131:752:86
L22557

30

F-Y79AA1001013

F-Y79AA1001056
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.2e-85:676:79
U50734

35

F-Y79AA1001062
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.
8.6e-17:293:65
U73643

40

F-Y79AA1001090
Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.
1.9e-05:223:63
AC004596

45

F-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds.
4.7e-162:763:98
AF038961

50

F-Y79AA1001264
Drosophila melanogaster DNA sequence (P1s DS00764 (D273) and DS00501 (D274)), complete sequence.
1.2e-32:599:63
AC005269

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F-Y79AA1001272

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Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.

1.2e-11:356:67

AJ009613

5

F-Y79AA1001328

Rattus norvegicus Delta 3 mRNA, complete cds.

2.1e-51:443:76

AF084576

10

F-Y79AA1001426

HS_3146_A1_A10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146

Col=19 Row=A, genomic survey sequence.

9.0e-23:106:91

AQ141090

15

F-Y79AA1001427

Bovine cytochrome b5 reductase mRNA, partial cds.

1.4e-55:670:70

M83104

20

F-Y79AA1001430

Homo sapiens mRNA for KIAA0469 protein, complete cds.

8.6e-123:577:99

AB007938

25

F-Y79AA1001523

Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds.

3.3e-91:496:93

AF009353

30

F-Y79AA1001530

Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.

1.8e-126:764:89

AL030996

35

F-Y79AA1001592

HS_3219_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=24 Row=I, genomic survey sequence.

5.2e-36:234:89

AQ180547

40

F-Y79AA1001727

F-Y79AA1001787

S.pombe chromosome III cosmid c1672.

8.8e-11:409:58

50

AL031324

F-Y79AA1001793

Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.

0.12:131:70

55

AL025355

F-Y79AA1001795

Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11

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- to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.
1.2e-140:672:98
AL031228
- 5
- F-Y79AA1001799
S.pombe chromosome I cosmid c8C9.
0.00031:300:60
Z99168
- 10
- F-Y79AA1001803
Mus musculus secretogranin III (SgIII) mRNA, complete cds.
4.6e-101:516:82
U02982
- 15
- F-Y79AA1001863
Homo sapiens DNA, anonymous heat-stable fragment RP5-6A.
5.2e-85:410:99
AB012170
- 20
- F-Y79AA1002022
CIT-HSP-2053H1.TF CIT-HSP Homo sapiens genomic clone 2053H1, genomic survey sequence.
4.3e-20:130:95
B68526
- 25
- F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence.
5.3e-153:740:98
AF052149
- 30
- F-Y79AA1002121
F-Y79AA1002129
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
5.5e-12:565:61
L14320
- 35
- F-Y79AA1002213
Rattus norvegicus brain specific Na+-dependent inorganic phosphate cotransporter mRNA, complete cds.
4.0e-12:434:60
U07609
- 40
- F-Y79AA1002334
F.rubripes GSS sequence, clone 174E24aB10, genomic survey sequence.
3.0e-10:171:72
AL019366
- 45
- F-Y79AA1002373
Rattus norvegicus Smad8 mRNA, complete cds.
0.96:420:61
AF012347
- 50
- F-Y79AA1002376
Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.
- 55

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1.1e-132:805:88
U39045

5 F-Y79AA1002378
Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.9e-64:521:78
D10630

10 F-Y79AA1002381
O.sativa mRNA for cdc2+/CDC28-related protein kinase.
3.3e-21:431:60
X58194

15 Homology search result 7

[0298] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 3'-ends. except EST and STS sequences.

20 Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

25 [0299] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone. Data were not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000006

30 R-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
2.2e-43:355:80
AL031291

35 R-HEMBA1000128
Homo sapiens chromosome X, PAC 671D9, complete sequence.
0.99:389:60
AF031078

40 R-HEMBA1000275
Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG
island.
3.4e-10:212:66
45 Z93023

R-HEMBA1000300
{Alu RNA transcript, clone NE461} [human, embryonal carcinoma cells, NTera2D1 pluripotent cells, Other RNA,
282 nt].
50 4.6e-42:246:89
S42653

R-nnnnnnnnnnnnn
Homo sapiens chromosome 17, clone hRPK.235_L_10, complete sequence.
55 1.0e-71:192:95
AC005922

R-HEMBA1000462

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- Homo sapiens clone 243 unknown mRNA, complete sequence.
8.3e-90:313:94
AF091094
- 5 R-HEMBA1000477
Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 8/11.
0.22:377:60
AB020865
- 10 R-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial.
8.0e-101:547:93
AJ007581
- 15 R-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.95:186:62
20 AC004480
- R-HEMBA1000671
RPC111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.
2.1e-09:165:73
25 AQ237194
- R-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
1.2e-117:575:97
30 AF053470
- R-HEMBA1000732
Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.
1.4e-108:581:93
35 Y13622
- R-nnnnnnnnnnnnn
- R-HEMBA1000875
40 Homo sapiens chromosome 17, clone hRPK.1090_M_7, complete sequence.
0.044:253:64
AC005274
- R-HEMBA1000940
45 ***ALU WARNING: Human Alu-J subfamily consensus sequence.
1.9e-33:222:82
U14567
- R-HEMBA1000962
- 50 R-HEMBA1001184
Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.00044:466:58
55 AC004688
- R-HEMBA1001221
Sequence 1 from patent US 5633147.

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- 7.1e-11:232:65
I43819
- 5 R-HEMBA1001228
Human gemline oligomeric matrix protein (COMP) mRNA, complete cds.
7.8e-89:358:96
L32137
- 10 R-HEMBA1001272
nbxb0003bDO1r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003G00r, genomic survey sequence.
0.00014:201:64
AQ050116
- 15 R-HEMBA1001296
Homo sapiens PAC clone DJ1168D11 from 7p21-p22, complete sequence.
0.13:440:58
AC004614
- 20 R-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.
5.0e-92:466:96
AF017789
- 25 R-HEMBA1001390
CIT-HSP-2314K10.TR CIT-HSP Homo sapiens genomic clone 2314K10, genomic survey sequence.
3.4e-43:196:85
AQ027191
- 30 R-HEMBA1001563
H.sapiens villin gene, exon 1.
2.1e-43:342:81
X71058
- 35 R-HEMBA1001621
Human G protein-coupled receptor APJ gene, complete cds.
1.2e-41:288:87
U03642
- 40 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
2.0e-79:434:93
AF090988
- 45 R-HEMBA1001886
Human zinc finger protein (ZNF141) mRNA, complete cds.
1.8e-59:530:80
L15309
- 50 R-HEMBA1002048
Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.
0.36:322:61
AC005355
- 55 R-HEMBA1002131
Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.
0.22:233:61
AL031730

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R-HEMBA1002163
 Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
 1.1e-16:275:69
 AC002489

5

R-HEMBA1002167
 Rattus norvegicus neuroligin I mRNA, complete cds.
 8.7e-23:193:84
 U22952

10

R-HEMBA1002178

 R-HEMBA1002195
 Homo sapiens DHPS gene, exons 8 to 9.
 1.4e-19:114:100
 AJ001704

15

R-HEMBA1002227
 Homo sapiens mRNA for 80K-L protein, complete cds.
 6.1e-115:567:97
 D10522

20

R-HEMBA1002316
 Homo sapiens mRNA for putative GTP-binding protein.
 1.5e-18:161:85
 Y14391

25

R-HEMBA1002420
 Caenorhabditis elegans cosmid C27A7, complete sequence.
 0.88:214:62
 Z81041

30

R-HEMBA1002421
 Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.
 6.0e-90:443:97
 J04621

35

R-HEMBA1002524
 Human MHC Class I region proline rich protein mRNA, complete cds.
 3.2e-110:551:96
 U63336

40

R-HEMBA1002551
 Mouse Bac 276o8, WORKING DRAFT SEQUENCE, 25 unordered pieces.
 7.0e-06:397:61
 AC003022

45

R-HEMBA1002767
 Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.
 4.2e-110:568:96
 AC005038

50

R-HEMBA1002985
 Homo sapiens chromosome 17, clone hRPK.15_K_2, complete sequence.
 3.4e-23:184:86
 AC005901

55

R-HEMBA1003047

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Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
5.0e-114:571:96
AF034611

5 R-HEMBA1003072
HS-1014-B1-F12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789
Col=23 Row=L, genomic survey sequence.
1.5e-62:340:94
B32084

10 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
3.8e-116:575:97
AF049891

15 R-HEMBA1003120
HS_3220_A1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=7 Row=K, genomic survey sequence.
3.6e-61:354:92
20 AQ184345

R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
1.3e-42:258:93
25 AF093118

R-HEMBA1003294
HS_3220_A1_D03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=5 Row=G, genomic survey sequence.
30 0.0095:204:63
AQ190655

R-HEMBA1003315
Sus scrofa DNA for LH beta, exons 1, 2, 3, complete cds.
35 6.6e-24:163:79
D00579

R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
40 2.6e-115:557:98
AF074264

R-HEMBA1003399
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.
45 1.8e-63:166:100
AC004971

R-HEMBA1003487

50 R-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27O5, WORKING DRAFT SEQUENCE.
1.4e-119:592:97
AL033529

55 R-HEMBA1003530

R-HEMBA1003602
Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.

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- 9.4e-79:468:91
AC002041
- 5 R-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
2.0e-118:586:98
AC006011
- 10 R-HEMBA1003945
Human calcineurin B mRNA, complete cds.
8.9e-82:410:97
M30773
- 15 R-HEMBA1004007
Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.
6.7e-56:404:75
AC004851
- 20 R-HEMBA1004085
G.gallus microsatellite DNA (LEI0311 (= EC12A05)).
0.66:144:65
Z95196
- 25 R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds.
2.1e-115:569:97
AF064243
- 30 R-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
3.8e-98:478:98
AC005752
- 35 R-HEMBA1004391
Plasmodium falciparum MAL3P8, complete sequence.
0.29:126:65
AL034560
- 40 R-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
8.4e-52:308:78
AC004938
- 45 R-HEMBA1004454
CIT-HSP-2337122.TF CIT-HSP Homo sapiens genomic clone 2337122, genomic survey sequence.
0.78:59:77
AQ038475
- 50 R-HEMBA1004505
R-HEMBA1004785
R-HEMBA1004797
- 55 R-HEMBA1004952
Mus musculus diabetic embryopathy (Dep-1) mRNA.
3.4e-39:327:82
AF032130

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- R-HEMBA1004971
Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.
0.00040:251:66
AC005099
- 5 R-HEMBA1004982
Strongyloides fulleborni 18S ribosomal RNA and 5.8S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, complete sequence.
0.092:191:63
10 U43581
- R-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
1.2e-94:381:91
15 AB002308
- R-HEMBA1005084
- R-HEMBA1005145
20 Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.
5.7e-58:283:84
AJ003147
- R-HEMBA1005230
25 CIT-HSP-2333N15.TR CIT-HSP Homo sapiens genomic clone 2333N15, genomic survey sequence.
5.5e-31:363:73
AQ040189
- R-HEMBA1005246
30 Homo sapiens full length insert cDNA clone YX52E07.
1.6e-11:173:72
AF086040
- R-HEMBA1005267
35 Sequence 1 from patent US 5618695.
2.4e-73:536:81
I40055
- R-HEMBA1005337
40 Caenorhabditis elegans cosmid K07D4.
0.16:157:63
AF077534
- R-HEMBA1005430
45 R-HEMBA1005449
- R-HEMBA1005489
50 Anopheles rangeli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.
0.020:271:61
U35272
- R-HEMBA1005522
55 R-HEMBA1005545
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

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1.8e-115:579:96
U29589

5 R-HEMBA1005698
0.0065:223:65
AG004952

10 R-HEMBA1005913
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
3.7e-15:272:68
AC003037

15 R-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
9.4e-55:502:76
AC005581

20 R-HEMBA1005945
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SE-
QUENCE.
0.45:245:62
AL034410

25 R-HEMBA1006016
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
3.5e-25:415:66
AC005562

30 R-HEMBA1006171
Human DNA sequence from PAC 433M19 on chromosome Xq26.3-Xq27.1. Contains ESTs, STSs and polymorphic
CA repeat.
1.0:176:64
Z95703

35 R-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
2.8e-118:592:96
AC005261

40 R-HEMBA1006299

R-HEMBA1006311

45 R-HEMBA1006335
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
6.1e-111:578:96
AL023582

50 R-HEMBA1006357
Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.
4.8e-11:174:74
AC004469

55 R-HEMBA1006430
Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.
8.7e-45:402:79
AC004086

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R-HEMBA1006482
 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
 1.7e-105:537:96
 AF026852

5

R-HEMBA1006517
 345A19.TV CIT978SKA1 Homo sapiens genomic clone A-345A19, genomic survey sequence.
 1.5e-44:176:88
 B15409

10

R-HEMBA1006544
 Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
 2.5e-66:310:83
 AC004997

15

R-HEMBA1006572
 Homo sapiens reduced folate carrier (RFC1) gene, exons 1a, 1c and 1b.
 0.028:255:64
 U92868

20

R-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds.
 7.3e-1 11:570:94
 AB014587

25

R-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial.
 5.1e-78:389:97
 AJ007581

30

R-HEMBA1006724
 HS_2052_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
 Plate=2052 Col=15 Row=F, genomic survey sequence.
 2.6e-46:309:88
 AQ305998

35

R-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial.
 3.2e-88:472:94
 AJ007581

40

R-HEMBA1006770
 Homo sapiens CAGH4 mRNA, partial cds.
 6.5e-25:145:82
 U80746

45

R-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial.
 9.3e-112:540:98
 AJ007581

50

R-HEMBA1006912
 ***ALU WARNING: Human Alu-Sc subfamily consensus sequence.
 6.6e-48:279:92
 U14571

55

R-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds.

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- 1.8e-114:346:99
L76687
- 5 R-HEMBA1006960
Homo sapiens chromosome 19, cosmid F16403, complete sequence.
0.78:203:62
AC005777
- 10 R-HEMBA1007013
Human mRNA for DNA-binding protein TAXREB302, complete cds.
6.3e-31:163:100
D28468
- 15 R-HEMBA1007057
CIT-HSP-517F5.TP CIT-HSP Homo sapiens genomic clone 517F5, genomic survey sequence.
1.0:128:67
B49904
- 20 R-HEMBA1007063
Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein
S6 kinase, EST, GSS, STS. CpG island, complete sequence.
5.0e-43:300:88
AL022069
- 25 R-HEMBA1007241
HIV-1 RNA V3 region (patient Y, sample Y1, clone 05).
0.74:148:66
Z47529
- 30 R-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
3.6e-36:300:80
AC004755
- 35 R-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
7.3e-15:148:80
U56430
- 40 R-HEMBA1000106
Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.
8.0e-05:313:60
L40609
- 45 R-HEMBA1000276
HS_3048_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3048 Col=14 Row=E, genomic survey sequence.
0.91:234:58
AQ099411
- 50 R-HEMBA1000309
- R-HEMBA1000407
Mus musculus clone OST5976, genomic survey sequence.
6.4e-28:226:81
AF046768
- 55 R-HEMBA1000447

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- Homo sapiens JWA protein mRNA, complete cds.
1.7e-107:533:97
AF070523
- 5 R-HEM BB1000542
Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
4.4e-72:547:80
AF084259
- 10 R-HEM BB1000567
Human insulin-like growth factor (IGF-II) gene, exon 1 of 4.
4.3e-60:368:88
M13970
- 15 R-HEM BB1000642
Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.
2.9e-42:431:75
ZB4483
- 20 R-HEM BB1000668
CITBI-E1-2508D15.TR CITBI-E1 Homo sapiens genomic clone 2508D15, genomic survey sequence.
2.5e-40:249:91
AQ261535
- 25 R-HEM BB1000679
HS_3061_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061
Col=5 Row=E, genomic survey sequence.
1.8e-48:257:96
AQ127602
- 30 R-HEM BB1000881
CIT-HSP-2350O20.TR CIT-HSP Homo sapiens genomic clone 2350O20, genomic survey sequence.
0.0072:248:61
AQ062620
- 35 R-HEM BB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.5e-104:547:94
AC005089
- 40 R-HEM BB1001026

R-HEM BB1001048
- 45 R-HEM BB1001200
P.falciparum complete gene map of plastid-like DNA (IR-A).
1.5e-11:521:59
X95275
- 50 R-HEM BB1001407
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
3.0e-29:308:77
AL033529
- 55 R-HEM BB1001530
Homo sapiens chromosome 19, cosmid R30538, complete sequence.
0.040:373:63
AC005943

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5 R-HEM BB1001547
Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.
0.027:291:62
AJ235270

10 R-HEM BB1001573
CIT-HSP-2307C1.TR CIT-HSP Homo sapiens genomic clone 2307C1, genomic survey sequence.
1.3e-13:90:98
AQ020395

15 R-HEM BB1001847
Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence.
3.4e-27:147:80
AF064864

20 R-HEM BB1001959
Homo sapiens clone 24781 mRNA sequence.
4.4e-103:504:97
AF070640

25 R-HEM BB1001978
CIT-HSP-2328G6.TF CIT-HSP Homo sapiens genomic clone 2328G6, genomic survey sequence.
7.9e-29:220:86
AQ040310

30 R-HEM BB1002039
Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.
2.7e-37:550:68
AC005014

35 R-HEM BB1002041
Sequence 1 from patent US 5633147.
2.7e-23:322:70
I43819

40 R-HEM BB1002051
Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.
9.2e-35:302:79
AC004825

45 R-HEM BB1002120
Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.
6.0e-05:479:59
AC003106

50 R-HEM BB1002162
Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS,
complete sequence.
3.7e-30:238:84
AL031289

55 R-HEM BB1002228
Homo sapiens BAC clone NH0436H22 from 2, complete sequence.
6.6e-57:274:86
AC005234

R-HEM BB1002245
Sequence 25 from patent US 5747660.

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4.8e-30:361:73
AR005295

5 R-HEM BB1002302
Methanococcus jannaschii section 84 of 150 of the complete genome.
0.00019:362:59
U67542

10 R-HEM BB1002427
Genomic sequence from Human 9q34, complete sequence.
3.9e-105:533:96
AC001643

15 R-HEM BB1002465
Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.
2.9e-05:335:62
AE001382

20 R-HEM BB1002661
R-HEM BB1002663
***ALU WARNING: Human Alu-Sq subfamily consensus sequence.
8.3e-43:268:89
U14573

25 R-HEM BB1002693
Human BAC clone RG126M09 from 7q21-q22, complete sequence.
2.4e-24:220:76
AC002067

30 R-MAMMA1000046
Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8
unordered pieces.
0.032:402:57
35 AC005505

R-MAMMA1000102
Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.
2.0e-84:428:96
40 Z79996

R-MAMMA1000106
Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.
0.095:138:66
45 AP000031

R-MAMMA1000118

50 R-MAMMA1000141
Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
9.0e-91:480:95
AC004024

55 R-MAMMA1000204
Homo sapiens mRNA for LGMD2B protein.
1.5e-107:544:96
AJ007670

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R-MAMMA1000226
 H.sapiens VASP gene, exons 4 to 13.
 0.99:244:63
 X98534

5

R-MAMMA1000403
 CIT-HSP-2372A15.TF CIT-HSP Homo sapiens genomic clone 2372A15, genomic survey sequence.
 8.0e-38:187:81
 AQ112406

10

R-MAMMA1000449
 Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.
 1.2e-41:422:76
 AC004491

15

R-MAMMA1000457
 Homo sapiens clone 638 unknown mRNA, complete sequence.
 7.4e-116:570:97
 AF091084

20

R-MAMMA1000473
 Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
 9.6e-09:136:77
 AC004131

25

R-MAMMA1000496
 Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
 2.6e-48:272:93
 AC004997

30

R-MAMMA1000528
 Human BAC clone RG114A06 from 7q31, complete sequence.
 1.8e-13:109:80
 AC002542

35

R-MAMMA1000591
 Human cosmid g1572c264, complete sequence.
 1.6e-22:329:71
 AC000359

40

R-MAMMA1000614

R-MAMMA1000652
 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28A10.
 0.81:158:65
 Z84499

45

R-MAMMA1000681
 Homo sapiens full length insert cDNA clone YY85D04.
 1.0e-107:560:94
 AF088014

50

R-MAMMA1000706
 Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.
 1.1e-46:232:100
 AF067223

55

R-MAMMA1000788

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- Bos taurus P14 (p14) mRNA, complete cds.
3.8e-72:493:84
AF037349
- 5 R-MAMMA1000810
Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.
5.0e-37:318:79
AC003002
- 10 R-MAMMA1000814
Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.
7.7e-15:140:85
AC003071
- 15 R-MAMMA1000881
Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.
8.8e-46:457:75
AL031311
- 20 R-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
7.7e-44:343:82
AF001550
- 25 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds.
3.6e-108:552:96
AB003184
- 30 R-MAMMA1001043
- R-MAMMA1001066
Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.
1.3e-42:302:82
AC006120
- 35 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence.
5.4e-115:567:97
AF091094
- 40 R-MAMMA1001141
HS_3059_B1_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3059 Col=11 Row=P, genomic survey sequence.
1.3e-68:388:92
AQ214896
- 45 R-MAMMA1001150
H.sapiens mRNA for protein kinase C mu.
5.4e-20:340:66
X75756
- 50 R-MAMMA1001237
Mouse DNA fragment that hybridizes to HSV- 1 Smal A fragment.
0.15:222:65
M11041
- 55

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R-MAMMA1001284
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SE-
 QUENCE.
 1.2e-33:344:76
 5 AL034423

R-MAMMA1001310
 Human Bruton agammaglobulinemia (BTK) gene, exons 10-12.
 1.8e-39:332:80
 10 L31565

R-MAMMA1001418
 Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.
 4.4e-42:411:76
 15 U07563

R-MAMMA1001532
 Homo sapiens PAC clone DJ0728D04, complete sequence.
 2.3e-10:196:73
 20 AC004865

R-MAMMA1001609
 HS-1054-B2-H01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=2
 Row=P, genomic survey sequence.
 25 1.6e-34:170:79
 B42016

R-MAMMA1001615
 30 R-MAMMA1001623
 Homo sapiens 12q24.2 BAC RPC111-407A16 (Roswell Park Cancer Institute Human BAC Library) complete se-
 quence.
 8.8e-21:180:82
 35 AC006065

R-MAMMA1001634
 Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.
 2.6e-40:283:86
 40 AC005695

R-MAMMA1001893
 Homo sapiens clone DJ0782K24, WORKING DRAFT SEQUENCE, 16 unordered pieces.
 0.73:132:67
 45 AC006003

R-MAMMA1001901
 Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG
 island.
 4.0e-43:288:77
 50 Z93023

R-MAMMA1001957
 Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.
 1.2e-41:298:86
 55 AC005212

R-MAMMA1001978

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- R-MAMMA1002070
Homo sapiens clone DJ400N23, WORKING DRAFT SEQUENCE, 10 unordered pieces.
2.1e-104:530:97
AC005003
- 5 R-MAMMA1002080 rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].
5.9e-47:449:76
S72304
- 10 R-MAMMA1002087
Human Cosmid g1572c037 from 7q31.3, complete sequence.
1.7e-11:120:83
AC000125
- 15 R-MAMMA1002095
Rat alternatively spliced mRNA.
5.3e-30:289:74
M93018
- 20 R-MAMMA1002128

R-MAMMA1002142

R-MAMMA1002165
- 25 Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.
1.1e-28:350:72
AC005871
- 30 R-MAMMA1002205
Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING
PROTEIN (CNBP) like gene and STSs.
1.2e-42:282:75
Z83843
- 35 R-MAMMA1002224
Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project).
0.99:210:60
AL022224
- 40 R-MAMMA1002234
Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).
1.7e-61:310:81
X53744
- 45 R-MAMMA1002586
Streptomyces collinus coenzyme B12-dependent mutase (meaA) gene, complete cds.
0.99:348:60
AF008569
- 50 R-MAMMA1002633
Homo sapiens, clone hRPK. 1_A_1, complete sequence.
2.6e-13:381:64
AC006196
- 55 R-MAMMA1003126

R-NT2RM4000100
Plasmodium falciparum MAL3P2, complete sequence.

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0.00047:296:61
AL034558

R-NT2RM4000115

5 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SE-
QUENCE.

0.079:270:64
AL031746

10 R-NT2RM4000198

Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-
ordered pieces.

7.7e-24:244:78
AC006171

15 R-NT2RM4000284

Human IgG Fc receptor hFcRn mRNA, complete cds.

1.7e-93:440:100
U12255

20 R-NT2RM4000295

, complete sequence.

0.89:351:58
AC005663

25 R-NT2RM4000326

Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterra-
nean Fever gene disease.

2.3e-112:602:94
AJ003147

30 R-NT2RM4000417

Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.

0.78:229:62
Z82170

R-NT2RM4000444

R-NT2RM4000587

40 R-NT2RM4000593

R-NT2RM4000648

0.010:260:61
AG005508

R-NT2RM4000761

H.sapiens mitochondrial genome (consensus sequence).

3.2e-95:476:97
X62996

R-NT2RM4000965

R-NT2RM4000997

55 R-NT2RM4001321

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-bind-
ing Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

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6.0e-19:282:73
AL031277

5 R-NT2RM4001325

R-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.9e-111:553:96
AB014538

10 R-NT2RM4001735
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:553:94
AF052129

15 R-NT2RM4001768
Human HepG2 3'region Mbol cDNA, clone hmd3c03m3.
4.1e-29:187:91
D17194

20 R-NT2RM4001843
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.95:366:58
AC005828

25 R-NT2RM4002352
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.
5.5e-108:557:95
AB009462

30 R-NT2RP2000092
HS_3070_B1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070
Col=7 Row=D, genomic survey sequence.
1.1e-23:247:77
AQ120714

35 R-NT2RP2000178
E.amylovora lon gene.
1.1e-15:422:62
X77706

40 R-NT2RP2000240
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.00010:260:62
AC004480

45 R-NT2RP2000394
HS_3211_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211
Col=12 Row=N, genomic survey sequence.
1.1e-61:316:97
AQ174850

50 R-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
8.7e-67:357:94
AC005630

55

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- 5 R-NT2RP2000479
Homo sapiens chromosome 17, clone 193h18, complete sequence.
5.7e-51:551:73
AC002546
- 10 R-NT2RP2000514
P.falciparum parasite antigen reactive with the parasite inhibitory mouse monoclonal antibody (mMAb) 43E5, clone #366, partial cds.
2.1e-08:192:68
M21323
- 15 R-NT2RP2000533
Mus musculus cornichon mRNA, complete cds.
3.5e-59:243:82
AF022811
- 20 R-NT2RP2000616
Human DNA sequence from clone 694E4 on chromosome 22 Contains exon similar to phosphatidylserine decarboxylase, EST, GSS, complete sequence.
0.0064:105:67
AL031255
- 25 R-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.4e-65:326:98
AB016068
- 30 R-NT2RP2000663
Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.
7.9e-110:555:96
Z73913
- 35 R-NT2RP2000712
Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
9.8e-32:308:78
AC006001
- 40 R-NT2RP2000739
Bos taurus TATA box binding protein (TBP) gene, partial cds.
0.19:128:68
L47974
- 45 R-NT2RP2000818
Caenorhabditis elegans cosmid C48D5, complete sequence.
0.010:429:58
Z36237
- 50 R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen.
4.0e-99:505:96
Z29083
- 55 R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds.
2.0e-57:306:95
AB014576

R-NT2RP2001223

R-NT2RP2001276
 Mouse regulatory protein (npdc-1) mRNA, complete cds.
 5 5.8e-14:353:65
 L03814

R-NT2RP2001388
 Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.
 10 1.7e-31:291:77
 AC004971

R-NT2RP2001469
 M.musculus tex292 mRNA (3'region).
 15 3.7e-26:188:89
 X80433

R-NT2RP2001480
 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
 20 6.6e-83:426:95
 L38969

R-NT2RP2001495
 transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
 25 6.3e-43:238:96
 S77359

R-NT2RP2001514
 Homo sapiens cyclin K (CPR4) mRNA, complete cds.
 30 6.6e-06:57:100
 AF060515

R-NT2RP2001538
 Mus musculus transcriptional regulatory protein (mSin3) gene, complete cds.
 35 6.9e-12:179:75
 L36831

R-NT2RP2001562
 Human PAC clone DJ0800B09 from 7q11.23-q21, complete sequence.
 40 0.074:257:61
 AC004028

R-NT2RP2001662
 Homo sapiens clone 24615 mRNA sequence.
 45 3.2e-94:485:95
 AF055012

R-NT2RP2001755
 Homo sapiens mRNA for KIAA0762 protein, partial cds.
 50 1.3e-103:576:92
 AB018305

R-NT2RP2001769
 CIT-HSP-2376O23.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.
 55 1.5e-74:381:96
 AQ111163

R-NT2RP2001817

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HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=18 Row=B, genomic survey sequence.
3.9e-60:430:84
AQ243047

5

R-NT2RP2001878
Human DNA sequence from PAC 296K21 on chromosome X contains cytokeratin exon, delta-aminolevulinate synthase (erythroid); 5-aminolevulinic acid synthase.(EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.
0.018:148:67
Z83821

10

R-NT2RP2001903
Human Not1 linking clone from chromosome 1q32.
0.99:160:63
U36769

15

R-NT2RP2001915

20

R-NT2RP2001921
Homo sapiens clone NH0332L11, complete sequence.
6.5e-86:295:98
AC005538

25

R-NT2RP2001948
Homo sapiens chromosome 19, cosmid R33590, complete sequence.
2.3e-79:440:91
AC005620

30

R-NT2RP2001956

R-NT2RP2002015
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
1.1e-16:254:72
AL031277

35

R-NT2RP2002063
Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
5.8e-105:550:95
AC004050

40

R-NT2RP2002188
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.
0.47:212:62
AL034555

45

R-NT2RP2002232

50

R-nnnnnnnnnnnnn
Human mRNA for KIAA0383 gene, partial cds.
2.5e-100:511:96
AB002381

55

R-NT2RP2002409
S.pombe chromosome I cosmid c17H9.
1.0:241:63

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Z98597

R-NT2RP2002510

Homo sapiens chromosome 19, cosmid F19847, complete sequence.

5 1.6e-38:307:81

AC005952

R-NT2RP2002527

10 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.5e-18:165:83

AC004770

R-NT2RP2002533

15 Homo sapiens alpha 2 delta calcium channel subunit isoform II mRNA, complete cds.

9.7e-116:580:96

AF042793

R-NT2RP2002564

20 Homo sapiens clone DJ0800G07, complete sequence.

3.8e-110:580:94

AC004890

R-NT2RP2002674

25 Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.

1.0:244:60

AE001374

R-NT2RP2002721

30 Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.

1.2e-10:221:73

AC003962

R-NT2RP2002824

35 Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.

3.0e-07:108:77

D17237

R-NT2RP2002942

40 Human DNA sequence from clone 88D7 on chromosome Xq25-26.3 Contains F9 (coagulation factor IX (plasma thromboplastic component, Christmas disease, haemophilia B)), dbl oncogene. EST, STS, GSS, complete sequence.

2.0e-37:491:71

AL033403

R-NT2RP2002974

H.sapiens DMAHP gene.

4.0e-118:585:97

X84813

R-NT2RP2002976

50 CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.

8.4e-45:233:98

AQ059444

R-NT2RP2003042

R-NT2RP2003179

R-NT2RP2003210

R-NT2RP2003302
Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.
5 1.5e-24:255:78
Z95704

R-NT2RP2003369
Homo sapiens chromosome 7q22 sequence, complete sequence.
10 3.1e-95:514:92
AF053356

R-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds.
15 3.9e-111:549:97
AB007927

R-NT2RP2003390
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.
20 4.9e-102:413:99
AL024507

R-NT2RP2003469
Genomic sequence from Human 9q34, complete sequence.
25 1.4e-35:376:74
AC001644

R-NT2RP2003545
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
30 QUENCE.
1.5e-09:503:61
AL034557

R-NT2RP2003593
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SE-
35 QUENCE.
7.8e-81:433:93
AL021396

R-NT2RP2003599
HS_3240_A1_C04_T7 C|T Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240
40 Col=7 Row=E, genomic survey sequence.
0.091:341:58
AQ206348

R-NT2RP2003655
Homo sapiens PAC clone DJ0015I23 from 22, complete sequence.
45 2.0e-08:249:69
AC004819

R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein.
50 1.7e-110:549:96
Y12670

R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds.
55 5.4e-112:571:96

AB002363

R-NT2RP2003940

Human Chromosome 11 pac pDJ1173a5, complete sequence.

5 2.4e-20:353:70

AC000378

R-NT2RP2003950

Homo sapiens clone 24778 unknown mRNA.

10 1.5e-96:494:95

AF070572

R-NT2RP2004069

Human DNA sequence from clone 618F1 on chromosome Xq25 Contains part of gene similar to DOC4, CA repeat, GSS, complete sequence.

15 2.6e-50:539:75

AL023878

R-NT2RP2004108

RPCII1-91F9.TV RPCI11 Homo sapiens genomic clone R-91F9, genomic survey sequence. 0.00013:281:63

20 AQ283338

R-NT2RP2004141

cSRL-115f11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-115f11, genomic survey sequence.

25 2.3e-05:239:64

B00539

R-NT2RP2004179

Genomic sequence from Human 9q34, complete sequence.

30 0.43:130:68

AC002322

R-NT2RP2004205

Homo sapiens chromosome 7q22 sequence, complete sequence.

35 1.4e-42:324:83

AF053356

R-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

40 5.5e-35:285:84

AC000353

R-NT2RP2004495

transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].

45 3.4e-44:238:97

S77359

R-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

50 7.4e-113:572:96

AC001644

R-NT2RP2004556

CIT-HSP-2306F6.TF CIT-HSP Homo sapiens genomic clone 2306F6, genomic survey sequence.

55 8.1e-99:514:95

AQ019229

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- R-NT2RP2004606 cDNA encoding NIC(Natural Inhibitor of Collagenase).
8.2e-116:576:96
E00985
- 5 R-NT2RP2004648
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.98:369:57
AC005828
- 10 R-NT2RP2004670
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
4.5e-43:592:69
L22557
- 15 R-NT2RP2004794
- R-NT2RP2004837
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
20 AC001232
- R-NT2RP2004847
Homo sapiens full length insert cDNA clone YY87C09.
1.0e-68:333:100
25 AF086055
- R-NT2RP2005027
Human glucose transporter-like protein-III (GLUT3), complete cds.
7.8e-103:508:97 -
30 M20681
- R-NT2RP2005069
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.
3.8e-42:463:73
35 U35245
- R-NT2RP2005163
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
7.4e-44:233:96
40 AQ059444
- R-NT2RP2005181
Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.
7.6e-53:567:73
45 AB000113
- R-NT2RP2005247
Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC11-93D11 (from Roswell
Park Cancer Center) complete sequence.
50 5.8e-38:341:76
AC002357
- R-NT2RP2005378
Homo sapiens full length insert cDNA clone YW25A12.
55 0.13:152:66
AF086029
- R-NT2RP2005391

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HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3056 Col=5 Row=E, genomic survey sequence.
1.1e-14:140:84
AQ134064

5 R-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds.
8.2e-100:526:94
AB018346

10 R-NT2RP2005463

R-NT2RP2005514

15 R-NT2RP2005535
Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.
1.9e-11:488:62
AC003973

20 R-NT2RP2005541
CIT-HSP-2034G23.TF CIT-HSP Homo sapiens genomic clone 2034G23, genomic survey sequence.
2.7e-61:311:98
B74709

25 R-NT2RP2005597

R-nnnnnnnnnnnnn
{FRA16A, folate-sensitive fragile site} [human, Genomic, 160 nt].
0.92:104:65

30 S70397

R-NT2RP2005666

35 R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence.
2.2e-94:440:96
AF035364

40 R-NT2RP2005878
Homo sapiens chromosome 19, cosmid F17987, complete sequence.
1.3e-32:340:76
AC004790

45 R-NT2RP2005883
Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-
GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
1.3e-117:581:97
AL023578

50 R-NT2RP2005887
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces
2.5e-61:367:90
AC001232

55 R-nnnnnnnnnnnnn
Human paired box gene (PAX6) homologue, complete cds.
5.0e-115:578:96
M93650

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R-NT2RP2005994
 Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
 2.4e-116:594:96
 AC004050

5

R-NT2RP2006004
 Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.
 1.8e-45:264:93
 U42975

10

R-NT2RP2006042
 T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.
 0.42:111:70
 B78148

15

R-NT2RP2006092
 Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
 1.7e-73:385:95
 AC005214

20

R-NT2RP2006099
 Homo sapiens PAC clone DJ0903G02, complete sequence.
 1.3e-27:335:74
 AC004924

25

R-NT2RP2006134
 Homo sapiens chromosome 4 clone B139M23 map 4q25, complete sequence.
 1.0:143:63
 AC004045

30

R-NT2RP2006269
 Phreatamoeba balamuthi-UBI3 sequence, putative polyubiquitin gene.
 0.82:153:63
 AJ000657

35

R-NT2RP2006512
 Homo sapiens clone 23904 mRNA sequence.
 4.6e-106:531:96
 AF052129

40

R-NT2RP3000011
 HS_2196_A2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196
 Col=16 Row=1, genomic survey sequence.
 1.3e-36:292:83
 AQ210450

45

R-NT2RP3000022
 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence.
 0.28:248:60
 Z98550

50

R-NT2RP3000059
 Homo sapiens chick ovalbumin upstream promoter transcription factor II (COUP-TFII) mRNA, partial cds.
 0.047:393:61
 M62760

55

R-NT2RP3000063
 HS_3190_B2_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone

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Plate=3190 Col=20 Row=H, genomic survey sequence.

0.88:232:63

AQ172428

- 5 R-nnnnnnnnnnnnn
RPCI11-35A1.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-35A1, genomic survey sequence.
3.8e-29:159:99
AQ045699
- 10 R-NT2RP3000148
Homo sapiens full length insert cDNA clone ZE03A07.
2.8e-112:574:95
AF086510
- 15 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
4.4e-110:551:96
AF093239
- 20 R-NT2RP3000171

R-NT2RP3000172
Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.
1.3e-40:554:70
- 25 L22557

R-NT2RP3000201
Homo sapiens BAC clone NH0353P23 from 2, complete sequence.
6.4e-96:478:97
- 30 AC005035

R-NT2RP3000232
Plasmodium falciparum MAL3P2, complete sequence.
0.93:262:61
- 35 AL034558

R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.4e-109:546:97
- 40 AF074264

R-NT2RP3000378
Mus musculus mSin3A (sin3A) mRNA, complete cds.
3.0e-27:411:72
- 45 U22394

R-NT2RP3000436
Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.
1.1e-06:440:57
- 50 AE001398

R-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 889J22, WORKING DRAFT SEQUENCE.
5.9e-105:543:95
- 55 AL031406

R-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.

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- 2.8e-12:292:68
M96629
- 5 R-NT2RP3000481
WORKING DRAFT SEQUENCE, 8 unordered pieces.
0.99:160:65
AC005992
- 10 R-NT2RP3000616
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.00087:412:57
AC005308
- 15 R-NT2RP3000645
- R-NT2RP3000652
Homo sapiens DNA from chromosome 19, cosmid R32532, complete sequence.
1.9e-44:539:74
20 AC004004
- R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
3.1e-103:542:94
25 AB007915
- R-NT2RP3000677
Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epitherium cancer, segment 4/10.
0.067:235:61
30 AB020872
- R-NT2RP3000721
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
4.0e-45:233:98
35 AQ059444
- R-NT2RP3000789
- R-NT2RP3000818
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
5.7e-95:510:93
Z97201
- R-NT2RP3000820
45 RPCI11-77B13.TJ RPCI11 Homo sapiens genomic clone R-77B13, genomic survey sequence.
2.1e-50:266:96
AQ283547
- R-NT2RP3000838
50 Homo sapiens mRNA for KIAA0638 protein, partial cds.
4.6e-99:522:94
AB014538
- R-NT2RP3000871
55 Homo sapiens clone DJ0703P08, WORKING DRAFT SEQUENCE, 23 unordered pieces.
0.68:249:61
AC005481

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R-NT2RP3000907
X.laevis oocyte repetitive sequence (XLOREP) mRNA.
2.9e-30:386:69
X65290

5

R-NT2RP3000921
HS_2026_A1_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026
Col=11 Row=C, genomic survey sequence.
2.2e-54:311:92
AQ232644

10

R-NT2RP3001012
Rattus norvegicus mRNA for TIP120, complete cds.
9.2e-63:456:83
D87671

15

R-NT2RP3001044
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
AC001232

20

R-NT2RP3001061
Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7
unordered pieces.
0.17:357:61
AC005506

25

R-NT2RP3001159
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519c13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
8.8e-111:561:96
AC004228

30

R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds.
8.8e-117:561:98
AB018327

35

R-NT2RP3001195
Genomic sequence from Human 9q34, complete sequence.
1.4e-35:376:74
AC001644

40

R-NT2RP3001240
Canis familiaris sec61 homologue mRNA, complete cds.
2.8e-12:292:68
M96629

45

R-NT2RP3001271
Homo sapiens chromosome 19, BAC CIT-B-470f8 (BC330812), complete sequence.
7.9e-17:260:71
AC006115

50

R-NT2RP3001322
Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.
0.035:451:60
Z97629

55

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R-NT2RP3001542
 Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8
 unordered pieces.
 4.1e-08:500:61
 5 AC004153

R-NT2RP3001560
 Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
 1.0e-30:523:65
 10 D67067

R-NT2RP3001592

R-NT2RP3001685
 15 Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome
 C oxidase gene, EST, CpG island, complete sequence.
 2.4e-30:147:85
 AL024474

R-NT2RP3001738
 20 Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
 complete sequence.
 9.2e-107:553:95
 AC004228

R-NT2RP3001754
 25 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
 2.0e-67:345:97
 AL034380

R-NT2RP3001858

R-NT2RP3001976
 Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence.
 35 4.4e-14:302:62
 AC006239

R-NT2RP3002015
 Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.
 40 6.2e-65:492:82
 AC004832

R-NT2RP3002160
 Genomic sequence from Human 9q34, complete sequence.
 45 2.1e-82:431:95
 AC001643

R-NT2RP3002281
 Homo sapiens mRNA for KIAA0765 protein, partial cds.
 50 1.1e-81:446:93
 AB018308

R-NT2RP3002286
 Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
 55 1.0e-80:378:90
 U57368

R-NT2RP3002311

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- Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.57:366:58
AC005828
- 5 R-NT2RP3002324
H.sapiens gene for nitric oxide synthase (promoter region).
1.6e-30:337:72
Z49251
- 10 R-NT2RP3002342
transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
6.5e-45:238:98
S77359
- 15 R-NT2RP3002353
Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence. 0.00015:164:70
AC002044
- NNNNNNNNNNNNNNNN
- 20 Homo sapiens mRNA for KIAA0788 protein, partial cds.
4.5e-98:493:96
AB018331
- NNNNNNNNNNNNNNNN
- 25 R-NT2RP3002448
S.cerevisiae DNA for ori 2.
0.52:91:71
X59535
- 30 R-NT2RP3002571
- R-NT2RP3002664
Homo sapiens full length insert cDNA clone ZC48G09.
9.9e-103:522:96
AF086209
- 35 R-NT2RP3002721
- 40 R-NT2RP3002737
- R-NT2RP3002738
Sequence 4 from patent US 5541109.
2.9e-22:171:74
I24014
- 45 R-NT2RP3002790
- R-NT2RP3002836
Bos taurus retina specific RGS protein (RET-RGS1) mRNA, complete cds.
2.3e-34:384:75
U89254
- 50 R-NT2RP3002887
Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.
1.6e-05:435:62
AF051726
- 55

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R-NT2RP3002900
Homo sapiens mRNA from chromosome 5q21-22, clone:A3-B.
1.3e-116:569:97
AB002451

5

R-NT2RP3002958
Homo sapiens clone 23851 mRNA sequence.
2.0e-117:575:98
AF035313

10

R-NT2RP3002983
Homo sapiens genomic DNA, chromosome 21q11.1, segment 17/28, WORKING DRAFT SEQUENCE.
5.1e-59:295:99
AP000046

15

R-NT2RP3003000
Homo sapiens clone 24597 mRNA sequence.
6.1e-109:562:95
AF070604

20

R-NT2RP3003076

R-NT2RP3003354
Human protocadherin 42 mRNA, complete cds for abbreviated PC42.
0.87:208:61
L11370

25

R-NT2RP3003448
High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.
1.3e-41:287:80
AC005840

30

R-NT2RP3003469
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
2.1e-18:223:77
AL031277

35

R-NT2RP3003473
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.
1.5e-54:294:96
Z99716

40

R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B.
5.1e-91:445:97
Y17999

45

R-NT2RP3003532
Mus musculus cell surface molecule OX-2 mRNA, complete cds.
1.2e-30:529:67
AF004023

50

R-nnnnnnnnnnnnn
Homo sapiens PAC clone DJ0531G15 from 7p21, complete sequence.
0.13:294:61
AC004739

55

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R-NT2RP3003559
 CIT-HSP-2307F17.TR CIT-HSP Homo sapiens genomic clone 2307F17, genomic survey sequence.
 1.4e-15:342:68
 AQ016972
 5

R-NT2RP3003614
 Homo sapiens chromosome 19, cosmid F21967, complete sequence.
 0.013:174:64
 AC005256
 10

R-NT2RP3003729
 R-NT2RP3003849
 Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 6 unordered pieces.
 15 8.9e-106:557:94
 AC002320

R-NT2RP3003874
 Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.
 20 1.6e-55:302:94
 AJ001381

R-NT2RP3003963
 cSRL-66f9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-66f9, genomic
 25 survey sequence.
 0.028:78:76
 B05608

R-NT2RP3004000
 Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 861 nt, segment 7 of 7].
 30 0.87:212:62
 S45012

R-NT2RP3004025
 Homo sapiens chromosome 19, cosmid F17987, complete sequence.
 35 0.71:197:62
 AC004790

R-NT2RP3004075
 40

R-NT2RP3004083
 Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5.
 0.27:375:59
 Z97340
 45

R-NT2RP3004090
 CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.
 2.2e-40:243:91
 B99962
 50

R-NT2RP3004119
 Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.
 8.3e-42:475:73
 AC004953
 55

R-NT2RP3004130
 R-NT2RP3004133

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- CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
0.00037:194:64
AQ022229
- 5 R-NT2RP3004202
Homo sapiens BAC clone GS285F21 from 7q21-q22, complete sequence.
0.65:209:62
AC004012
- 10 R-NT2RP3004294

R-NT2RP3004309
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.
15 7.4e-99:500:96
AC004228

R-NT2RP3004321
Human chromosome 11 168h3 cosmid, complete sequence.
20 1.7e-105:540:96
U73637

R-NT2RP3004345
Human BAC clone RG016J04 from 7q21, complete sequence.
25 0.00033:348:61
AC002064

R-NT2RP3004355
Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.
30 0.0029:180:66
AC004709

R-NT2RP3004374
35 Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.
4.3e-18:223:77
AL031277

40 R-NT2RP3004406
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-70, complete sequence.
1.0:201:62
AL010239

45 R-NT2RP3004481

R-NT2RP3004552
Human germline immunoglobulin lambda light chain pseudogene (VII.1).
1.0:165:63
50 X57825

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds.
8.2e-49:352:84
55 AF082516

R-NT2RP3004640
Homo sapiens full length insert cDNA clone ZC45E05.

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- 1.2e-96:471:98
AF086205
- 5 R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds.
1.5e-109:555:96
AB007915
- 10 R-NT2RP4000108
Mouse neurofilament protein (NF-L) gene, 3' flank.
1.0e-09:344:63
M55424
- 15 R-NT2RP4000634
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
1.6e-16:267:71
AC003037
- 20 R-NT2RP4000962
Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).
0.026:176:67
AL021069
- 25 R-NT2RP4001001
Drosophila melanogaster Oregon-R mitochondrial A+T region.
0.00026:354:61
U11584
- 30 R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.6e-82:408:98
AB016068
- 35 R-NT2RP4001467
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
1.8e-111:545:97
X55740
- 40 R-NT2RP4001877
Yeast (S.cerevisiae) mitochondrial cob gene, intron 4.
0.19:384:59
J01469
- 45 R-NT2RP4001879
Homo sapiens full length insert cDNA clone ZD76G10.
4.4e-107:548:94
AF086408
- 50 R-NT2RP4002187
RPC111-69F22.TK RPC111 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.1e-37:240:89
AQ238297
- 55 R-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
5.8e-111:575:96
Z98200

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R-NT2RP4002715
 Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
 2.5e-61:367:90
 AC001232

5

R-NT2RP4002750
 Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.
 1.2e-52:527:74
 AB000113

10

R-OVARC1000003
 Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
 2.3e-10:140:77
 AC004909

15

R-OVARC1000090
 Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SE-
 QUENCE.
 2.8e-59:323:78
 D84394

20

R-OVARC1000105
 H.sapiens gene for ribosomal protein L38.
 2.7e-12:83:100
 Z26876

25

R-OVARC1000137

R-OVARC1000208
 Homo sapiens PAC clone DJ0817I18 from 7p11.2p13, complete sequence.
 2.7e-52:464:79
 AC004901

30

R-OVARC1000255
 H.sapiens syk mRNA for protein-tyrosine kinase.
 1.9e-105:511:98
 Z29630

35

R-OVARC1000275

40

R-OVARC1000298
 Plasmodium falciparum carbamoyl phosphate synthetase II gene, complete cds.
 0.66:364:59
 L32150

45

R-OVARC1000307

R-OVARC1000313
 Homo sapiens mRNA for KIAA0573 protein, partial cds.
 1.6e-96:534:93
 AB011145

50

R-OVARC1000331
 Sequence 2 from patent US 5763589.
 8.1e-66:335:97
 AR012692

55

R-OVARC1000410

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- Homo sapiens clone 23767 and 23782 mRNA sequences.
1.0e-88:462:94
AF007150
- 5 R-OVARC1000439
E.coli fanG and fanH genes.
0.99:424:58
Y00531
- 10 R-OVARC1000467
HS_3235_A2_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235
Col=24 Row=A, genomic survey sequence.
9.2e-09:125:76
AQ206826
- 15 R-OVARC1000529
- R-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894, complete sequence.
2.0e-84:437:96
AC005594
- 20 R-OVARC1000775
CIT-HSP-2060P5.TF CIT-HSP Homo sapiens genomic clone 2060P5, genomic survey sequence. 0.29:223:63
B70025
- 25 R-OVARC1000811
Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
2.8e-89:438:98
AC004235
- 30 R-OVARC1000853
RPCI11-16C11.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16C11, genomic survey sequence.
5.3e-53:317:92
B76661
- 35 R-OVARC1000873
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-
COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
1.2e-102:511:97
AL034418
- 40 R-OVARC1000916
H.sapiens PISSLRE mRNA.
5.8e-111:588:94
X78342
- 45 R-OVARC1000956
Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains poly-
morphic VNTR pYNZ32.
2.7e-89:478:94
Z69708
- 50 R-OVARC1000995
Human DNA sequence from clone 885E17 on chromosome 1p33-34.1. Contains STSs and GSSs and genomic
marker D1S1302, complete sequence.
9.5e-46:325:84
AL031294
- 55

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5 R-OVARC1001030
Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds.
1.2e-05:197:63
L10335

10 R-OVARC1001049

R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds.
4.3e-105:569:94
AF048731

15 R-OVARC1001132
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
2.2e- 111:569:96
AP000038

20 R-OVARC1001163
Sus scrofa MHC SLA class III steroid 21-hydroxylase (CYP21) gene, complete cds, ORF human-like gene, last 5
exons.
0.010:349:60
M83939

25 R-OVARC1001222
Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived
ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.
0.58:184:60
U28972

30 R-OVARC1001260
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
1.1e-10:140:78
AC004909

35 R-OVARC1001336
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
2.3e-10:140:77
AC004909

40 R-OVARC1001338

R-OVARC1001569

45 R-OVARC1001570

R-OVARC1001596
Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
5.9e-47:361:83
AC005951

50 R-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
3.3e-112:559:96
U15128

55 R-OVARC1001725
Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
3.9e-56:318:95

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AF064800

R-OVARC1001727

Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.

6.1e-101:533:94

AL031132

R-OVARC1001807

Human TR3 orphan receptor mRNA, complete cds.

2.8e-87:426:97

L13740

R-OVARC1001833

Mouse fork head related protein (HNF-3beta) mRNA, complete cds.

1.1e-21:263:76

L10409

R-OVARC1001991

H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 301e3, reverse read 301e3.r.

0.90:151:59

Z79826

R-OVARC1002058

Homo sapiens full length insert cDNA clone ZD58C02.

1.9e-105:547:95

AF088043

R-OVARC1002178

Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.

0.26:429:58

AL031053

R-PLACE1000033

Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.

0.098:467:59

AC004688

R-PLACE1000231

Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.

0.91:141:64

AC003083

R-PLACE1000258

Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myotubularin-related protein, EST, STS and GSS, complete sequence.

3.8e-53:524:75

AL034408

R-PLACE1000442

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence.

3.0e-07:413:62

AB016873

R-PLACE1000560

Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.

6.3e-59:323:94

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AC005368

R-PLACE1000740
H.sapiens PEX gene.
5 0.0065:202:63
Y10196

R-PLACE1000912

10 R-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
3.4e-68:452:86
AC002093

15 R-PLACE1000927
Cowpox virus strain GRI-90 DNA (49 kb fragment).
1.8e-46:432:76
Y15035

20 R-PLACE1000986
HS_2037_A2_B06_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=12 Row=C, genomic survey sequence.
0.087:48:89
AQ232754

25 R-PLACE1001016
M.fascicularis gene for apolipoprotein A-IV.
0.016:226:61
X68361

30 R-PLACE1001100
Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear in-
hibitor of protein phosphatase-1, ESTs, and a CA repeat.
3.4e-37:320:80

35 AL020997

R-PLACE1001114
RPC111-5C23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5C23, genomic survey sequence.
9.2e-44:173:85

40 B49180

R-PLACE1001123

R-PLACE1001183
45 Plasmodium falciparum MAL3P8, complete sequence.
0.47:217:63
AL034560

R-PLACE1001229
50 Mitochondrion Culex torrentium A+T rich mitochondrial control region.
3.3e-09:356:63
U69573

R-PLACE1001231
55 Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
1.2e-09:186:72
AF026554

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R-PLACE1001340
 Homo sapiens mRNA for KIAA0719 protein, complete cds.
 2.0e-51:265:98
 AB018262

5

R-PLACE1001401
 Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.
 0.0073:203:60
 AF033929

10

R-PLACE1001407
 Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
 5.8e-70:360:96
 AL023582

15

R-PLACE1001464
 Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
 3.1e-90:457:96
 X55740

20

R-PLACE1001500
 Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.
 1.0:232:62
 AC004929

25

R-PLACE1001516
 Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.
 1.9e-26:168:88
 AC002425

30

R-PLACE1001536
 Human Chromosome X clone bW XD187, complete sequence.
 6.5e-61:310:98
 AC004383

35

R-PLACE1001564
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
 QUENCE.
 2.9e-100:504:97
 AL033377

40

R-PLACE1001655
 Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.
 3.8e-1 17:578:97
 AF043472

45

R-PLACE1001788
 Sequence 9 from Patent WO9722695.
 1.9e-05:91:82
 A63556

50

R-PLACE1001795

R-PLACE1001836
 , complete sequence.
 4.1e-14:269:69
 AC005406

55

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- 5 R-PLACE1001918
Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.
7.3e-25:151:95
D17237
- 10 R-PLACE1001949
Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.
0.54:165:63
Z94056
- 15 R-PLACE1002080
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.
3.7e-60:289:95
AC004150
- 20 R-PLACE1002095
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig.3-52, complete sequence.
0.00052:422:59
AL008982
- 25 R-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
4.6e-100:514:95
AF095791
- 30 R-PLACE1002329
Homo sapiens chromosome 19, cosmid R31855, complete sequence.
1.3e-46:257:95
AC005782
- 35 R-PLACE1002355
HS_2057_B1_D01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2057 Col=1 Row=H, genomic survey sequence.
0.089:132:65
AQ245227
- 40 R-PLACE1002374
Human mRNA for pro-cathepsin L (major excreted protein MEP).
2.6e-101:501:97
X12451
- 45 R-PLACE1002518
HS_2176_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=8 Row=G, genomic survey sequence.
1.7e-43:221:100
AQ014851
- 50 R-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-53:276:97
AB018262
- 55 R-PLACE1002726
Human DNA-binding protein ABP/ZF mRNA, complete cds.
1.1e-37:212:94
U82613

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- 5 R-PLACE1002905
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SE-
QUENCE.
1.2e-42:302:86
AL034417
- R-PLACE1002911
- 10 R-PLACE1002967
Homo sapiens chromosome 16, BAC clone 461A8, complete sequence.
2.3e-39:310:82
AC006111
- 15 R-PLACE1003135
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
2.2e-07:418:60
AL034557
- 20 R-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds.
4.7e-110:547:96
AF069301
- 25 R-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.
1.7e-47:287:91
AF068227
- 30 R-PLACE1003428
Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2,
ESTs, GSSs,, complete sequence.
1.1e-75:268:98
AL032821
- 35 R-PLACE1003438
- 40 R-PLACE1003460
HS_3026_B1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026
Col=15 Row=B, genomic survey sequence.
0.30:100:69
AQ093523
- 45 R-NNNNNNNNNNNN
Homo sapiens clone DJ0981007, complete sequence.
3.3e-46:135:98
AC006017
- 50 R-PLACE1003573
HS_3079_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079
Col=4 Row=B, genomic survey sequence.
1.1e-49:261:96
AQ121751
- 55 R-PLACE1003598
- R-PLACE1003644
Caenorhabditis elegans cosmid F52H3, complete sequence.

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0.38:345:62
Z66512

- 5 R-PLACE1003737
Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.
1.9e-77:406:96
AC005859
- 10 R-PLACE1003772
Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.
2.2e-29:454:70
AL020997
- 15 R-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
3.0e-52:272:97
AC004131
- 20 R-PLACE1003845
HS_3219_A1_A10_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=19 Row=A, genomic survey sequence.
1.5e-13:231:70
AQ181482
- 25 R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds.
6.8e-86:439:96
AB018301
- 30 R-PLACE1004028
- R-PLACE1004078
Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
35 5.0e-36:310:80
AC006064
- 40 R-PLACE1004166
Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.
0.95:224:62
U19361
- 45 R-NNNNNNNNNNNN
Fugu rubripes GSS sequence, clone 076D01bH10, genomic survey sequence.
3.0e-08:107:77
AL026605
- 50 R-PLACE1004199
Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.
0.0028:157:67
M98538
- 55 R-PLACE1004279
Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3. Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j genes, histone pH2b.i and hypothetical protein A4 pseudogenes, histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene, olfactory receptor OL1 like gene, ESTs STSs and predicted CpG islands.

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0.00065:228:58
Z98744

5 R-PLACE1004282

R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds.
2.0e-77:377:99
AB018283

10 R-PLACE1004441
RPC111-76P13.TV RPC111 Homo sapiens genomic clone R-76P13, genomic survey sequence.
1.8e-73:370:97
AQ281810

15 R-PLACE1004450
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.
0.87:269:59
AB012242

20 R-PLACE1004482
Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.
5.2e-33:356:75
AF009513

25 R-PLACE1004492
Mus musculus mRNA for Doc2, partial cds.
4.1e-28:268:77
D50000

30 R-PLACE1004519
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.

35 1.8e-14:330:67
AL021808

R-PLACE1004520
Human pregnancy specific beta-1-glycoprotein 1 (PSG1) gene.
40 1.4e-73:397:93
M93705

R-PLACE1004630

45 R-PLACE1004637
Human Chromosome 11 Cosmid cSRL16b6, complete sequence.
5.5e-108:625:91
U73638

50 R-PLACE1004648

R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds.
5.6e-103:586:90
55 D88587

R-PLACE1004887
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

- 1.2e-31:177:97
B99962
- 5 R-PLACE1005003
Mus musculus clone OST13719, genomic survey sequence.
0.0043:159:64
AF046703
- 10 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.
2.1e-56:299:95
AF032456
- 15 R-PLACE1005031
Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.
1.0:155:65
AC005821
- 20 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).
4.4e-85:450:93
AJ223351
- 25 R-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
7.7e-19:232:73
U50734
- 30 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.0e-77:471:88
AF093118
- 35 R-PLACE1005410
Canis familiaris sec61 homologue mRNA, complete cds.
6.4e-12:132:82
M96629
- 40 R-PLACE1005426
Human pregnancy specific beta-1-glycoprotein 4 (PSG4) mRNA, complete cds.
2.3e-109:574:94
M94891
- 45 R-PLACE1005519
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
4.1e-08:426:61
AL034557
- 50 R-PLACE1005539
- R-PLACE1005544
Homo sapiens chromosome 19, cosmid F20887, complete sequence.
1.0e-17:202:73
- 55 AC005578
- R-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

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3.8e-89:470:95
AL034397

5 R-PLACE 1005601
Homo Sapiens angiotensin II receptor gene, complete cds.
8.0e-52:301:90
L48211

10 R-PLACE1005660

R-PLACE1005669
Mitochondrion Culex torrentium A+T rich mitochondrial control region.
9.5e-09:338:63
U69573

15 R-PLACE1005682
Caenorhabditis elegans cosmid M70.
0.012:226:62
AF047661

20 R-PLACE1005725
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48E1, WORKING DRAFT SE-
QUENCE.
0.42:435:59
25 Z92856

R-PLACE1005736
Rattus norvegicus DD6A4-1 mRNA, partial sequence.
9.0e-21:282:73
30 AF034237

R-PLACE1005745
RPC111-88L20.TJ RPC111 Homo sapiens genomic clone R-88L20, genomic survey sequence.
2.4e-62:310:99
35 AQ281511

R-PLACE1005768
Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
5.6e-94:511:93
40 Z82185

R-PLACE1005815
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
9.0e-55:586:73
45 AC002310

R-PLACE1005878

50 R-PLACE1005927

R-PLACE1006071
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
1.6e-76:410:95
55 AQ022149

R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds.
2.2e-97:513:93

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AB009598

R-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5 5.4e-57:333:91

AF028233

R-PLACE1006093

10 R-nnnnnnnnnnnnn

Caenorhabditis elegans mRNA for GAP-2-7, partial cds.

1.9e-08:251:60

AB011283

15 R-PLACE1006219

HS_3219_A1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=19 Row=A, genomic survey sequence.

3.1e-12:228:69

AQ181482

20

R-PLACE1006277

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

7.8e-96:557:91

AL034397

25

R-PLACE1006290

Bacillus whitei clone pWH/CugI satellite DNA.

0.37:209:62

U90159

30

R-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

8.9e-76:451:91

AC002093

35

R-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

2.1e-76:413:94

AB011148

40

R-PLACE1006716

M.musculus gene encoding prostaglandin D synthase, putative.

1.0:199:59

Y10138

45

R-PLACE1006786

HS_2037_A2_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037

Col=12 Row=C, genomic survey sequence.

0.33:47:91

50

AQ232754

R-PLACE1006809

Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.

55

0.67:241:59

U52112

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- R-PLACE1006959
- R-PLACE1007028
- 5 R-PLACE1007040
Rabbit angiotensin-converting enzyme (ACE-P) gene, 5' end.
0.0037:208:65
M58579
- 10 R-PLACE1007077
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
3.0e-76:411:94
AQ022149
- 15 R-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
1.9e-06:88:84
AQ016433
- 20 R-PLACE1007096
H.sapiens DMD gene microsatellite (147-200bp).
1.0:142:59
X77677
- 25 R-PLACE1007296
- R-PLACE1007591
Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.
- 30 1.6e-11:203:66
AL023574
- R-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
- 35 4.9e-29:183:91
AF047439
- R-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
- 40 2.3e-75:445:90
AC002348
- R-PLACE1007845
CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
- 45 0.00045:194:64
AQ022229
- R-PLACE1007881
CITBI-E1-2503C21.TF CITBI-E1 Homo sapiens genomic clone 2503C21, genomic survey sequence.
- 50 0.43:104:69
AQ263355
- R-PLACE1007971
- 55 R-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
7.7e-73:396:94
AC005995

- 5 R-PLACE1008297
N.frontalis enolase gene, promotor region.
1.2e-08:457:57
X81451
- 10 R-PLACE1008359
Plasmodium falciparum MAL3P1, complete sequence.
0.00044:443:56
Z97348
- 15 R-PLACE1008469
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
4.4e-78:536:84
AC002093
- 20 R-PLACE1008549
Mus musculus E74-like factor 5 (Elf5) mRNA, complete cds.
3.4e-30:256:75
AF049702
- 25 R-PLACE1008657
Homo sapiens BAC clone GS067A24 from 7q21.q21.2, complete sequence.
1.9e-40:320:82
AC005009
- 30 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
8.2e-118:591:96
U15128
- 35 R-PLACE1008744
Sequence 1 from patent US 5691147.
3.1e-108:559:94
I76197
- 40 R-PLACE1008984
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
1.6e-102:503:96
AL031427
- 45 R-PLACE1008985
Mus musculus synaptotagmin VIII mRNA, partial cds.
9.7e-29:255:77
U20107
- 50 R-PLACE1009067
- 55 R-PLACE1009196
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SE-
QUENCE.
0.0094:206:65
Z92854
- 60 R-PLACE1009279
Homo sapiens serine protease (PRSS11) mRNA, partial cds.
2.4e-26:553:62
AF097709

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R-PLACE1009527
 Human DNA-binding protein ABP/ZF mRNA, complete cds.
 7.9e-91:497:91
 U82613
 5

R-PLACE1009546
 Human PAC clone DJ218B13 from Xq23, complete sequence.
 0.29:147:64
 AC002072
 10

R-PLACE1009600
 Mouse mRNA for tetracycline transporter-like protein, complete cds.
 6.1e-81:466:90
 D88315
 15

R-PLACE1009735
 Homo sapiens clone NH0523H20, complete sequence.
 2.0e-74:268:99
 AC005041
 20

R-nnnnnnnnnnnnn
 Homo sapiens DNA sequence from PAC 833B2 on chromosome Xq26.1-27.2. Contains an EST, complete se-
 quence.
 1.9e-05:255:65
 25 AL023800

R-PLACE1010011
 , complete sequence.
 2.9e-77:174:100
 30 AC005409

R-PLACE1010078
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.
 1.0:108:65
 35 Z84465

R-PLACE1010081
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
 9.2e-105:560:93
 40 AF027706

R-PLACE1010251
 Plasmodium falciparum MAL3P4, complete sequence.
 5.0e-07:468:58
 45 AL008970

R-PLACE1010445
 Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.
 1.2e-49:303:90
 50 AF077058

R-PLACE1010713
 RPCI11-69F22.TK RPCI11 Homo sapiens genomic clone R-69F22, genomic survey sequence.
 7.4e-11:114:80
 55 AQ238297

R-PLACE1010784
 Capra hircus strain Saanen, genomic survey sequence.

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- 7.4e-24:182:87
AF083406
- 5 R-PLACE1010827
nbxb0026K23f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026K23f, genomic survey sequence.
1.0:252:61
AQ271546
- 10 R-PLACE1010968
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.0038:295:57
AC005308
- 15 R-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.6e-90:453:96
AF094516
- 20 R-PLACE1011116
Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds.
4.6e-72:385:94
AF006621
- 25 R-PLACE1011236
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0289H06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.98:142:65
AC004580
- 30 R-PLACE1011364
- R-PLACE1011407
Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some
35 similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1).
Contains GSSs, complete sequence.
9.1e-27:293:74
AL031575
- 40 R-PLACE1011516
Fugu rubripes GSS sequence, clone 190N14aC12, genomic survey sequence.
1.0:96:68
AL030602
- 45 R-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
2.4e-91:521:91
AF034611
- 50 R-PLACE1011824
Figure 6. DNA sequence of three 3'apoB VNTR alleles.
2.2e-06:264:65
M23046
- 55 R-PLACE1011978
Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.
4.8e-50:553:69
M27877

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- 5 R-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.
3.9e-107:567:94
AL022578
- 10 R-PLACE2000219
Homo sapiens clone RG132J19, complete sequence.
4.7e-39:317:82
AC005163
- 15 R-PLACE3000181
Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8.
3.9e-81:441:94
L11369
- 20 R-PLACE3000213
Sequence 1 from patent US 5691147.
1.5e-109:559:95
I76197
- 25 R-PLACE4000354
Sequence 1 from patent US 5691147.
2.7e-106:548:95
I76197
- 30 R-PLACE4000455
Arabidopsis thaliana genomic DNA chromosome 3, P1 clone: MEBS, complete sequence.
9.3e-07:357:60
AB019230
- 35 R-THYRO1000036
Sequence 11 from patent US 5773248.
4.0e-99:527:93
AR014074
- 40 R-THYRO1000061
Homo sapiens chromosome 19, cosmid R34382, complete sequence.
7.3e-90:460:96
AC005329
- 45 R-THYRO1000099
- 50 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.
1.1e-104:530:96
AF016272
- 55 R-THYRO1000400
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.
1.0:308:61
AC004685
- R-THYRO1000580
Human Kox26 mRNA for zinc finger protein, partial.
0.11:105:67

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X52357

R-THYRO1000584

5 *** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.

1.4e-14:241:68

AC004480

R-THYRO1000678

10 Belonogaster petiolata 16S ribosomal RNA gene, mitochondrial gene for mitochondrial rRNA, partial sequence.

0.049:150:64

AF066910

R-THYRO1000776

15 CITBI-E1-2505N5.TF.1 CITBI-E1 Homo sapiens genomic clone 2505N5, genomic survey sequence.

0.38:179:63

AQ241670

R-THYRO1000795

20

R-THYRO1000846

Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.

3.6e-06:425:61

AF029779

25

R-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds.

4.0e-42:251:92

AF015913

30

R-THYRO1000956

R-THYRO1000964

35 Human Chromosome 11 Cosmid cSRL186g7, complete sequence.

0.18:292:61

U73627

R-THYRO1000999

40 CIT-HSP-2288E24.TR CIT-HSP Homo sapiens genomic clone 2288E24, genomic survey sequence.

3.6e-18:292:71

AQ002356

R-THYRO1001063

45 Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.

1.5e-27:292:76

AF001552

R-THYRO1001071

50 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.

1.7e-105:513:98

Z83844

R-THYRO1001102

55 Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.

3.2e-62:429:86

AC004832

R-THYRO1001113

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Caenorhabditis elegans cosmid C25F9, complete sequence.

0.026:338:58

Z81476

5 R-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

5.3e-12:132:79

AC002096

10 R-THYRO1001205

Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE, 5 unordered pieces.

1.9e-60:251:85

AC004987

15 R-THYRO1001237

R-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

1.5e-45:525:75

20 D67067

R-THYRO1001266

H.sapiens DNA containing a polymorphic (CA)_n repeat (436bp).

6.0e-05:258:67

25 X65457

R-THYRO1001327

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

30 2.8e-104:541:95

AL021578

R-THYRO1001456

35

R-THYRO1001457

H.sapiens mRNA for protein kinase C mu.

2.9e-23:391:66

X75756

40

R-THYRO1001471

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence.

0.39:271:61

AC004787

45

R-THYRO1001478

R-THYRO1001495

Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.

50 2.8e-88:446:88

AC006006

R-THYRO1001523

CIT-HSP-2333F9.TF CIT-HSP Homo sapiens genomic clone 2333F9, genomic survey sequence.

55 1.4e-05:126:71

AQ039390

R-THYRO1001529

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5 R-THYRO1001593
Homo sapiens chromosome 19, cosmid R33632, complete sequence.
3.7e-100:514:96
AC005781

10 R-THYRO1001608
Homo sapiens clone DJ0635O05, WORKING DRAFT SEQUENCE, 7 unordered pieces.
2.3e-40:369:79
AC004845

15 R-THYRO1001641
Homo sapiens clone 24448 unknown mRNA, partial cds.
3.4e-110:562:96
AF070638

20 R-THYRO1001700

R-THYRO1001702
Mus musculus mRNA for myeloid associated differentiation protein.
1.1e-11:367:66
AJ001616

25 R-THYRO1001725
Homo sapiens, clone hRPK.1_A_1, complete sequence.
9.1e-12:329:65
AC006196

30 R-THYRO1001770
Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.
0.12:339:59
AC004879

R-THYRO1001803

35 R-Y79AA1000030
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
2.0e-98:515:95
AC005214

40 R-Y79AA1000127
Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
3.2e-115:551:99
AP000034

45 R-Y79AA1000207
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
1.8e-38:282:85
AC005562

50 R-Y79AA1000226
Homo sapiens full length insert cDNA YN52F10.
4.8e-09:104:85
AF075033

55 R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion.
1.0e-105:564:93
D16469

- 5 R-Y79AA1000426
Rattus norvegicus activin beta E mRNA, complete cds.
6.1e-50:562:72
AF089825
- 10 R-Y79AA1000521
Rattus norvegicus steroid sulfatase (Sts) mRNA, complete cds.
0.48:233:62
U37138
- 15 R-Y79AA1000750
Human DNA from cosmid f23280 from chromosome 19q13.2, genomic sequence.
6.8e-07:320:60
L47334
- 20 R-Y79AA1000776
R-Y79AA1000777
Homo sapiens full length insert cDNA clone ZD93D10.
2.9e-110:574:95
AF088072
- 25 R-Y79AA1000876
Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.
0.0096:105:71
U73520
- 30 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.0e-78:453:92
AF093420
- 35 R-Y79AA1000967
Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.
2.3e-43:263:84
L22557
- 40 R-Y79AA1001013
R-Y79AA1001056
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.5e-22:269:73
U50734
- 45 R-Y79AA1001062
D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val.
1.1e-07:494:57
X54011
- 50 R-Y79AA1001090
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.
1.2e-26:269:77
AC002300
- 55 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds.
5.7e-82:407:97
AF038961

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R-Y79AA1001264
 HS_2195_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195
 Col=14 Row=A, genomic survey sequence.
 3.4e-07:101:82
 5 AQ191092

R-Y79AA1001272
 Hansenula wingei mitochondrial DNA, complete sequence.
 2.1e-05:435:60
 10 D31785

R-Y79AA1001328
 Rattus norvegicus Delta 3 mRNA, complete cds.
 1.0e-29:356:72
 15 AF084576

R-Y79AA1001426

R-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds.
 6.2e-111:555:96
 20 AB007938

R-Y79AA1001523
 Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8
 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete
 sequence.
 3.7e-71:259:90
 25 ZB4480

R-Y79AA1001530
 Human beta-tubulin gene (5-beta) with ten Alu family members.
 2.6e-56:301:96
 30 X00734

R-Y79AA1001592
 HS_2175_A2_B11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175
 Col=22 Row=C, genomic survey sequence.
 1.0:237:59
 35 AQ307634

R-Y79AA1001727

R-Y79AA1001787
 Homo sapiens mRNA for putative ATPase, partial.
 7.2e-80:405:97
 45 AJ009947

R-Y79AA1001795
 Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11
 to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein
 S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-
 SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4
 (RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-
 DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and
 55 GSSs, complete sequence.
 4.2e-110:555:97
 AL031228

- R-Y79AA1001799
- R-Y79AA1001803
Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
5 6.2e-60:499:77
U02983
- R-Y79AA1001863
10 Human DNA sequence from PAC 365E2 on chromosome 6p22.3-24.1. Contains EST and STS.
1.4e-45:261:75
AL009177
- R-Y79AA1002022
15 H.sapiens mRNA for basement membrane heparan sulfate proteoglycan.
1.0:311:61
X62515
- R-nnnnnnnnnnnnn
20 Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence.
1.0:208:62
AE001381
- R-nnnnnnnnnnnnn
25 Homo sapiens DNA, trinucleotide repeats region, clone CAG83.
0.17:132:67
AB018494
- R-Y79AA1002213
30 Human DNA sequence from PAC 340G1 on chromosome 6 contains STS.
5.6e-46:490:73
Z84719
- R-Y79AA1002334
35 Japanese Quail (C.coturnix) troponin T isoform mRNA, clone cC501.
0.96:210:63
M26599
- R-Y79AA1002373
40 Human BAC clone RG126M09 from 7q21-q22, complete sequence.
9.7e-82:544:85
AC002067
- R-Y79AA1002376
45 Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
1.9e-111:546:97
M10546
- R-Y79AA1002378
50 Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.5e-33:244:74
D10630
- R-Y79AA1002381
55 Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.
0.0046:177:68
Z95152

Homology search result 8.

[0300] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 5'-ends.

5

Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

10

[0301] Data were not shown for the clones in which the P-value was higher than 1.

15

F-BNGH41000020
ESTs
6.6e-72:412:92
Hs.153375:AI287812

20

F-BNGH41000087
Homo sapiens mRNA for MIFR-1, complete cds
0.027:499:57
Hs.58269:AB010962

25

F-BNGH41000091
Homo sapiens voltage-gated potassium channel eag (EAG) mRNA, complete cds
5.2e-81:687:76
Hs.158305:AJ001366

30

F-HEMBA1000006
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [*S.cerevisiae*]
2.0e-25:167:91
Hs.9252:R53360

35

F-HEMBA1000121
ESTs, Moderately similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [*Caenorhabditis elegans*]
3.0e-34:180:98
Hs.149509:N24022

40

F-HEMBA1000128
EST
0.00069:177:62
Hs.158854:AI377837

45

F-HEMBA1000275
Human modulator recognition factor I (MRF-1) mRNA, 3'end
0.012:508:58
Hs.920:M62324

50

F-HEMBA1000300
Human mRNA for KIAA0355 gene, complete cds
1.6e-46:402:78
Hs.153014:AB002353

55

F-HEMBA1000349
EST
6.7e-08:65:95

Hs.54372:N80032

F-HEMBA1000443
ESTs
5 6.1e-23:278:76
Hs.69492:AA116026

F-HEMBA1000462

10 F-HEMBA1000477
ESTs
6.9e-78:414:94
Hs.152861:AA287444

15 F-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial
7.3e-95:482:96
Hs.129361:AJ007581

20 F-HEMBA1000634
ESTs
1.3e-38:246:86
Hs.6145:W26640

25 F-HEMBA1000671
Zinc finger protein 140 (clone pHZ-39)
2.4e-53:469:68
Hs.154205:U09368

30 F-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds
2.1e-127:442:97
Hs.5300:AF053470

35 F-HEMBA1000732
Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, complete cds
1.0e-45:258:94
Hs.85087:AF051344

40 F-HEMBA1000745
Human cardiotrophin-1 (CTF1) mRNA, complete cds
1.1e-07:316:61
Hs.25537:U43030

45 F-HEMBA1000835
ESTs
4.2e-11:188:72
Hs.116265:AI184988

50 F-HEMBA1000875
Zinc finger protein 133 (clone pHZ-13)
1.5e-27:169:93
Hs.78434:U09366

55 F-HEMBA1000907
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-06:545:60
Hs.143551:AF048693

5 F-HEMBA1000940
Homo sapiens connexin46.6 (Cx46.6) gene, complete cds
4.1e-18:307:66
Hs.100072:AF014643

10 F-HEMBA1000962
Homo sapiens mRNA for MEGF8, partial cds
0.0018:391:62
Hs.158200:AB011541

15 F-HEMBA1001184
Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds
2.7e-24:404:67
Hs.14368:AF042081

20 F-HEMBA1001221
Human transmembrane protein mRNA, complete cds
7.7e-44:858:63
Hs.78531:U19878

25 F-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds
2.2e-85:463:93
Hs.1584:AC003107

30 F-HEMBA1001272
Antidiuretic hormone receptor
0.064:616:57
Hs.2524:L22206

35 F-HEMBA1001296
Homo sapiens delta-catenin mRNA, complete cds
0.031:410:59
Hs.80220:U96136

40 F-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds
3.0e-15:143:81
Hs.13063:AF017789

45 F-HEMBA1001390
ESTs, Highly similar to polymerase I-transcript release factor [M.musculus]
1.6e-49:297:91
Hs.25581:AI246284

50 F-HEMBA1001563
ESTs
4.9e-12:160:74
Hs.162813:AA524616

55 F-HEMBA1001621
Human P2U nucleotide receptor mRNA, complete cds
0.00098:314:61
Hs.339:U07225

F-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
3.4e-172:810:98

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Hs.10290:AF090988

F-HEMBA1001886
Human repressor transcriptional factor (ZNF85) mRNA, complete cds
5 1.1e-115:849:80
Hs.37138:U35376

F-HEMBA1002048
Homo sapiens mRNA for APC 2 protein, complete cds
10 0.96:266:62
Hs.20912:AB012162

F-HEMBA1002131
Homo sapiens mRNA for KIAA0584 protein, partial cds
15 1.1e-45:709:66
Hs.106794:AB011156

F-HEMBA1002163
ASPARTYL-TRNA SYNTHETASE
20 0.026:568:58
Hs.80758:J05032

F-HEMBA1002164
Pregnancy-associated plasma protein A
25 0.0049:274:60
Hs.158229:U28727

F-HEMBA1002167

30 F-HEMBA1002178
Homo sapiens mRNA for KIAA0584 protein, partial cds
8.3e-48:794:65
Hs.106794:AB011156

35 F-HEMBA1002195
EST
2.0e-05:177:70
Hs.145935:AI275921

40 F-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
1.2e-138:382:95
Hs.75607:D10522

45 F-HEMBA1002239
Homo sapiens mRNA, chromosome I specific transcript KIAA0488
1.2e-47:570:71
Hs.67619:AB007957

50 F-HEMBA1002316
EST
1.8e-28:246:79
Hs.136950:AA825638

55 F-HEMBA1002420
Homo sapiens GABA-B receptor mRNA, complete cds
1.7e-05:303:63
Hs.12307:AF056085

- 5 F-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
4.3e-167:778:98
Hs.1501:J04621
- 10 F-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
8.5e-128:751:89
Hs.41548:U63336
- 15 F-HEMBA1002551
ESTs
2.4e-25:207:84
Hs.158172:N24325
- 20 F-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
4.4e-170:798:98
Hs.19154:AF038660
- 25 F-HEMBA1002985
ESTs
2.6e-09:124:76
Hs.118620:T60326
- 30 F-HEMBA1002992
ESTs
2.4e-21:121:97
Hs.143571:AI089396
- 35 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.5e-188:873:99
Hs.148318:AF034611
- 40 F-HEMBA1003072
ESTs
1.2e-33:387:71
Hs.59628:W91959
- 45 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.7e-140:671:98
Hs.26350:AF049891
- 50 F-HEMBA1003120
Zinc finger protein 91 (HPF7, HTF10)
1.0e-24:143:76
Hs.8597:L11672
- 55 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
1.8e-184:856:98
Hs.11494:AF093118
- F-HEMBA1003294
Human antiseecretory factor-1 mRNA, complete cds
5.1e-45:324:83

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Hs.148495:AF050199

F-HEMBA1003315
Homo sapiens mRNA for TIP49, complete cds
5 4.2e-19:377:64
Hs.155541:AF070735

F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
10 9.2e-185:851:99
Hs.23672:AF074264

F-HEMBA1003399
H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase
15 0.00042:297:61
Hs.118929:X79568

F-HEMBA1003487
Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds
20 0.0011:237:63
Hs.88145:AF030339

F-HEMBA1003497
ESTs, Weakly similar to similar to zinc finger 5 protein from Gallus gallus, U51640 [H.sapiens]
25 2.5e-09:303:63
Hs.143723:H86048

F-HEMBA1003530
Homo sapiens mRNA for ephrin-A2
30 0.024:396:60
Hs.158306:AJ007292

F-HEMBA1003602
Homo sapiens DNA from chromosome 19, cosmid R29144
35 0.0072:663:57
Hs.155647:AC004221

F-HEMBA1003732
ESTs
40 1.0e-106:494:100
Hs.157568:AI356515

F-HEMBA1003945
Homo sapiens clone 638 unknown nRNA, complete sequence
45 5.9e-78:310:93
Hs.159515:AF091085

F-HEMBA1004007
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC
50 0.56:165:64
Hs.115742:AF077754

F-HEMBA1004067
Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]
55 0.048:581:58
Hs.83190:U29344

F-HEMBA1004085

- ESTs
1.7e-15:92:98
Hs.98138:AI183561
- 5 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds
1.2e-159:779:96
Hs.66392:AF064244
- 10 F-HEMBA1004250
Human mRNA for KIAA0327 protein, complete cds
2.1e-23:676:59
Hs.149323:AB002325
- 15 F-HEMBA1004391
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR
0.43:157:63
Hs.1757:U52112
- 20 F-HEMBA1004444
H.sapiens mRNA for gp25L2 protein
1.5e-54:544:73
Hs.159569:X90872
- 25 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds
1.1e-05:230:62
Hs.20709:AF065389
- 30 F-HEMBA1004505
ESTs
9.1e-61:345:93
Hs.4814:AA631254
- 35 F-HEMBA1004785
Homo sapiens Polycomb 2 homolog (hPc2) mRNA, complete cds
3.7e-18:294:65
Hs.123085:AF013956
- 40 F-HEMBA1004797
ESTs
3.9e-06:107:73
Hs.42302:AI032142
- 45 F-HEMBA1004952
Human cardiotrophin-1 (CTF1) mRNA, complete cds
0.00021:175:68
Hs.25537:U43030
- 50 F-HEMBA1004971

F-HEMBA1004982
Human metabotropic glutamate receptor 8 mRNA, complete cds
0.31:288:60
- 55 Hs.86204:U92459

F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds

- 7.9e-67:370:93
Hs.5716:AB002308
- 5 F-HEMBA1005084
Homo sapiens mRNA for KIAA0612 protein, partial cds
0.00022:400:59
Hs.112499:AB014512
- 10 F-HEMBA1005145
Lymphocyte-activation gene 3
3.4e-05:480:59
Hs.74011:X51985
- 15 F-HEMBA1005230
ESTs
2.3e-103:481:99
Hs.135112:AI090827
- 20 F-HEMBA1005246
Homo sapiens ALR mRNA, complete cds
2.0e-05:220:62
Hs.153638:AF010403
- 25 F-HEMBA1005267
ESTs
5.6e-16:305:64
Hs.125699:AA868017
- 30 F-HEMBA1005337
EST
2.1e-59:304:97
Hs.48956:N64339
- 35 F-HEMBA1005430
ESTs
6.9e-19:333:65
Hs.116567:AI332643
- 40 F-HEMBA1005449
Human plectin (PLEC1) mRNA, complete cds
0.026:576:56
Hs.79706:U53204
- 45 F-HEMBA1005489
Homo sapiens mRNA for KIAA0291 gene, partial cds
0.14:551:59
Hs.104717:AB006629
- 50 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR
1.8e-12:298:64
Hs.36989:M13232
- 55 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
2.6e-143:672:98
Hs.7138:U29589

F-HEMBA1005698
 ESTs
 1.8e-124:611:97
 Hs.144441:AI338335
 5

F-HEMBA1005913

 F-HEMBA1005929
 H.sapiens mRNA for serine/threonine protein kinase EMK
 10 1.5e-86:847:72
 Hs.157199:X97630

F-HEMBA1005945
 ESTs, Weakly similar to F17E5.2 [C.elegans]
 15 4.2e-26:159:92
 Hs.126571:AI038963

F-HEMBA1006016
 ESTs
 20 1.3e-22:145:93
 Hs.33728:H97503

F-HEMBA1006171

 F-HEMBA1006276
 Homo sapiens KIAA0412 mRNA, partial cds
 25 5.1e-19:371:65
 Hs.6200:AB007872

F-HEMBA1006299
 30

F-HEMBA1006311

 F-HEMBA1006335
 ESTs
 35 0.00021:327:62
 Hs.146044:AI089998

F-HEMBA1006357
 40 Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
 7.4e-28:389:67
 Hs.10761:AF005038

F-HEMBA1006430
 ESTs
 45 9.7e-92:463:95
 Hs.143702:AI084062

F-HEMBA1006482
 50 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
 6.2e-146:575:98
 Hs.14511:AF026852

F-HEMBA1006517
 ESTs
 55 3.6e-63:381:87
 Hs.11611:W21919

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F-HEMBA1006544
 Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds
 2.0e-50:503:76
 Hs.43543:AF042800
 5

F-HEMBA1006572
 Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
 0.031:611:57
 Hs.96253:U79666
 10

F-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds
 1.2e-128:646:95
 Hs.3628:AB014587
 15

F-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial
 1.7e-101:476:98
 Hs.129361:AJ007581
 20

F-HEMBA1006724
 ESTs
 8.3e-86:450:95
 Hs.10056:AA210796
 25

F-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial
 6.1e-97:457:98
 Hs.129361:AJ007581
 30

F-HEMBA1006770
 ESTs, Highly similar to BRAIN PROTEIN F41 [Mus musculus]
 1.6e-31:237:85
 Hs.31612:H41366
 35

F-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial
 9.4e-113:541:97
 Hs.129361:AJ007581
 40

F-HEMBA1006912
 ESTs
 1.4e-94:460:97
 Hs.88672:AA279956
 45

F-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds
 5.2e-120:651:92
 Hs.83070:L76687
 50

F-HEMBA1006960
 Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
 0.011:628:57
 Hs.159234:U89995
 55

F-HEMBA1007013
 ESTs
 2.6e-05:139:69

- Hs.113817:AA702497
- F-HEMBA1007057
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
5 7.5e-12:389:64
Hs.143641:AB009462
- F-HEMBA1007063
- 10 F-HEMBA1007226
ESTs
1.8e-35:202:94
Hs.105140:N32669
- 15 F-HEMBA1007241
ESTs, Weakly similar to No definition line found [C.elegans]
4.1e-27:361:67
Hs.114062:AI421699
- 20 F-HEMBA1007291
ESTs
0.96:114:69
Hs.121411:AA770241
- 25 F-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.5e-81:405:97
Hs.3727:AA205887
- 30 F-HEMBA1000106
ESTs
2.2e-76:393:96
Hs.151874:AI023405
- 35 F-HEMBA1000276
EST
0.81:239:63
Hs.149811:AI286277
- 40 F-HEMBA1000309
Homo sapiens zinc finger protein (MBLL) mRNA, complete cds
2.4e-35:180:100
Hs.44806:AF061261
- 45 F-HEMBA1000407
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
0.026:218:65
Hs.106070:U22398
- 50 F-HEMBA1000447
Homo sapiens JWA protein mRNA, complete cds
4.6e-160:750:98
Hs.92384:AF070523
- 55 F-HEMBA1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
6.8e-07:130:77
Hs.18171:AA524327

F-HEMBB1000567
 ESTs
 8.8e-13:271:71
 Hs.19934:AA455673
 5
 F-HEMBB1000642
 F-HEMBB1000668
 EST
 10 0.83:192:58
 Hs.126372:AA912193
 F-HEMBB1000679
 H.sapiens mRNA for TRAMP protein
 15 4.1e-96:727:80
 Hs.4147:X63679
 F-HEMBB1000881
 Homo sapiens chromosome 4p homeobox mRNA sequence
 20 2.2e-06:512:60
 Hs.104134:M99587
 F-HEMBB1000905
 Homo sapiens mRNA for voltage gated potassium channel
 25 0.93:337:58
 Hs.4975:Y15065
 F-HEMBB1001026
 Human p76 mRNA, complete cds
 30 6.1e-08:410:61
 Hs.28757:U81006
 F-HEMBB1001048
 Human Hpast (HPAST) mRNA, complete cds
 35 2.1e-56:524:75
 Hs.155119:AF001434
 F-HEMBB 1001200
 EST
 40 0.10:300:61
 Hs.161647:AA133367
 F-HEMBB1001407
 Homo sapiens PRKY exon 1 and joined CDS
 45 2.6e-40:271:81
 Hs.56336:Y15801
 F-HEMBB1001530
 ESTs
 50 1.2e-98:477:98
 Hs.135208:AI093908
 F-HEMBB1001547
 55 F-HEMBB1001573
 EST
 2.2e-06:115:75
 Hs.138275:R43976

5 F-HEM BB1001847
ESTs
5.3e-79:389:98
Hs.16141:W56079

10 F-HEM BB1001959
Homo sapiens clone 24781 mRNA sequence
1.0e-58:322:93
Hs.108112:AF070640

15 F-HEM BB1001978
EST
4.7e-23:245:74
Hs.136356:AA493225

20 F-HEM BB1002039
EST
2.3e-25:345:70
Hs.128248:AA972858

25 F-HEM BB1002041
Human plectin (PLEC1) mRNA, complete cds
2.2e-08:477:60
Hs.79706:U53204

30 F-HEM BB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
9.9e-97:454:99
Hs.159267:AF049703

35 F-HEM BB1002120
ESTs
7.6e-10:68:100
Hs.146335:AI262660

40 F-HEM BB1002162
Homo sapiens genethonin 1 mRNA, complete cds
2.2e-68:328:99
Hs.109590:AF062534

45 F-HEM BB1002228
Homo sapiens unknown mRNA, complete cds
5.3e-41:208:98
Hs.11441:AF047439

50 F-HEM BB1002245
Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds
5.6e-05:299:63
Hs.92614:M62302

55 F-HEM BB1002302

F-HEM BB1002427
Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds
0.84:108:68
Hs.8786:AB014680

- 5 F-HEMBB1002465
ESTs, Highly similar to ACYL-COA DEHYDROGENASE [Bacillus subtilis]
3.2e-18:159:84
Hs.14791:AA741056
- 10 F-HEMBB1002661
ESTs
0.023:424:55
Hs.154029:AI380603
- 15 F-HEMBB1002663
F-HEMBB1002693
- 20 F-MAMMA1000046
Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)
3.2e-43:454:74
Hs.144563:AF057280
- 25 F-MAMMA1000102
Homo sapiens mRNA for cathepsin V, complete cds
0.70:222:65
Hs.87417:AB001928
- 30 F-MAMMA1000106
Homo sapiens mRNA for KIAA0754 protein, partial cds
0.00076:331:61
Hs.159183:AB018297
- 35 F-MAMMA1000118
B94 PROTEIN
1.5e-07:511:61
Hs.75522:M92357
- 40 F-MAMMA1000141
ESTs
2.3e-18:268:73
Hs.155334:AA827904
- 45 F-MAMMA1000204
Homo sapiens dysferlin mRNA, complete cds
2.5e-167:781:98
Hs.143897:AF075575
- 50 F-MAMMA1000226
Human involucrin mRNA
0.0010:414:61
Hs.157091:M13903
- 55 F-MAMMA1000403
ESTs
2.0e-24:163:90
Hs.44281:AI342377
- 60 F-MAMMA1000449
ESTs
0.99:211:60
Hs.143715:AI167929

F-MAMMA1000457
 NADH-CYTOCHROME B5 REDUCTASE
 7.7e-37:551:66
 Hs.75666:M28713
 5

F-MAMMA1000473

 F-MAMMA1000496
 Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
 10 1.1e-107:543:96
 Hs.8003:AC004997

F-MAMMA1000528
 EST
 15 0.22:227:59
 Hs.161400:AI423879

F-MAMMA1000591
 H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
 20 3.3e-23:470:62
 Hs.55823:X92689

F-MAMMA1000614
 H.sapiens mRNA for CCAAT/enhancer binding protein alpha
 25 1.9e-06:492:61
 Hs.76171:Y11525

F-MAMMA1000652
 Homo sapiens mRNA, chromosome I specific transcript KIAA0487
 30 1.5e-61:449:75
 Hs.92381:AB007956

F-MAMMA1000681
 Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
 35 4.0e-34:636:65
 Hs.159543:AJ000479

F-MAMMA1000706
 COAGULATION FACTOR VII PRECURSOR
 40 9.7e-16:378:65
 Hs.36989:M13232

F-MAMMA1000788
 ESTs, Weakly similar to M01E11.2 [C.elegans]
 45 3.4e-118:571:97
 Hs.78389:AI191127

F-MAMMA1000810
 EST
 50 0.065:211:61
 Hs.116798:AA633813

F-MAMMA1000814
 EST
 55 3.1e-08:224:66
 Hs.141620:N63316

F-MAMMA1000881

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- Homo sapiens sgk gene
3.5e-08:165:69
Hs.159640:AJ000512
- 5 F-MAMMA1000986
Homo sapiens clone 24796 mRNA sequence
2.3e-115:320:99
Hs.27191:AF070596
- 10 F-MAMMA1000994
Human HOX4C mRNA for a homeobox protein
0.050:178:64
Hs.74061:X59372
- 15 F-MAMMA1001043
Latent transforming growth factor beta binding protein 2
0.0013:376:60
Hs.83337:Z37976
- 20 F-MAMMA1001066
ESTs
1.1e-18:128:77
Hs.114031:AA700958
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
2.0e-182:844:99
Hs.20423:AF091094
- 30 F-MAMMA1001141
Homo sapiens achaete scute homologous protein (ASH1) mRNA, complete cds
6.1e-07:492:58
Hs.1619:L08424
- 35 F-MAMMA1001150
Protein kinase C, mu
8.3e-51:691:67
Hs.2891:X75756
- 40 F-MAMMA1001237
Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds
8.2e-08:386:60
Hs.85838:U81800
- 45 F-MAMMA1001284
ESTs
1.1e-91:452:97
Hs.114756:AI279440
- 50 F-MAMMA1001310
Homo sapiens mRNA for KIAA0708 protein, partial cds
0.014:512:57
Hs.117177:AB014608
- 55 F-MAMMA1001344
ESTs, Weakly similar to No definition line found [C.elegans]
8.3e-80:406:96
Hs.121619:AI188389

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F-MAMMA1001418
 Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds
 1.9e-36:622:63
 Hs.97207:U62966
 5

F-MAMMA1001532
 Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds
 2.1e-33:282:68
 Hs.158174:U66561
 10

F-MAMMA1001609
 Insulin-like growth factor-binding protein 4
 0.00026:596:57
 Hs.1516:U20982
 15

F-MAMMA1001615
 Homo sapiens DNA from chromosome 19, cosmid R29144
 1.1e-05:504:59
 Hs.155647:AC004221
 20

F-MAMMA1001623
 Excision repair protein ERCC6
 1.2e-38:274:86
 Hs.99924:L04791
 25

F-MAMMA1001634
 ESTs
 1.5e-26:176:90
 Hs.16187:AI139901
 30

F-MAMMA1001893
 Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
 0.00030:170:68
 Hs.106070:U22398
 35

F-MAMMA1001901
 ESTs
 1.5e-36:201:76
 Hs.161660:AA167744
 40

F-MAMMA1001957
 Prostaglandin I2 (prostacyclin) receptor (IP)
 0.041:277:61
 Hs.393:D38128
 45

F-MAMMA1001978
 EST
 4.0e-43:359:81
 Hs.136494:AA587773
 50

F-MAMMA1002070
 Human PAC clone DJ515N1 from 22q11.2-q22
 5.1e-135:652:97
 Hs.26670:AC002073
 55

F-MAMMA1002080
 Calcium channel, voltage-dependent, L type, alpha 1C subunit
 0.0019:574:57

- Hs.89925:L04569
- F-MAMMA1002087
Human mRNA for KIAA0009 gene, complete cds
5 0.71:228:63
Hs.79972:D13634
- F-MAMMA1002091
Homo sapiens CD39L2 (CD39L2) mRNA, complete cds
10 5.2e-158:743:98
Hs.12330:AF039916
- F-MAMMA1002095
Homo sapiens mRNA for KIAA0703 protein, complete cds
15 4.9e-55:657:68
Hs.6168:AB014603
- F-MAMMA1002128
Human leucine zipper on the D14S46E locus mRNA, complete cds
20 0.77:449:59
Hs.89606:M95925
- F-MAMMA1002142
- F-MAMMA1002165
Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
25 1.2e-35:182:98
Hs.139340:AF083500
- F-MAMMA1002205
ESTs
30 4.7e-32:385:71
Hs.46158:AI160121
- F-MAMMA1002224
TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT
35 1.3e-34:248:85
Hs.3006:X63468
- F-MAMMA1002234
ESTs
40 1.1e-100:501:97
Hs.158161:AA312511
- F-MAMMA1002586
Human mRNA for KIAA0183 gene, partial cds
45 0.00041:388:61
Hs.76666:D80005
- F-MAMMA1002633
Landsteiner-Wiener blood group glycoprotein
50 1.1e-37:477:71
Hs.108287:L27670
- F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds
55 4.1e-84:801:74
Hs.155119:AF001434

F-NT2RM1000407
 ESTs
 4.1e-19:132:92
 Hs.133484:D80522
 5
 F-NT2RM1000462
 F-NT2RM1000542
 Beta-galactosidase (GLB1)
 10 1.3e-17:436:61
 Hs.79222:M34423
 F-NT2RM1000580
 ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
 15 6.2e-51:254:98
 Hs.132096:AA314601
 F-NT2RM1000789
 Homo sapiens mRNA for hTCF-4
 20 3.5e-96:299:92
 Hs.154485:Y11306
 F-NT2RM1000855
 Hydroxysteroid (11-beta) dehydrogenase 2
 25 0.021:178:67
 Hs.1376:U26726
 F-NT2RM1000858
 F-NT2RM1000899
 30 Homo sapiens BAC clone RG119C02 from 7p15
 0.037:222:63
 Hs.22900:AC004520
 F-NT2RM2000241
 35 ESTs
 2.9e-31:166:97
 Hs.156175:AI334328
 F-NT2RM2000306
 40
 F-NT2RM2000410
 ESTs
 3.2e-12:81:97
 45 Hs.72116:AA151564
 F-NT2RM2000423
 Beta-galactosidase (GLB1)
 0.074:163:63
 50 Hs.79222:M34423
 F-NT2RM2000497
 ESTs, Weakly similar to CHL1 protein [H.sapiens]
 3.7e-21:121:97
 55 Hs.97515:AA435715
 F-NT2RM2000514

F-NT2RM2000565

F-NT2RM2000582
EST
5 1.7e-42:218:98
Hs.160262:AI146610

F-NT2RM2000589

10 F-NT2RM2000622
Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
0.00018:409:62
Hs.99915:M23263

15 F-NT2RM2000632
Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds
0.00017:331:59
Hs.14244:AF038362

20 F-NT2RM2000773
Human zinc finger protein (MAZ) mRNA
7.2e-47:274:91
Hs.7647:M94046

25 F-NT2RM2001126
Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds
5.1e-163:663:99
Hs.21301:AF093419

30 F-NT2RM2001558
Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds
3.9e-166:770:98
Hs.98397:AF093408

35 F-NT2RM2001626
Human mRNA for KIAA0231 gene, partial cds
2.8e-40:562:67
Hs.7938:D86984

40 F-NT2RM2001643
ESTs
7.9e-112:548:97
Hs.12610:W56112

45 F-NT2RM2001738
FACTOR VIII INTRON 22 PROTEIN
0.32:452:59
Hs.83363:M34677

50 F-NT2RM2001767
Homo sapiens mRNA for B120, complete cds
5.0e-24:131:100
Hs.123090:AB001895

55 F-NT2RM2001792
Homo sapiens mRNA for serum lectin P35, complete cds
8.2e-14:244:67

	Hs.54517:D63160
	F-NT2RM2001818
	EST
5	0.051:152:61
	Hs.157619:AI357718
	F-NT2RM2001902
	Human p21-activated protein kinase (Pak1) gene, complete cds
10	4.4e-39:568:66
	Hs.62402:U24152
	F-NT2RM2001939
	Human G protein-coupled receptor GPR-NGA gene, complete cds
15	4.2e-141:664:98
	Hs.92458:U55312
	F-NT2RM2001941
	Dopamine receptor D4
20	1.3e-14:547:61
	Hs.99922:L12398
	F-NT2RM4000100
	Human involucrin mRNA
25	1.1e-09:487:62
	Hs.157091:M13903
	F-NT2RM4000115
30	F-NT2RM4000198
	ESTs
	9.3e-101:496:98
	Hs.128676:AA464413
35	F-NT2RM4000284
	Human IgG Fc receptor hFcRn mRNA, complete cds
	2.4e-38: 194:98
	Hs.110804:U12255
40	F-NT2RM4000295
	Homo sapiens SOX22 protein (SOX22) mRNA, complete cds
	1.7e-06:479:60
	Hs.43627:U35612
45	F-NT2RM4000326
	Phosphorylase kinase, gamma 2 (testis)
	0.95:204:63
	Hs.87452:M31606
50	F-NT2RM4000417
	H.sapiens Syt V gene (genomic and cDNA sequence)
	0.97:143:67
	Hs.23179:X96783
55	F-NT2RM4000444
	Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
	0.45:194:64
	Hs.90319:Z21507

F-NT2RM4000587
 Human proto-oncogene (FRATI) gene, complete cds
 3.8e-05:495:60
 Hs.143005:U58975
 5

F-NT2RM4000593

F-NT2RM4000648
 Homo sapiens glypican-4 (GPC4) mRNA, complete cds
 1.0e-50:610:70
 Hs.58367:AF030186
 10

F-NT2RM4000761
 EST
 0.89:53:79
 Hs.161967:AA494423
 15

F-NT2RM4000965
 H.sapiens mRNA for PHAPI2b protein
 0.18:148:68
 Hs.84264:U70439
 20

F-NT2RM4000997

F-NT2RM4001321
 ESTs
 1.8e-94:467:97
 Hs.12610:W56112
 25

F-NT2RM4001325
 Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds
 2.1e-13:384:64
 Hs.158304:AB012192
 30

F-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 3.1e-156:719:99
 Hs.77864:AB014538
 35

F-NT2RM4001735
 40

F-NT2RM4001768
 ESTs
 0.00012:123:68
 Hs.128045:AA970231
 45

F-NT2RM4001843

F-NT2RM4002352
 Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
 4.4e-157:761:97
 Hs.143641:AB009462
 50

F-NT2RP1000002
 EST
 0.00023:170:68
 Hs.135504:AI091717
 55

	F-NT2RP1000050
	Histidine-rich calcium binding protein
	0.0047:257:61
	Hs.1480:M60052
5	
	F-NT2RP1000181
	Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
	6.9e-99:510:94
	Hs.132898:AC004770
10	
	F-NT2RP1000239
	ESTs
	1.7e-34:240:67
	Hs.33020:N31946
15	
	F-NT2RP1000261
	ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
	9.1e-92:484:94
20	Hs.7870:AI078137
	F-NT2RP1000271
	Homo sapiens DNA-binding protein mRNA, complete cds
	1.4e-140:678:97
25	Hs.137582:AF038951
	F-NT2RP1000300
	Human endosome-associated protein (EEA1) mRNA, complete cds
	1.0:205:61
30	Hs.2864:L40157
	F-NT2RP1000325
	Phosphate carrier, mitochondrial
	7.7e-84:444:93
35	Hs.78713:X60036
	F-NT2RP1000448
	ESTs
	9.5e-73:405:93
40	Hs.24054:N46499
	F-NT2RP1000465
	ESTs
	8.5e-10:81:87
45	Hs.18619:AI202769
	F-NT2RP1000468
	Homo sapiens clone 24781 mRNA sequence
	2.1e-20:133:92
50	Hs.108112:AF070640
	F-NT2RP1000551
	Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds
	2.4e-140:742:93
55	Hs.75402:U09585
	F-NT2RP1000579
	SUCCINATE DEHYDROGENASE

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	1.1e-141:798:91 Hs.469:L21936
5	F-NT2RP1000613 Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds 5.5e-11:468:58 Hs.5338:AF037335
10	F-NT2RP1000679 ESTs 0.79:127:65 Hs.146093:AA100242
15	F-NT2RP1000740 Homo sapiens Trio isoform mRNA, complete cds 0.24:160:66 Hs.150625:AF091395
20	F-NT2RP1000903 F-NT2RP1000981
25	F-NT2RP1001004 Human mRNA for Doc2 beta, complete cds 0.00072:520:57 Hs.54402:D70830
30	F-NT2RP1001020 ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae] 2.1e-73:392:94 Hs.4789:AI418298
35	F-NT2RP1001031 Miller-Dieker syndrome chromosome region 4.5e-07:383:61 Hs.77318:L13385
40	F-NT2RP1001563 Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds 0.086:398:59 Hs.57783:U78525
45	F-NT2RP2000092 Zinc finger protein 136 (clone pHZ-20) 5.5e-56:652:70 Hs.69740:U09367
50	F-NT2RP2000178 Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence 0.14:231:62 Hs.159402:AC005609
55	F-NT2RP2000240 Homo sapiens KIAA0415 mRNA, complete cds 3.0e-61:554:76 Hs.7289:AB007875
	F-NT2RP2000394

- ESTs
0.0063:210:63
Hs.134272:AI220363
- 5 F-NT2RP2000447
Human (clone SY11) golgin-95 mRNA, complete cds
3.8e-22:498:65
Hs.24049:L06147
- 10 F-NT2RP2000479
ESTs
1.3e-46:298:90
Hs.15641:W63676
- 15 F-NT2RP2000514
Homo sapiens roundabout 1 (robo1) mRNA, complete cds
1.2e-37:543:67
Hs.36702:AF040990
- 20 F-NT2RP2000533
ESTs, Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION [Saccha-
romyces cerevisiae]
5.4e-132:647:96
Hs.18120:AA913148
- 25 F-NT2RP2000610
Homo sapiens antigen NY-CO-16 mRNA, complete cds
0.00027:182:66
Hs.132206:AF039694
- 30 F-NT2RP2000616
ESTs
0.44:235:60
Hs.31714:AA514389
- 35 F-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
6.2e-167:802:97
Hs.25846:AB016068
- 40 F-NT2RP2000663
Homo sapiens mRNA for KIAA0512 protein, complete cds
4.8e-15:305:64
Hs.48924:AB011084
- 45 F-NT2RP2000694
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.0e-113:558:96
Hs.82128:AJ012159
- 50 F-NT2RP2000712
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
1.5e-83:442:93
Hs.154226:AA468767
- 55 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds
2.1e-25:574:62

	Hs.6833:AB002324
	F-NT2RP2000818
5	F-NT2RP2000903 H.sapiens 5T4 gene for 5T4 Oncofetal antigen 3.5e-112:539:97 Hs.82128:AJ012159
10	F-NT2RP2001200 Homo sapiens mRNA for KIAA0676 protein, partial cds 1.1e-111:540:96 Hs.115763:AB014576
15	F-NT2RP2001223 ESTs 5.9e-91:461:95 Hs.103733:AA436929
20	F-NT2RP2001276 Homo sapiens mRNA for KIAA0634 protein, partial cds 2.4e-11:382:62 Hs.30898:AB014534
25	F-NT2RP2001388
	F-NT2RP2001469 ESTs 7.3e-39:213:95 Hs.151001:AA564706
30	
	F-NT2RP2001480 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds 2.9e-141:686:96 Hs.82165:L38969
35	
	F-NT2RP2001495 Human transporter protein (g17) mRNA, complete cds 6.0e-37:581:64 Hs.76460:U49082
40	
	F-NT2RP2001514
	F-NT2RP2001529 Homo sapiens mRNA for ZIP-kinase, complete cds 1.5e-153:757:96 Hs.25619:AB007144
45	
	F-NT2RP2001538 ESTs, Highly similar to co-repressor protein [M.musculus] 4.4e-63:329:94 Hs.22583:AA188168
50	
	F-NT2RP2001562 Homo sapiens GLE1 (GLE1) mRNA, complete cds 7.5e-119:572:97 Hs.81449:AF058922
55	

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5 F-NT2RP2001662
 H.sapiens mRNA for TGIF protein
 2.6e-29:448:67
 Hs.90077:X89750

10 F-NT2RP2001755
 ESTs, Highly similar to F-SPONDIN PRECURSOR [Rattus norvegicus]
 1.0e-47:275:92
 Hs.153657:H37929

15 F-NT2RP2001769
 Human protein kinase C-L (PRKCL) mRNA, complete cds
 1.9e-09:399:59
 Hs.89616:M55284

20 F-NT2RP2001817
 EST
 0.97:133:63
 Hs.145274:AI249468

25 F-NT2RP2001878
 Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
 3.6e-05:491:60
 Hs.159234:U89995

30 F-NT2RP2001903
 Human mRNA for apolipoprotein E receptor 2, complete cds
 0.0023:270:60
 Hs.54481:D86407

35 F-NT2RP2001915
 Homo sapiens Pig3 (PIG3) mRNA complete cds
 3.2e-05:493:60
 Hs.50649:AF010309

40 F-NT2RP2001921

45 F-NT2RP2001948
 ESTs
 0.55:213:61
 Hs.147805:AI221717

50 F-NT2RP2001956
 ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
 8.1e-45:510:70
 Hs.13144:T67556

55 F-NT2RP2002015
 ESTs
 4.3e-20:127:92
 Hs.12610:W56112

F-NT2RP2002063
 ESTs
 1.0e-08:73:91
 Hs.19814:T81721

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F-NT2RP2002188

F-NT2RP2002232
EST
5 0.82:99:67
Hs.148596:AI202232

F-NT2RP2002304
Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds
10 0.031:107:71
Hs.82210:U47742

F-NT2RP2002409
Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds
15 0.00063:302:65
Hs.105927:AF020044

F-NT2RP2002510
ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galacto-
20 syltransferase)
4.4e-09:298:64
Hs.144023:U15197

F-NT2RP2002527
25 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
5.2e-65:327:96
Hs.132898:AC004770

F-NT2RP2002533
30 Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete
cds
2.1e-142:726:95
Hs.127436:AF040709

F-NT2RP2002564
35 Homo sapiens mRNA for repressor protein, partial cds
3.5e-55:594:74
Hs.58167:D30612

F-NT2RP2002674
40 Epoxide hydrolase 2, cytoplasmic
2.5e-07:332:62
Hs.113:L05779

F-NT2RP2002721
45

F-NT2RP2002824
ESTs, Weakly similar to ZK858.6 [C.elegans]
5.2e-28:190:90
50 Hs.120416:AA057428

F-NT2RP2002942
Homo sapiens mRNA for KIAA0806 protein, complete cds
2.0e-146:758:94
55 Hs.24279:AB018349

F-NT2RP2002974
ESTs

4.9e-51:475:77
Hs.137840:AI123378

5 F-NT2RP2002976
ESTs, Weakly similar to No definition line found [C.elegans]
7.8e-50:315:89
Hs.159604:AI380827

10 F-NT2RP2003042
Lecithin-cholesterol acyltransferase
2.4e-25:454:65
Hs.112125:M12625

15 F-NT2RP2003138
H.sapiens mRNA for TGIF protein
2.0e-05:121:75
Hs.90077:X89750

20 F-NT2RP2003179
Homo sapiens mRNA for KIAA0537 protein, complete cds
1.0e-43:587:70
Hs.12836:AB011109

25 F-NT2RP2003210

F-NT2RP2003302
Zinc finger protein 136 (clone pHZ-20)
1.8e-64:691:69
Hs.69740:U09367

30 F-NT2RP2003369
Homo sapiens chromosome 7q22 sequence
5.1e-109:539:96
Hs.125742:AF053356

35 F-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
1.6e-159:801:95
Hs.7414:AB007927

40 F-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
2.2e-116:554:98
Hs.31575:AF100141

45 F-NT2RP2003469
ESTs
0.26:127:69
Hs.62649:AA115328

50 F-NT2RP2003545
ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]
4.2e-111:550:96
Hs.85768:W16504

55 F-NT2RP2003593
EST
8.7e-43:213:99

	Hs.130657:AI005473
	F-NT2RP2003599
	ESTs
5	7.8e-14:84:98
	Hs.107171:H53973
	F-NT2RP2003655
10	F-NT2RP2003664
	Homo sapiens mRNA for leptin receptor gene-related protein
	5.4e-134:630:98
	Hs.23581:Y12670
15	F-NT2RP2003931
	Human mRNA for KIAA0365 gene, partial cds
	4.3e-14:101:92
	Hs.84123:AB002363
20	F-NT2RP2003940
	Zinc finger protein 43 (HTF6)
	4.6e-99:693:82
	Hs.74107:X59244
25	F-NT2RP2003950
	Cell division cycle 25A
	0.00041:419:59
	Hs.1634:M81933
30	F-NT2RP2004069
	ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]
	1.3e-75:390:94
	Hs.13322:AA151730
35	F-NT2RP2004108
	Zinc finger protein 136 (clone pHZ-20)
	4.9e-69:548:78
	Hs.69740:U09367
40	F-NT2RP2004141
	TRICHOHYALIN
	4.8e-11:435:63
	Hs.82276:L09190
45	F-NT2RP2004179
	ESTs
	0.0054:180:66
	Hs.134917:AI092952
50	F-NT2RP2004205
	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
	0.27:474:56
	Hs.112049:U93181
55	F-NT2RP2004447
	Homo sapiens LDL receptor member LR3 mRNA, complete cds
	0.016:456:57
	Hs.6347:AF077820

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5 F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds
1.2e-26:497:61
Hs.76460:U49082

10 F-NT2RP2004524
Human bone morphogenetic protein-3b
0.0016:259:64
Hs.2171:D49493

15 F-NT2RP2004556
ESTs
1.1e-34:181:97
Hs.27160:AA421991

20 F-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
5.7e-107:587:92
Hs.148726:X03124

25 F-NT2RP2004648
TUBULIN ALPHA-4 CHAIN
0.59:186:61
Hs.75318:X06956

30 F-NT2RP2004670
Human mRNA for KIAA0369 gene, complete cds
0.097:309:61
Hs.21355:AB002367

35 F-NT2RP2004794
ESTs
1.3e-60:310:96
Hs.84926:N50073

40 F-NT2RP2004837

45 F-NT2RP2004847
Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)
1.4e-05:396:60
Hs.78247:M58297

50 F-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
7.2e-147:713:96
Hs.7594:M20681

55 F-NT2RP2005069
Human mRNA for KIAA0355 gene, complete cds
0.14:303:61
Hs.153014:AB002353

F-NT2RP2005163
ESTs, Weakly similar to No definition line found [C.elegans]
1.4e-23:334:70
Hs.159604:AI380827

F-NT2RP2005181

	Ecotropic retroviral receptor 8.3e-45:501:70 Hs.2928:X57303
5	F-NT2RP2005247 Oxysterol binding protein 4.2e-08:356:62 Hs.143065:M86917
10	F-NT2RP2005378 ESTs 1.7e-100:485:97 Hs.151572:AA588083
15	F-NT2RP2005391 EST 1.0:264:62 Hs.148259:AA905706
20	F-NT2RP2005425 Homo sapiens mRNA for KIAA0803 protein, partial cds 3.3e-118:566:97 Hs.58103:AB018346
25	F-NT2RP2005463
	F-NT2RP2005514 ESTs 3.6e-18:193:77
30	Hs.153344:R26293
	F-NT2RP2005535 Homo sapiens DNA-binding protein mRNA, complete cds 7.5e-127:726:90
35	Hs.137582:AF038951
	F-NT2RP2005541 Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID) 1.2e-06:225:64
40	Hs.2703:Z12173
	F-NT2RP2005597
	F-NT2RP2005632 ESTs 5.6e-67:344:96
45	Hs.112011:AA987961
	F-NT2RP2005666 ESTs 5.8e-71:453:87
50	Hs.122698:AI042484
	F-NT2RP2005774 Zinc finger protein 136 (clone pHZ-20) 1.3e-45:451:74
55	Hs.69740:U09367

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F-NT2RP2005878
 ESTs, Highly similar to ESTRADIOL 17 BETA-DEHYDROGENASE 3 [Homo sapiens]
 5.9e-10:67:100
 Hs.104523:AA584520
 5
 F-NT2RP2005883
 F-NT2RP2005887
 10 F-NT2RP2005941
 Human novel homeobox mRNA for a DNA binding protein
 6.2e-11:464:61
 Hs.37035:U07664
 15 F-NT2RP2005994
 F-NT2RP2006004
 Homo sapiens KIAA0405 mRNA, complete cds
 1.2e-13:273:63
 20 Hs.48998:AB007865
 F-NT2RP2006042
 Human mRNA for KIAA0144 gene, complete cds
 5.6e-12:220:69
 25 Hs.8127:D63478
 F-NT2RP2006092
 Human FE65-like protein (hFE65L) mRNA, partial cds
 2.6e-23:353:65
 30 Hs.24957:U62325
 F-NT2RP2006099
 EST
 2.5e-28:180:90
 35 Hs.160878:AI361890
 F-NT2RP2006134
 Neogenin (chicken) homolog 1
 0.035:219:60
 40 Hs.90408:U61262
 F-NT2RP2006269
 Homo sapiens mRNA for matrilin-3
 1.0:147:65
 45 Hs.119534:AJ224741
 F-NT2RP2006512
 ESTs
 1.6e-09:70:95
 50 Hs.118981:AA282396
 F-NT2RP3000011
 F-NT2RP3000022
 55 EST
 0.016:293:60
 Hs.127706:AA961478

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5 F-NT2RP3000059
Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds
0.0041:608:59
Hs.89449:L32976

10 F-NT2RP3000063
Excision repair protein ERCC6
1.0:264:59
Hs.99924:L04791

15 F-NT2RP3000125
Human mRNA for KIAA0314 gene, partial cds
6.9e-08:379:59
Hs.155045:AB002312

20 F-NT2RP3000148
Human Chromosome 16 BAC clone CIT987SK-A-635H12
4.5e-40:349:73
Hs.108604:AC002310

25 F-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds
1.1e-107:501:99
Hs.30985:AF093239

30 F-NT2RP3000171
Homo sapiens methionine synthase reductase (MTRR) mRNA, complete cds
1.0:279:64
Hs.153792:AF025794

35 F-NT2RP3000172
Homo sapiens mRNA for ZIP-kinase, complete cds
7.4e-09:463:59
Hs.25619:AB007144

40 F-NT2RP3000201
Homo sapiens mRNA for KIAA0687 protein, partial cds
3.0e-171:792:98
Hs.3628:AB014587

45 F-NT2RP3000232
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
8.6e-24:304:70
Hs.112094:AA447558

50 F-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
1.1e-172:797:98
Hs.23672:AF074264

55 F-NT2RP3000378
Homo sapiens mRNA for KIAA0700 protein, partial cds
4.3e-45:585:66
Hs.13999:AB014600

F-NT2RP3000427
Protein kinase, cAMP-dependent, catalytic, beta
1.2e-15:97:98

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Hs.87773:M34181

F-NT2RP3000436
Human protein disulfide isomerase-related protein P5 mRNA, partial cds
5 4.1e-06:353:59
Hs.85200:D49489

F-NT2RP3000444
Homo sapiens mRNA for KIAA0445 protein, complete cds
10 1.2e-08:542:60
Hs.154139:AB007914

F-NT2RP3000460
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
15 1.3e-17:181:75
Hs.131840:AI016073

F-NT2RP3000481
Homo sapiens RanBP7/importin 7 mRNA, complete cds
20 5.4e-164:770:98
Hs.5151:AF098799

F-NT2RP3000616
Homo sapiens KIAA0405 mRNA, complete cds
25 1.5e-32:579:62
Hs.48998:AB007865

F-NT2RP3000645
Human KH type splicing regulatory protein KSRP mRNA, complete cds
30 4.6e-06:245:64
Hs.91142:U94832

F-NT2RP3000652
Homo sapiens DNA from chromosome 19, BAC 33152
35 2.6e-135:853:84
Hs.55452:AC003973

F-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
40 8.8e-88:420:98
Hs.158286:AB007915

F-NT2RP3000677
ESTs
45 3.9e-09:67:97
Hs.98819:AA778727

F-NT2RP3000721
ESTs, Weakly similar to No definition line found [C.elegans]
50 1.2e-57:395:86
Hs.159604:AI380827

F-NT2RP3000789
Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds
55 4.8e-75:833:69
Hs.79440:U97188

F-NT2RP3000818

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- Homo sapiens chromosome 19, fosmid 39554
5.9e-08:313:63
Hs.129906:AC004410
- 5 F-NT2RP3000820
ESTs, Moderately similar to WSB-1 [M.musculus]
8.8e-127:613:97
Hs.24630:AI365246
- 10 F-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
8.3e-79:682:79
Hs.77864:AB014538
- 15 F-NT2RP3000871
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds
1.9e-08:350:60
Hs.29287:U72066
- 20 F-NT2RP3000907
Human Ini1 mRNA, complete cds
0.91:345:59
Hs.155626:U04847
- 25 F-NT2RP3000921
Homo sapiens mRNA for KIAA0806 protein, complete cds
2.0e-65:798:68
Hs.24279:AB018349
- 30 F-NT2RP3001012
Homo sapiens mRNA for KIAA0667 protein, partial cds
1.3e-21:383:64
Hs.154740:AB014567
- 35 F-NT2RP3001044

F-NT2RP3001061
KERATIN, TYPE II CYTOSKELETAL 7
3.4e-05:256:62
- 40 Hs.23881:M99063

F-NT2RP3001159
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.8e-81:527:70
- 45 Hs.132874:AC004770

F-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
7.3e-183:859:98
- 50 Hs.3657:AB018327

F-NT2RP3001 195
ESTs
3.5e-08:282:62
- 55 Hs.135168:AI394026

F-NT2RP3001240
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

- 2.8e-64:344:95
Hs.14038:R06800
- 5 F-NT2RP3001271
Centromere protein B (80kD)
7.6e-08:288:64
Hs.85004:X05299
- 10 F-NT2RP3001322
ESTs, Weakly similar to W09D10.2 [C.elegans]
1.2e-86:422:98
Hs.26107:R60661
- 15 F-NT2RP3001388
F-NT2RP3001542
- 20 F-NT2RP3001560
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.016:190:63
Hs.57764:S87759
- 25 F-NT2RP3001592
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 30 F-NT2RP3001650
Homo sapiens KIAA0415 mRNA, complete cds
1.6e-17:394:66
Hs.7289:AB007875
- F-NT2RP3001685
- 35 F-NT2RP3001738
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.9e-54:776:65
Hs.132898:AC004770
- 40 F-NT2RP3001754
Homo sapiens mRNA for B120, complete cds
2.4e-18:106:100
Hs.123090:AB001895
- 45 F-NT2RP3001858
Homo sapiens mRNA for KIAA0584 protein, partial cds
1.9e-40:770:63
Hs.106794:AB011156
- 50 F-NT2RP3001976
Zinc finger protein 140 (clone pHZ-39)
7.3e-33:493:68
Hs.154205:U09368
- 55 F-NT2RP3002015
Homo sapiens OPA-containing protein mRNA, complete cds
0.018:329:62
Hs.85313:AF071309

5 F-NT2RP3002160
Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds
0.53:182:64
Hs.113259:AF023456

10 F-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds
5.2e-151:713:98
Hs.62318:AB018308

15 F-NT2RP3002286
ESTs
0.034:48:95
Hs.124692:AA777421

20 F-NT2RP3002311
Beta-galactosidase (GEB1)
2.3e-28:633:61
Hs.79222:M34423

25 F-NT2RP3002324
ESTs
2.5e-28:296:75
Hs.22822:H06408

30 F-NT2RP3002342
Human transporter protein (g17) mRNA, complete cds
3.2e-37:565:65
Hs.76460:U49082

35 F-NT2RP3002353
Homo sapiens mRNA for KIAA0790 protein, partial cds
0.0055:271:60
Hs.12002:AB018333

40 F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.4e-191:897:98
Hs.21198:AB018262

45 F-NT2RP3002411
Hydroxysteroid (17-beta) dehydrogenase 3
2.9e-28:604:62
Hs.477:U05659

50 F-NT2RP3002448
Human mRNA for KIAA0233 gene, complete cds
1.6e-08:721:57
Hs.79077:D87071

55 F-NT2RP3002571
Homo sapiens mRNA for KIAA0603 protein, complete cds
9.7e-67:707:71
Hs.16909:AB011175

F-NT2RP3002664
Homo sapiens Trio isoform mRNA, complete cds
0.26:160:66

Hs.150625:AF091395

F-NT2RP3002721
Homo sapiens citrate synthase mRNA, complete cds
5 2.4e-180:873:96
Hs.132991:AF047042

F-NT2RP3002737
Homo sapiens mRNA for voltage gated potassium channel
10 7.1e-43:409:75
Hs.4975:Y15065

F-NT2RP3002738
Human BMK1 alpha kinase mRNA, complete cds
15 0.0070:722:57
Hs.3080:U29725

F-NT2RP3002790
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
20 7.2e-17:626:62
Hs.106070:U22398

F-NT2RP3002836
Homo sapiens mRNA for KIAA0463 protein, partial cds
25 2.2e-153:717:99
Hs.77738:AB007932

F-NT2RP3002887
Human plectin (PLEC1) mRNA, complete cds
30 2.5e-06:605:59
Hs.79706:U53204

F-NT2RP3002900
H.sapiens mRNA for transmembrane protein rnp24
35 3.1e-09:346:64
Hs.75914:X92098

F-NT2RP3002958
ESTs
40 8.3e-117:765:86
Hs.107119:AI198794

F-NT2RP3002983
ESTs
45 1.4e-07:270:67
Hs.160271:AI149075

F-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
50 2.5e-89:555:88
Hs.122359:AF051946

F-NT2RP3003076
Homo sapiens mRNA for APC 2 protein, complete cds
55 0.00016:522:60
Hs.20912:AB012162

F-NT2RP3003354

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Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds

4.0e-36:625:64

Hs.10761:AF005038

- 5 F-NT2RP3003448
Arginine vasopressin receptor 1B
0.77:149:69
Hs.1372:L37112
- 10 F-NT2RP3003469
ESTs
1.4e-42:239:93
Hs.12610:W56112
- 15 F-NT2RP3003473
ESTs, Highly similar to transcription factor ARF6 chain B [M.musculus]
8.7e-46:281:89
Hs.136172:W28257
- 20 F-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
4.6e-162:769:98
Hs.130988:Y17999
- 25 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR
1.5e-146:682:98
Hs.79015:M17229
- 30 F-NT2RP3003535
EST
6.7e-10:330:60
Hs.133239:AI052508
- 35 F-NT2RP3003559
Breakpoint cluster region protein BCR
1.0:143:66
Hs.2557:Y00661
- 40 F-NT2RP3003614
ESTs
3.7e-50:327:88
Hs.148873:T33582
- 45 F-NT2RP3003729
ESTs, Weakly similar to unknown [S.cerevisiae]
1.9e-96:449:99
Hs.100843:W28953
- 50 F-NT2RP3003849
ESTs, Weakly similar to raphilin [M.musculus]
1.7e-32:197:92
Hs.118457:AA019161
- 55 F-NT2RP3003874
Homo sapiens incomplete cDNA for a myosin class I, myh-1c
8.5e-84:494:90
Hs.109805:AJ001381

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F-NT2RP3003939
 Peroxisomal biogenesis factor 6
 1.5e-05:236:62
 Hs.30729:D83703
 5 F-NT2RP3003963

 F-NT2RP3004000
 Homo sapiens mRNA for APC 2 protein, complete cds
 10 4.8e-06:669:59
 Hs.20912:AB012162

 F-NT2RP3004025
 ESTs
 15 0.0015:68:86
 Hs.154835:AI289188

 F-NT2RP3004067
 ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cere-
 20 visiae]
 2.1e-76:416:94
 Hs.9252:R53360

 F-NT2RP3004075
 25 ESTs
 1.1e-54:298:94
 Hs.124051:T15786

 F-NT2RP3004083
 30
 F-NT2RP3004090
 Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
 2.4e-06:486:62
 Hs.135639:U77629
 35
 F-NT2RP3004119
 Human mRNA for KIAA0215 gene, complete cds
 4.1e-74:640:75
 Hs.82292:D86969
 40
 F-NT2RP3004130

 F-NT2RP3004133
 ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
 45 4.6e-52:259:98
 Hs.132096:AA314601

 F-NT2RP3004202
 ALPHA-2C-1 ADRENERGIC RECEPTOR
 50 1.0:229:62
 Hs.123022:J03853

 F-NT2RP3004294
 Homo sapiens mRNA for KIAA0741 protein, complete cds
 55 2.4e-05:404:59
 Hs.3615:AB018284

 F-NT2RP3004309

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Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
3.4e-71:756:71
Hs.132874:AC004770

- 5 F-NT2RP3004321
Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, complete polyA site
0.015:263:60
Hs.103944:L13283
- 10 F-NT2RP3004345
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 15 F-NT2RP3004355
EST
0.25:130:59
Hs.149436:AI274484
- 20 F-NT2RP3004374
ESTs
1.4e-95:480:96
Hs.12610:W56112
- 25 F-NT2RP3004406
Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds
3.4e-45:505:70
Hs.79136:U41060
- 30 F-NT2RP3004481
Homo sapiens mRNA for KIAA0476 protein, complete cds
0.00065:594:58
Hs.6684:AB007945
- 35 F-NT2RP3004552
Biglycan
0.92:347:57
Hs.821:J04599
- 40 F-NT2RP3004557
Human Ki nuclear autoantigen mRNA, complete cds
2.6e-121:626:94
Hs.152978:U11292
- 45 F-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
3.1e-152:710:98
Hs.26285:AF082516
- 50 F-NT2RP3004640
ESTs, Moderately similar to unknown [H.sapiens]
0.76:195:64
Hs.6487:T65302
- 55 F-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
6.6e-111:524:98
Hs.158286:AB007915

F-NT2RP4000108
 NEUROFILAMENT TRIPLET L PROTEIN
 5.3e-159:862:93
 Hs.159540:X05608
 5
 F-NT2RP4000634
 Human MEK kinase 3 mRNA, complete cds
 2.3e-54:370:71
 Hs.86201:U78876
 10
 F-NT2RP4000962
 ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
 2.3e-95:479:96
 Hs.4789:AI418298
 15
 F-NT2RP4001001
 EST
 0.98:93:64
 Hs.147598:AI217868
 20
 F-NT2RP4001009
 Homo sapiens mRNA for Hs Ste24p, complete cds
 3.1e-176:828:98
 Hs.25846:AB016068
 25
 F-NT2RP4001467
 5' nucleotidase (CD73)
 1.1e-160:742:98
 Hs.153952:X55740
 30
 F-NT2RP4001877
 ESTs, Weakly similar to siah binding protein 1 [H.sapiens]
 3.3e-103:495:98
 Hs.65648:AA600816
 35
 F-NT2RP4001879
 EST
 0.78:171:61
 Hs.112790:AA609949
 40
 F-NT2RP4002187
 Hydroxysteroid (17-beta) dehydrogenase 3
 9.9e-27:534:63
 Hs.477:U05659
 45
 F-NT2RP4002451
 ESTs
 1.5e-11:106:86
 Hs.163724:AA017689
 50
 F-NT2RP4002715
 EST
 4.2e-07:64:93
 Hs.160901:AI366910
 55
 F-NT2RP4002750
 Ecotropic retroviral receptor
 6.6e-51:581:68

Hs.2928:X57303

F-OVARC1000003

Solute carrier family 17 (sodium phosphate), member 2

5 6.9e-65:587:73

Hs.936:L13258

F-OVARC1000090

ESTs

10 4.8e-07:214:65

Hs.87456:AA434484

F-OVARC1000105

Human novel homeobox mRNA for a DNA binding protein

15 0.00095:204:64

Hs.37035:U07664

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds

20 4.0e-35:184:98

Hs.31531:U95735

F-OVARC1000208

Human calcium-dependent group X phospholipase A2 mRNA, complete cds

25 1.5e-61:365:90

Hs.136004:U95301

F-OVARC1000255

Spleen tyrosine kinase

30 2.2e-88:615:84

Hs.74101:L28824

F-OVARC1000275

ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]

35 4.7e-85:424:97

Hs.55165:AA573499

F-OVARC1000298

Homo sapiens GABA-B receptor mRNA, complete cds

40 0.00021:285:61

Hs.12307:AF056085

F-OVARC1000307

ESTs

45 0.00016:226:63

Hs.162935:AI393970

F-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds

50 5.5e-121:585:97

Hs.154023:AB011145

F-OVARC1000331

Glucose-6-phosphate dehydrogenase

55 5.3e-18:213:71

Hs.1435:M24470

F-OVARC1000410

Homo sapiens mRNA for angiopoietin-like factor
1.5e-27:538:62
Hs.146559:Y16132

5 F-OVARC1000439

F-OVARC1000467
ESTs
2.5e-26:173:90
10 Hs.105040:AA292817

F-OVARC1000529
Homo sapiens mRNA for C8FW phosphoprotein
1.1e-12:391:59
15 Hs.143513:AJ000480

F-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894
9.0e-111:425:99
20 Hs.157732:AC005594

F-OVARC1000775
Human chromosome 3p21.1 gene sequence
2.2e-70:380:95
25 Hs.82837:L13435

F-OVARC1000811
HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR
1.2e-06:446:61
30 Hs.104:D14012

F-OVARC1000853
ESTs
7.9e-09:268:63
35 Hs.92700:W37903

F-OVARC1000873
Homo sapiens mRNA for MIFR-1, complete cds
0.038:343:60
40 Hs.58269:AB010962

F-OVARC1000916
H.sapiens PISSLRE mRNA
1.3e-56:435:82
45 Hs.77313:X78342

F-OVARC1000956
Human TBP-associated factor (hTAFII130) mRNA, partial cds
7.7e-05:511:59
50 Hs.24644:U75308

F-OVARC1000995
ESTs
2.4e-39:205:98
55 Hs.163662:AA514348

F-OVARC1001030
EST

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- 1:1e-44:232:96
Hs.135504:AI091717
- 5 F-OVARC1001049
ESTs
6.1e-78:373:98
Hs.135022:AI417283
- 10 F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
6.0e-166:761:99
Hs.155478:AF048731
- 15 F-OVARC1001132
ESTs, Weakly similar to GC-RICH SEQUENCE DNA-BINDING FACTOR [Homo sapiens]
7.9e-121:610:96
Hs.26461:AI341685
- 20 F-OVARC1001163
ESTs
5.9e-39:215:94
Hs.126067:AI344351
- 25 F-OVARC1001222
ESTs
2.7e-93:467:95
Hs.10267:W27845
- 30 F-OVARC1001260
Pregnancy-zone protein
1.0:251:58
Hs.74094:X54380
- 35 F-OVARC1001336
Solute carrier family 17 (sodium phosphate), member 2
1.2e-31:304:74
Hs.936:L13258
- 40 F-OVARC1001338
Homo sapiens cam kinase I mRNA, complete cds
3.7e-17:570:60
Hs.118414:L41816
- 45 F-OVARC1001569
Human novel homeobox mRNA for a DNA binding protein
0.038:178:63
Hs.37035:U07664
- 50 F-OVARC1001570
ESTs
4.5e-10:75:93
Hs.120928:AA703165
- 55 F-OVARC1001596
Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)
0.0092:287:63
Hs.111301:M55593

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F-OVARC1001607
 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
 5.5e-41:323:80
 Hs.154844:U15128
 5 F-OVARC 1001725

 F-OVARC1001727
 EST
 10 3.2e-05:237:61
 Hs.119508:AA485732

 F-OVARC1001807
 Hormone receptor (growth factor-inducible nuclear protein N10)
 15 3.4e-91:564:88
 Hs.1119:D49728

 F-OVARC1001833
 ESTs
 20 1.2e-94:444:97
 Hs.155256:AA707750

 F-OVARC1001952
 Myristoylated alanine-rich C-kinase substrate
 25 2.9e-10:364:64
 Hs.75607:D10522

 F-OVARC1001991
 Human mRNA for KIAA0176 gene, partial cds
 30 0.0019:224:62
 Hs.4935:D79998

 F-OVARC1002058
 Human mRNA for KIAA0149 gene, complete cds
 35 5.0e-48:674:67
 Hs.57735:D86864

 F-OVARC1002178
 Homo sapiens zinc-finger protein of the cerebellum 3 (ZIC3) mRNA, complete cds
 40 0.010:310:61
 Hs.111227:AF028706

 F-PLACE1000033

 45 F-PLACE1000231
 Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
 0.00021:235:63
 Hs.1686:M69013

 50 F-PLACE1000258
 KRAB zinc finger protein {alternative products}
 1.2e-14:241:70
 Hs.22556:U37251

 55 F-PLACE1000442
 Zinc finger protein 136 (clone pHZ-20)
 7.3e-89:774:76
 Hs.69740:U09367

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5 F-PLACE1000560
ESTs
1.5e-36:200:96
Hs.86541:AA214554

10 F-PLACE1000740
Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA, complete cds
6.5e-05:283:62
Hs.113285:AF017988

15 F-PLACE1000907
ESTs, Moderately similar to zinc finger protein [H.sapiens]
8.1e-38:237:89
Hs.139115:AA325104

20 F-PLACE1000912
ESTs
4.6e-61:331:95
Hs.17558:AA155762

25 F-PLACE1000914
Homo sapiens PB39 mRNA, complete cds
3.1e-45:500:69
Hs.18910:AF045584

30 F-PLACE1000927
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
1.4e-123:655:94
Hs.8661:AI189791

35 F-PLACE1000986
ESTs
1.2e-105:494:99
Hs.19207:AA039595

40 F-PLACE1001016
Calcium channel, voltage-dependent, L type, alpha 1S subunit
0.011:432:59
Hs.1294:L33798

45 F-PLACE1001100
Human clone 23839 mRNA sequence
0.38:342:60
Hs.78362:U79249

50 F-PLACE1001114
Human mRNA for KIAA0303 gene, partial cds
0.085:339:59
Hs.54985:AB002301

55 F-PLACE1041123
ESTs
5.0e-14:505:61
Hs.99272:AI147740

F-PLACE1001183
ESTs, Weakly similar to gene pp21 protein [H.sapiens]
0.66:361:58

Hs.15984:A,1085974

F-PLACE1001229
ESTs, Weakly similar to D9481.15 gene product [S.cerevisiae]
5 9.3e-110:561:96
Hs.125155:W52093

F-PLACE1001231
ESTs, Weakly similar to sodium iodide symporter [H.sapiens]
10 1.0e-17:120:91
Hs.5167:AA053914

F-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds
15 4.1e-132:636:97
Hs.21198:AB018262

F-PLACE1001401
ESTs, Weakly similar to IgE receptor beta subunit [H.sapiens]
20 3.1e-100:516:95
Hs.43900:AA418443

F-PLACE 1001407
H.sapiens mRNA for B-HLH DNA binding protein
25 0.00015:244:66
Hs.66744:X99268

F-PLACE1001464
5' nucleotidase (CD73)
30 1.6e-152:742:96
Hs.153952:X55740

F-PLACE1001500
Bloom syndrome
35 5.7e-05:450:58
Hs.36820:U39817

F-PLACE1001516
Homo sapiens Rigui (RIGUI) mRNA, complete cds
40 2.3e-07:663:58
Hs.8114:AF022991

F-PLACE1001536
ESTs
45 4.6e-60:318:97
Hs.13026:H04491

F-PLACE1001564
H.sapiens mRNA for HE6 Tm7 receptor
50 8.8e-41:499:70
Hs.155681:X81892

F-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds
55 4.3e-125:585:98
Hs.47584:AF043472

F-PLACE1001788

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Homo sapiens mRNA for HYA22, complete cds
3.2e-22:234:75
Hs.147189:D88153

5 F-PLACE1001795

F-PLACE1001836
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1.1e-18:162:80

10 Hs.157223:AA309318

F-PLACE1001918
Human p76 mRNA, complete cds
1.3e-22:693:60

15 Hs.28757:U81006

F-PLACE1001949
ESTs
0.97:243:63

20 Hs.151143:AA576926

F-PLACE1002080
Homo sapiens mRNA for KIAA0600 protein, partial cds
2.4e-130:622:98

25 Hs.9028:AF039691

F-PLACE1002095

F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds
2.7e-162:764:98

30 Hs.90415:AF095791

F-PLACE1002329
ESTs
1.5e-107:556:95

35 Hs.28907:AI343292

F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds
9.0e-19:190:77

40 Hs.137574:AF055917

F-PLACE1002374
Cathepsin L
2.0e-163:716:94

45 Hs.78056:X12451

F-PLACE1002518
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds
7.0e-19:396:64

50 Hs.28285:AF064801

F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds
8.3e-173:819:98

55 Hs.21198:AB018262

5 F-PLACE1002726
Human mRNA for KIAA0362 gene, partial cds
1.0:310:59
Hs.25515:AB002360

10 F-PLACE1002905
ESTs
2.4e-74:415:92
Hs.110298:AA621807

15 F-PLACE1002911
ESTs, Weakly similar to Y53C12A.3 [C.elegans]
0.030:279:58
Hs.107747:AI357868

20 F-PLACE1002967
ESTs
3.3e-120:574:98
Hs.11090:W37646

25 F-PLACE1003135
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
1.5e-50:450:75
Hs.72292:AF024636

30 F-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds
1.5e-153:722:98
Hs.15250:AF069301

35 F-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds
2.0e-142:682:97
Hs.30213:AF068227

40 F-PLACE1003428
Biotinidase
8.2e-06:265:62
Hs.78885:AF018631

45 F-PLACE1003438
ESTs
0.018:470:60
Hs.119482:AI361002

50 F-PLACE1003460
ESTs
0.019:211:60
Hs.92700:W37903

55 F-PLACE1003529
130 KD LEUCINE-RICH PROTEIN
0.53:208:63
Hs.87157:M92439

F-PLACE1003573
F-PLACE1003598

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Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
0.00064:302:64
Hs.96253:U79666

5 F-PLACE1003644
ESTs
1.3e-06:265:63
Hs.163564:R43678

10 F-PLACE1003737

F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds
7.0e-09:448:61
15 Hs.155302:U57317

F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
7.7e-109:521:97
20 Hs.154050:AC004131

F-PLACE1003845
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.2e-92:432:100
25 Hs.153778:AI246000

F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.4e-172:814:98
30 Hs.22039:AB018301

F-PLACE1004028

F-PLACE1004078
35 GELSOLIN PRECURSOR, PLASMA
3.1e-49:616:67
Hs.80562:X04412

F-PLACE1004166
40 ESTs
7.6e-79:415:94
Hs.163741:AA551077

F-PLACE1004168

45 F-PLACE1004199
EST
6.8e-15:147:80
Hs.128205:AA972308

50 F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
3.9e-20:456:62
Hs.23965:AF057039

55 F-PLACE1004282

F-PLACE1004305

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- Homo sapiens mRNA for KIAA0740 protein, complete cds
8.7e-123:612:96
Hs.15099:AB018283
- 5 F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds
8.6e-99:501:96
Hs.159248:U13666
- 10 F-PLACE1004450
AMINOPEPTIDASE N
1.1e-09:587:57
Hs.1239:M22324
- 15 F-PLACE1004482
- F-PLACE1004492
ESTs
2.1e-25:134:100
- 20 Hs.154475:AI199037
- F-PLACE1004519
ESTs
1.0e-110:518:99
- 25 Hs.128505:AA306435
- F-PLACE1004520
Pregnancy-specific beta 1-glycoprotein 7
1.3e-110:606:92
- 30 Hs.119662:M34715
- F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds
2.0e-139:749:92
- 35 Hs.82582:AB008375
- F-PLACE1004637
- F-PLACE1004648
- 40 F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds
1.2e-99:590:90
Hs.9225:D88587
- 45 F-PLACE1004887
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
5.1e-06:486:62
Hs.135639:U77629
- 50 F-PLACE1005003
Human SNC19 mRNA sequence
1.5e-21:472:63
Hs.56937:U20428
- 55 F-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
4.7e-42:245:93

- Hs.151614:AF032456
- F-PLACE1005031
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]
5 2.9e-43:538:70
Hs.118991:AA675919
- F-PLACE1005239
ESTs
10 2.4e-42:209:100
Hs.154475:AI199037
- F-PLACE1005250
- F-PLACE1005383
15 Homo sapiens UP50 mRNA, complete cds
8.5e-128:633:96
Hs.11494:AF093118
- F-PLACE1005410
20 ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
1.3e-17:181:75
Hs.131840:AI016073
- F-PLACE1005426
25 Pregnancy-specific beta-1 glycoprotein 4
2.3e-109:596:93
Hs.108936:X17097
- F-PLACE1005519
30 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
3.3e-55:521:74
Hs.72292:AF024636
- F-PLACE1005539
35 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U
5.8e-05:277:63
Hs.103804:AF068846
- F-PLACE1005544
40
- F-PLACE1005569
EST
0.38:60:75
45 Hs.137086:AA912486
- F-PLACE1005601
Homo Sapiens angiotensin II receptor gene, complete cds
0.016:72:84
50 Hs.20954:AI054441
- F-PLACE1005660
- F-PLACE1005669
55 Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
3.5e-08:461:60
Hs.113286:U77783

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F-PLACE1005682

F-PLACE1005725
Huntingtin (Huntington disease)
5 1.1e-06:401:61
Hs.79391:L12392

F-PLACE1005736
ESTs
10 3.6e-63:343:94
Hs.17757:AA875839

F-PLACE1005745
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
15 6.9e-66:351:94
Hs.7870:AI078137

F-PLACE1005768
ESTs
20 7.9e-60:318:95
Hs.143856:AI186351

F-PLACE1005815
Mutated in colorectal cancers
25 0.0029:199:62
Hs.1345:M62397

F-PLACE1005878
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]
30 5.0e-38:464:70
Hs.118991:AA675919

F-PLACE1005927
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR
35 0.010:511:59
Hs.839:M86826

F-PLACE1006071
EST
40 0.68:224:59
Hs.161788:AA371859

F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
45 5.5e-96:464:98
Hs.26492:AB009598

F-PLACE1006079
Homo sapiens BAC clone RG300E22 from 7q21-q31.1
50 1.5e-18:402:65
Hs.99348:AC004774

F-PLACE1006093
Homo sapiens mRNA for protein phosphatase 1 (PPP1R6)
55 0.0022:306:59
Hs.106471:Y18206

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5 F-PLACE1006208
HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1
0.022:425:57
Hs.74095:L20433

10 F-PLACE1006219
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.7e-61:294:100
Hs.153778:AI246000

15 F-PLACE1006277
EST
0.42:60:75
Hs.137086:AA912486

20 F-PLACE1006290
ESTs, Weakly similar to similar to M. musculus MERS and other AHPC/TSA proteins [C.elegans]
1.3e-51:260:98
Hs.132096:AA314601

25 F-PLACE1006443
Homo sapiens PB39 mRNA, complete cds
1.2e-53:553:70
Hs.18910:AF045584

30 F-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
1.3e-141:655:99
Hs.14687:AB011148

35 F-PLACE1006716
EST
7.2e-12:148:75
Hs.162969:AA677315

40 F-PLACE1006786
ESTs
0.0050:125:72
Hs.109156:AA193501

45 F-PLACE1006809
ESTs
4.5e-99:477:98
Hs.135208:AI093908

50 F-PLACE1006959
ESTs
7.4e-72:381:93
Hs.4963:W29030

55 F-PLACE1007028
Homo sapiens p17-Beckwith-Wiedemann region 1 C (BWR1C) mRNA, complete cds
1.8e-18:364:65
Hs.154036:AF035444

F-PLACE1007040
H.sapiens NF-H gene, exon 1 (and joined CDS)
1.4e-09:501:61

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Hs.75735:X15306

F-PLACE1007077
ESTs, Moderately similar to testis-specific TCP20 [H.sapiens]
5 0.88:192:62
Hs.85818:AI216525

F-PLACE1007081
Human plectin (PLEC1) mRNA, complete cds
10 0.079:403:60
Hs.79706:U53204

F-PLACE1007096
YY1 transcription factor
15 0.64:173:64
Hs.97496:M77698

F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1
20 4.2e-73:542:83
Hs.78040:X55885

F-PLACE1007591
EST
25 0.026:136:64
Hs.130897:AI014389

F-PLACE1007626
Homo sapiens unknown mRNA, complete cds
30 2.6e-105:516:97
Hs.11441:AF047439

F-PLACE1007702
Homo sapiens mRNA for UTF1, complete cds
35 0.033:297:62
Hs.158307:AB011076

F-PLACE1007845
ESTs
40 4.8e-22:158:89
Hs.23445:AA489015

F-PLACE1007881

F-PLACE1007971
ESTs, Weakly similar to K07F5.14 [C.elegans]
45 1.1e-128:599:99
Hs.157918:AA313781

F-PLACE1008282
ESTs, Highly similar to HEME-EGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctola-
gus cuniculus]
50 2.4e-65:353:94
Hs.130830:W27380

F-PLACE1008297

F-PLACE1008359

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- Human arginine-rich protein (ARP) gene, complete cds
0.020:197:64
Hs.75412:M83751
- 5 F-PLACE1008469
Homo sapiens PB39 mRNA, complete: cds
5.3e-20:620:60
Hs.18910:AF045584
- 10 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
1.8e-145:693:98
Hs.159267:AF049703
- 15 F-PLACE1008657
VILLIN
2.3e-10:356:61
Hs.3046:X12901
- 20 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
1.5e-31:191:92
Hs.154844:U15128
- 25 F-PLACE1008744

F-PLACE1008984
Pregnancy-associated plasma protein A
0.0085:268:60
30 Hs.158229:U28727

F-PLACE1008985
Signal transducer and activator of transcription 5A
0.0047:249:64
35 Hs.14203:U43185

F-PLACE1009067
Human density enhanced phosphatase-1 mRNA, complete cds
2.0e-06:453:60
40 Hs.1177:U10886

F-PLACE1009196

F-PLACE1009279
45 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
1.9e-11:327:64
Hs.75111:D87258

F-PLACE1009527
50 Human DNA-binding protein ABP/ZF mRNA, complete cds
6.8e-21:125:96
Hs.86185:U82613

F-PLACE1009546
55 TRANSCRIPTION FACTOR RELB
0.051:248:61
Hs.858:M83221

5 F-PLACE1009600
ESTs
1.0:124:64
Hs.52794:W51887

10 F-PLACE1009735
ESTs
0.022:387:61
Hs.132253:AI027207

15 F-PLACE1009982
F-PLACE1010011
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-09:330:66
Hs.143551:AF048693

20 F-PLACE1010078
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
8.3e-47:474:72
Hs.13144:T67556

25 F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
2.2e-151:733:97
Hs.103755:AF027706

30 F-PLACE1010251
Homo sapiens Na⁺/H⁺ exchanger regulatory factor 2 (NHERF-2) mRNA, complete cds
0.0037:405:60
Hs.101813:AB016243

35 F-PLACE1010445
ESTs
1.7e-45:235:97
Hs.144501:N39767

40 F-PLACE1010713
Hydroxysteroid (17-beta) dehydrogenase 3
2.8e-20:447:62
Hs.477:U05659

45 F-PLACE1010784
Human protease-activated receptor 3 (PAR3) mRNA, complete cds
0.56:199:59
Hs.159196:U92971

50 F-PLACE 1010827
H.sapiens mRNA for transmembrane protein rnp24
2.9e-09:346:64
Hs.75914:X92098

55 F-PLACE1010968
ESTs
0.00062:52:98
Hs.119408:T87544

- 5 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
6.0e-129:595:99
Hs.28190:AF094516
- F-PLACE1011116
- 10 F-PLACE1011181
ESTs
1.0:301:58
Hs.80285:AI092519
- 15 F-PLACE1011236
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
1.1e-41:776:62
Hs.23965:AF057039
- 20 F-PLACE1011364
ESTs, Weakly similar to HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II [C.elegans]
3.7e-53:276:96
Hs.106499:W28299
- 25 F-PLACE1011407
ESTs, Moderately similar to ZINC FINGER PROTEIN 140 [H.sapiens]
3.2e-15:228:70
Hs.152174:AI199619
- 30 F-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
1.7e-85:444:95
Hs.110978:AA843431
- 35 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
5.9e-145:722:96
Hs.148318:AF034611
- 40 F-PLACE1011824
Human Ste20-like kinase (MST2) mRNA, complete cds
1.6e-101:561:92
Hs.92317:U26424
- 45 F-PLACE1011978
Homo sapiens DNA from chromosome 19, BAC 33152
3.8e-67:733:72
Hs.55452:AC003973
- 50 F-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence)
7.8e-115:568:95
55 Hs.120856:AL022578
- F-PLACE2000219
EST

8.7e-11:137:75
Hs.98191:AA417044

5 F-PLACE3000181
Human protocadherin 42 mRNA, complete cds for abbreviated PC42
1.5e-128:745:90
Hs.79769:L11370

10 F-PLACE3000213
EST
1.0:219:63
Hs.98452:AA426058

15 F-PLACE4000354
ESTs
1.4e-13:190:71
Hs.138841:R94879

20 F-PLACE4000455
F-SKNMC1000004
Homo sapiens GABA-B receptor mRNA, complete cds
0.00039:275:62
Hs.12307:AF056085

25 F-SKNMC1000014
ESTs
3.3e-38:196:98
Hs.113307:H16716

30 F-SKNMC1000082
Complement component 4A
0.98:324:63
Hs.76682:K02403

35 F-THYRO1000036
Homo sapiens mRNA for putative ATPase, partial
0.98:199:60
Hs.91471:AJ006268

40 F-THYRO1000061
Human kinase Myt1 (Myt1) mRNA, complete cds
1.0:210:62
Hs.77783:AF014118

45 F-THYRO1000099
ESTs
2.5e-119:605:96
Hs.11782:W07369

50 F-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
1.6e-126:475:98
Hs.115418:AF016272

55 F-THYRO1000400
Human R kappa B mRNA, complete cds
0.64:223:63

Hs.95262:U08191

F-THYRO1000580
ESTs, Weakly similar to ZINC FINGER PROTEIN 7 [H.sapiens]
5 5.4e-27:248:76
Hs.25465:AA528105

F-THYRO1000584
Alpha mannosidase II isozyme
10 2.2e-06:528:60
Hs.155961:L28821

F-THYRO1000678
Gap junction protein, beta 2, 26kD (connexin 26)
15 1.3e-33:266:80
Hs.81795:M86849

F-THYRO1000776
Human involucrin mRNA
20 0.0025:497:59
Hs.157091:M13903

F-THYRO1000795
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN
25 4.1e-19:532:62
Hs.3816:AF070548

F-THYRO1000846
Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds
30 0.029:387:60
Hs.27910:AF049105

F-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds
35 1.1e-92:529:89
Hs.12912:AF015913

F-THYRO1000956
Homo sapiens mRNA for G-protein coupled receptor
40 1.8e-15:474:64
Hs.155235:Y13583

F-THYRO1000964
Human OB binding protein-2 (OB-BP2) mRNA, complete cds
45 0.22:303:61
Hs.117005:U71383

F-THYRO1000999
EST
50 2.0e-05:198:63
Hs.146520:AI130948

F-THYRO1001063
Human mRNA for cerebroside sulfotransferase, complete cds
55 0.51:448:60
Hs.17958:D88667

F-THYRO1001071

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- ESTs
2.1e-29:237:83
Hs.155582:AI125241
- 5 F-THYRO1001102
ESTs, Weakly similar to growth arrest inducible gene product [H.sapiens]
4.7e-32:208:88
Hs.7854:W21970
- 10 F-THYRO1001113
Homo sapiens dysferlin mRNA, complete cds
3.2e-53:684:68
Hs.143897:AF075575
- 15 F-THYRO1001128
ESTs
2.1e-120:589:97
Hs.62595:AA306052
- 20 F-THYRO1001205

F-THYRO1001237
ESTs
0.66:326:60
- 25 Hs.148352:U80757

F-THYRO1001242
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.017:188:63
- 30 Hs.57764:S87759

F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds
8.6e-43:806:62
- 35 Hs.103983:U66088

F-THYRO1001327
ESTs
2.8e-50:264:96
- 40 Hs.154667:AI343524

F-THYRO1001456
EST
0.90:84:72
- 45 Hs.130049:AA902650

F-THYRO1001457
Protein kinase C, mu
6.0e-53:705:67
- 50 Hs.2891:X75756

F-THYRO1001471
ESTs
8.0e-52:278:94
- 55 Hs.7604:W31115

F-THYRO1001478
Human mRNA for KIAA0150 gene, partial cds

0.79:150:66
Hs.98508:D63484

5 F-THYRO1001495
Homo sapiens KIAA0415 mRNA, complete cds
9.5e-75:550:82
Hs.7289:AB007875

10 F-THYRO1001523
ESTs
7.2e-19:142:86
Hs.140588:H60533

15 F-THYRO1001529
ESTs
5.7e-24:141:95
Hs.114172:AA703201

20 F-THYRO1001593
H.sapiens mRNA for serine/threonine protein kinase EMK
1.4e-70:643:74
Hs.157199:X97630

25 F-THYRO1001608
Human mRNA for KIAA0227 gene, partial cds
2.6e-07:533:59
Hs.79170:D86980

30 F-THYRO1001641
ESTs
0.87:269:59
Hs.14599:AA522511

35 F-THYRO1001700
Homo sapiens c-Jun N-terminal kinase kinase 2 (JNKK2) mRNA, complete cds
3.3e-05:441:59
Hs.110299:AF013589

40 F-THYRO1001702
Human plectin (PLEC1) mRNA, complete cds
0.00017:346:62
Hs.79706:U53204

45 F-THYRO1001725
Homo sapiens mRNA for procollagen I-N proteinase
1.3e-06:275:64
Hs.120330:AJ003125

50 F-THYRO1001770
Homo sapiens mRNA for HsGAK, complete cds
0.046:265:58
Hs.153227:D88435

55 F-THYRO1001803
EST
0.0085:201:63
Hs.158782:AI376601

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F-Y79AA1000030
 ESTs
 0.00051:276:60
 Hs.111999:AA465020
 5

F-Y79AA1000127
 ESTs
 1.3e-85:430:96
 Hs.49932:W58552
 10

F-Y79AA1000207
 ESTs
 4.5e-81:407:96
 Hs.125308:AI376737
 15

F-Y79AA1000226
 ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis elegans]
 0.00081:76:84
 Hs.11221:AI192291
 20

F-Y79AA1000270
 Human mRNA for ORF, Xq terminal portion
 9.9e-97:590:88
 Hs.6551:D16469
 25

F-Y79AA1000426
 CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
 0.045:507:59
 Hs.82914:X68264
 30

F-Y79AA1000521
 Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
 0.0029:489:58
 Hs.159543:AJ000479
 35

F-Y79AA1000750
 ESTs
 9.9e-12:252:65
 Hs.52885:H29851
 40

F-Y79AA1000776
 ESTs
 1.4e-50:340:87
 Hs.144198:AI017555
 45

F-Y79AA1000777
 Homo sapiens mRNA for putative transcription factor, partial
 3.9e-10:501:61
 Hs.26782:AJ009770
 50

F-Y79AA1000876
 Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds
 1.3e-11:323:66
 Hs.30250:AF055376
 55

F-Y79AA1000888
 Homo sapiens mRNA for KIAA0469 protein, complete cds

- 1.5e-05:641:58
Hs.7764:AB007938
- 5 F-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
5.3e-54:277:96
Hs.53066:AF093420
- 10 F-Y79AA1000967
Human mRNA for KIAA0369 gene, complete cds
8.1e-10:517:61
Hs.21355:AB002367
- 15 F-Y79AA1001013
ESTs
2.4e-44:259:93
Hs.109468:W52074
- 20 F-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
4.7e-07:90:87
Hs.36794:AI038407
- 25 F-Y79AA1001062
ESTs, Weakly similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]
1.6e-60:320:96
Hs.13982:W27344
- 30 F-Y79AA1001090
H.sapiens DAP-kinase mRNA
2.3e-06:465:59
Hs.153924:X76104
- 35 F-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.5e-163:763:98
Hs.6710:AF038961
- 40 F-Y79AA1001264
Homo sapiens mRNA for MSJ-1, complete cds
5.3e-15:367:64
Hs.3845:AB014888
- 45 F-Y79AA1001272
Human plectin (PLEC1) mRNA, complete cds
6.3e-05:325:63
Hs.79706:U53204
- 50 F-Y79AA1001328
Homo sapiens Delta mRNA, complete cds
1.8e-07:271:61
Hs.144631:AF003522
- 55 F-Y79AA1001426
Aldehyde dehydrogenase 7
0.94:485:56
Hs.83155:U10868

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F-Y79AA1001427
 NADH-CYTOCHROME B5 REDUCTASE
 1.7e-56:649:69
 Hs.75666:M28713
 5

F-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds
 2.8e-124:577:99
 Hs.7764:AB007938
 10

F-Y79AA1001523
 Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds
 1.1e-92:496:93
 Hs.128763:AF009353
 15

F-Y79AA1001530
 Human beta-tubulin gene (5-beta) with ten Alu family members
 1.0e-131:669:95
 Hs.108014:X00734
 20

F-Y79AA1001592
 ESTs
 1.2e-88:212:97
 Hs.131180:AA594251
 25

F-Y79AA1001727
 F-Y79AA1001787
 Human mRNA for KIAA0315 gene, partial cds
 0.48:248:63
 Hs.3989:AB002313
 30

F-Y79AA1001793
 ESTs
 1.4e-67:192:98
 Hs.118559:AA887084
 35

F-Y79AA1001795
 Homo sapiens mRNA for GalT4 protein
 5.3e-89:431:98
 Hs.21495:AL031228
 40

F-Y79AA1001799
 NUCLEAR FACTOR RIP140
 0.54:182:62
 Hs.155017:X84373
 45

F-Y79AA1001803
 ESTs, Highly similar to MELANOMA-ASSOCIATED ANTIGEN XP [Homo sapiens]
 0.72:169:63
 Hs.94011:AA627644
 50

F-Y79AA1001863
 EST
 1.0:114:63
 Hs.152260:AA489703
 55

F-Y79AA1002022

B94 PROTEIN
5.7e-13:469:65
Hs.75522:M92357

- 5 F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence
1.7e-154:740:98
Hs.21970:AF052149
- 10 F-Y79AA1002121
EST
0.14:104:66
Hs.100070:M91493
- 15 F-Y79AA1002129
ESTs
5.1e-90:431:98
Hs.40719:AI183452
- 20 F-Y79AA1002213

F-Y79AA1002334
ESTs
5.0e-20:187:80
25 Hs.111900:AA397579
- F-Y79AA1002373
ESTs
4.5e-37:192:98
30 Hs.118559:AA887084
- F-Y79AA1002376
Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
1.2e-36:657:64
35 Hs.65248:AF063228
- F-Y79AA1002378
Homo sapiens KIAA0426 mRNA, complete cds
4.9e-38:424:72
40 Hs.97476:AB007886
- F-Y79AA1002381
CELL DIVISION PROTEIN KINASE 3
8.4e-17:580:61
45 Hs.100009:X66357

Homology search result 9

50 **[0302]** The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 3'-ends.

Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
55 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0303] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0304] Data were not shown for the clones in which the P-value was higher than 1.

5 R-HEMBA1000006
ESTs
1.0:85:71
Hs.130699:AA621478

10 R-HEMBA1000121
ESTs
1.3e-111:545:97
Hs.153432:AA098922

15 R-HEMBA1000128
ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae]
3.0e-98:532:93
Hs.7745:H92988

20 R-HEMBA1000275
ESTs
6.5e-11:81:81
Hs.163492:AI334460

25 R-HEMBA1000300
Homo sapiens mRNA for putative lipoic acid synthetase, partial
1.2e-39:309:81
Hs.53531:AJ224162

30 R-aaaaaaaaaaaa
ESTs
4.9e-95:455:98
Hs.154009:AI284184

35 R-HEMBA1000462
Homo sapiens clone 243 unknown mRNA, complete sequence
3.6e-91:313:94
Hs.20423:AF091094

40 R-HEMBA1000477
ESTs
4.7e-111:541:97
Hs.84526:AI341541

45 R-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial
2.6e-102:547:93
Hs.129361:AJ007581

50 R-HEMBA1000634
ESTs
0.85:189:62
Hs.131268:AA909162

55 R-HEMBA1000671
ESTs
6.5e-84:432:96
Hs.31991:T78668

R-HEMBA1000713
 Homo sapiens 10kD protein (BC10) mRNA, complete cds
 4.0e-119:575:97
 Hs.5300:AF053470
 5

R-HEMBA1000732
 EST
 3.9e-81:435:92
 Hs.146718:AI146722
 10

R-nnnnnnnnnnnnn
 R-HEMBA1000875
 EST
 0.023:207:62
 Hs.148275:AA907849
 15

R-HEMBA1000940
 Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
 7.4e-31:211:81
 Hs.97203:U83171
 20

R-HEMBA1000962
 ESTs
 1.1e-104:515:97
 Hs.8978:W63573
 25

R-HEMBA1001 184
 EST
 7.1e-07:382:62
 Hs.124559:AA847550
 30

R-HEMBA1001221
 ESTs, Weakly similar to transmembrane protein [H.sapiens]
 1.2e-95:487:95
 Hs.22791:AI056665
 35

R-HEMBA1001228
 Human germline oligomeric matrix protein (COMP) mRNA, complete cds
 4.0e-42:170:92
 Hs.1584:AC003107
 40

R-HEMBA1001272
 ESTs
 5.7e-71:514:84
 Hs.26966:N74056
 45

R-HEMBA1001296
 EST
 1.7e-93:494:95
 Hs.102465:N27272
 50

R-HEMBA1001297
 Homo sapiens putative transcription factor CA150 mRNA, complete cds
 1.5e-93:466:96
 Hs.13063:AF017789
 55

R-HEMBA1001390

- ESTs
1.6e-42:181:89
Hs.139190:N55515
- 5 R-HEMBA1001563
Homo sapiens DEC-205 mRNA, complete cds
8.4e-42:311:83
Hs.153563:AF011333
- 10 R-HEMBA1001621
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
4.2e-56:386:86
Hs.9305:W84893
- 15 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
1.1e-80:433:93
Hs.10290:AF090988
- 20 R-HEMBA1001886
Zinc finger protein 141 (clone pHZ-44)
5.9e-61:530:80
Hs.159596:L15309
- 25 R-HEMBA1002048
ESTs
0.95:127:63
Hs.98690:AA431162
- 30 R-HEMBA1002131

R-HEMBA1002163
ESTs, Weakly similar to K09E9.2 [C.elegans]
5.9e-36:225:90
Hs.26813:AI339473
- 35 R-HEMBA1002167
ESTs
1.5e-35:325:80
Hs.124171:N98933
- 40 R-HEMBA1002178
MICROSOMAL DIPEPTIDASE PRECURSOR
0.99:243:61
Hs.109:J05257
- 45 R-HEMBA1002195
Deoxyhypusine synthase
1.9e-19:109:100
Hs.79064:U79262
- 50 R-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
2.0e-116:567:97
Hs.75607:D10522
- 55 R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein

- 8.2e-20:160:85
Hs.101033:Y14391
- 5 R-HEMBA1002420
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.7e-78:402:97
Hs.108354:W19984
- 10 R-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1.9e-91:443:97
Hs.1501:J04621
- 15 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
1.0e-111:551:96
Hs.41548:U63336
- 20 R-HEMBA1002551
ESTs
3.4e-107:553:96
Hs.92071:W80592
- 25 R-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
5.5e-108:568:95
Hs.19154:AF038660
- 30 R-HEMBA1002985
ESTs
4.4e-39:211:96
Hs.126894:AA932538
- 35 R-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.6e-115:571:96
Hs.148318:AF034611
- 40 R-HEMBA1003072
EST
0.044:220:61
Hs.136349:AA490873
- 45 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.2e-117:575:97
Hs.26350:AF049891
- 50 R-HEMBA1003120
Zinc finger protein 10 (KOX 1)
5.8e-41:412:73
Hs.2479:X78933
- 55 R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
4.2e-44:258:93
Hs.11494:AF093118

5
R-HEMBA1003294
ESTs
4.3e-84:410:98
Hs.113517:AA418756

10
R-HEMBA1003315
ESTs, Weakly similar to TIP49 [R.norvegicus]
7.3e-73:476:87
Hs.6455:AA515838

15
R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
8.3e-117:557:98
Hs.23672:AF074264

20
R-HEMBA1003399
ESTs, Highly similar to MVP1 PROTEIN [Saccharomyces cerevisiae]
8.0e-94:526:92
Hs.12169:N38744

25
R-HEMBA1003487
ESTs
4.5e-84:417:96
Hs.21835:AA458524

30
R-HEMBA1003497
ESTs
1.4e-72:346:99
Hs.129837:AA778570

35
R-HEMBA1003530
ESTs
8.5e-82:459:91
Hs.22140:R41751

40
R-HEMBA1003602
ESTs
1.0e-101:592:90
Hs.124342:AA829829

45
R-HEMBA1003732
ESTs
2.1e-111:530:99
Hs.101660:AA481200

50
R-HEMBA1003945
Calcineurin B
2.9e-83:410:97
Hs.1335:M30773

55
R-HEMBA1004007
Homo sapiens PYRIN (MEFV) mRNA, complete cds
3.8e-57:382:77
Hs.113283:AF018080

R-HEMBA1004085
ESTs
3.0e-59:396:87

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Hs.102480:AA520980

R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds
5 2.0e-116:569:97
Hs.66392:AF064244

R-HEMBA1004250
ESTs
10 1.6e-97:469:97
Hs.125529:AA883986

R-HEMBA1004391
EST
15 0.085:113:63
Hs.157582:AI356856

R-HEMBA1004444
ESTs
20 2.3e-88:430:98
Hs.141680:N98441

R-HEMBA1004454
ESTs
25 1.7e-71:338:100
Hs.103913:AA740543

R-HEMBA1004505
ESTs
30 2.2e-63:329:95
Hs.4814:AA631254

R-HEMBA1004785
EST
35 1.0:77:67
Hs.144066:AA905236

R-HEMBA1004797
ESTs
40 4.1e-11:71:100
Hs.27206:AA626782

R-HEMBA1004952
ESTs
45 6.0e-93:435:99
Hs.115120:AA935633

R-HEMBA1004971
ESTs
50 0.98:152:58
Hs.112621:AA608964

R-HEMBA1004982
ESTs
55 2.3e-109:516:98
Hs.14877:AA749081

R-HEMBA1005070

- Human mRNA for KIAA0310 gene, complete cds
4.0e-96:381:91
Hs.5716:AB002308
- 5 R-HEMBA1005084
ESTs
1.0:75:80
Hs.62119:AA043299
- 10 R-HEMBA1005145
Homo sapiens LIM protein mRNA, complete cds
1.6e-58:278:84
Hs.154103:AF061258
- 15 R-HEMBA1005230
ESTs
3.7e-65:336:95
Hs.124946:AI026708
- 20 R-HEMBA1005246

R-HEMBA1005267
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds
7.8e-75:536:81
- 25 Hs.44566:U28831

R-HEMBA1005337
EST
8.7e-58:291:97
- 30 Hs.48956:N64339

R-HEMBA1005430
ESTs
7.6e-83:388:100
- 35 Hs.28968:AA524690

R-HEMBA1005449
ESTs
5.0e-47:317:86
- 40 Hs.23650:H21144

R-HEMBA1005489
ESTs
1.8e-96:504:94
- 45 Hs.8028:AA053817

R-HEMBA1005522
EST
1.0:98:64
- 50 Hs.157385:AI364194

R-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
6.3e-117:579:96
- 55 Hs.7138:U29589

R-HEMBA1005698
ESTs

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	1.6e-113:562:96
	Hs.12942:AI042353
5	R-HEMBA1005913
	ESTs
	2.8e-109:564:94
	Hs.28827:AI125541
10	R-HEMBA1005929
	Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
	9.6e-63:497:77
	Hs.97203:U83171
15	R-HEMBA1005945
	ESTs
	1.1e-74:412:92
	Hs.32246:AA464020
20	R-HEMBA1006016
	ESTs
	1.4e-18:162:82
	Hs.149448:AI082465
25	R-HEMBA1006171
	EST
	0.049:94:69
	Hs.159919:AA961766
30	R-HEMBA1006276
	ESTs
	6.3e-22:257:75
	Hs.138847:N64493
35	R-HEMBA1006299
	ESTs, Weakly similar to R06B9.b [C.elegans]
	3.9e-107:596:91
	Hs.30432:W28988
40	R-HEMBA1006311
	Homo sapiens SALL1 gene, partial
	0:99:273:60
	Hs.123094:X98833
45	R-HEMBA1006335
	ESTs
	2.5e-72:447:89
	Hs.23579:W38893
50	R-HEMBA1006357
	ESTs
	6.3e-15:187:74
	Hs.161714:AA229078
55	R-HEMBA1006430
	Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds
	2.9e-47:303:88
	Hs.129708:AF064090

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R-HEMBA1006482
 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
 5.5e-107:537:96
 Hs.14511:AF026852
 5

R-HEMBA1006517
 ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
 2.7e-43:173:86
 Hs.141505:N30650
 10

R-HEMBA1006544
 Homo sapiens mRNA for small GTP-binding protein, complete cds
 5.8e-60:329:80
 Hs.115325:D84488
 15

R-HEMBA1006572
 ESTs
 7.2e-94:450:99
 Hs.123933:AA758566
 20

R-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds
 2.3e-112:570:94
 Hs.3628:AB014587
 25

R-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial
 1.7e-79:389:97
 Hs.129361:AJ007581
 30

R-HEMBA1006724
 R-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial
 1.0e-89:472:94
 Hs.129361:AJ007581
 35

R-HEMBA1006770
 ESTs, Moderately similar to CAGH4 [H.sapiens]
 2.0e-112:554:96
 Hs.41641:AA428519
 40

R-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial
 3.0e-113:540:98
 Hs.129361:AJ007581
 45

R-HEMBA1006912
 H.sapiens mRNA for phosphoinositide 3-kinase
 5.9e-45:297:86
 Hs.101238:Y11312
 50

R-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds
 5.8e-116:346:99
 Hs.83070:L76687
 55

R-HEMBA1006960

ESTs
1.7e-110:519:99
Hs.22015:AI359551

5 R-HEMBA1007013
ESTs
0.53:280:59
Hs.143532:AI087321

10 R-HEMBA1007057

R-HEMBA1007063
EST
3.2e-41:310:83
15 Hs.163333:AA879053

R-HEMBA1007241
ESTs
1.8e-103:492:98
20 Hs.127478:AI188768

R-HEMBA1007291
Human mRNA for KIAA0266 gene, complete cds
8.7e-46:283:89
25 Hs.78878:D87455

R-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.8e-17:161:80
30 Hs.3727:AA205887

R-HEMBA1000106
ESTs
1.3e-100:491:97
35 Hs.27774:AA576731

R-HEMBA1000276

R-HEMBA1000309
EST
1.0:150:64
40 Hs.125409:AA879096

R-HEMBA1000407
ESTs, Weakly similar to C47D12.2 [C.elegans]
4.1e-110:535:97
45 Hs.14328:AA503393

R-HEMBA1000447
Homo sapiens JWA protein mRNA, complete cds
5.6e-109:533:97
50 Hs.92384:AF070523

R-HEMBA1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
1.6e-88:497:91
55 Hs.18171:AA524327

5 R-HEMBB1000567
 Insulin-like growth factor 2 (somatomedin A)
 8.9e-61:369:88
 Hs.155487:J03242

 R-HEMBB1000642
 ESTs
 2.2e-44:308:84
 Hs.141318:N71080
 10
 R-HEMBB1000668
 ESTs, Weakly similar to hTAFII100 [H.sapiens]
 2.5e-102:520:95
 Hs.3830:AA167691
 15
 R-HEMBB1000679
 ESTs
 6.7e-36:188:97
 Hs.154218:AA169554
 20
 R-HEMBB1000881
 ESTs
 8.4e-105:519:96
 Hs.110967:AA570505
 25
 R-HEMBB1000905
 ESTs
 1.1e-94:454:98
 Hs.52515:AA464314
 30
 R-HEMBB1001026
 ESTs
 0.22:93:69
 Hs.119510:AA630235
 35
 R-HEMBB1001048
 EST
 0.42:127:66
 Hs.147466:AI215091
 40
 R-HEMBB1001200
 ESTs
 3.7e-07:330:62
 Hs.10109:AI148628
 45
 R-HEMBB1001407
 MHC class II transactivator
 3.8e-35:414:71
 Hs.3076:U18259
 50
 R-HEMBB1001530
 ESTs
 2.4e-95:455:98
 Hs.8956:AI146421
 55
 R-HEMBB1001547
 ESTs
 1.0e-111:533:98

Hs.33979:AI074147

R-HEM BB1001573

ESTs, Moderately similar to LL5 protein [R.norvegicus]

5

1.7e-06:64:95

Hs.131327:AI148746

R-HEM BB1001847

ESTs

10

1.4e-54:280:96

Hs.109755:AA180809

R-HEM BB1001959

Homo sapiens clone 24781 mRNA sequence

15

1.5e-104:504:97

Hs.108112:AF070640

R-HEM BB1001978

Homo sapiens mRNA for TRAFS, complete cds

20

7.0e-28:220:84

Hs.29736:AB000509

R-HEM BB1002039

ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]

25

1.5e-34:423:72

Hs.154912:N63897

R-HEM BB1002041

ESTs, Weakly similar to transmembrane protein [H.sapiens]

30

7.0e-122:575:98

Hs.22791:AI056665

R-HEM BB1002051

ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]

35

4.2e-43:298:84

Hs.141429:AA631915

R-HEM BB1002120

ESTs

40

1.4e-91:438:99

Hs.145014:AI218562

R-HEM BB1002162

ESTs

45

1.0e-34:238:86

Hs.164036:AA845659

R-HEM BB1002228

Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds

50

1.7e-59:583:77

Hs.129735:AF010144

R-HEM BB1002245

ESTs

55

9:1e-66:383:91

Hs.8989:R71365

R-HEMBB1002302
 ESTs
 3.6e-54:329:89
 Hs.37706:AA005120
 5
 R-HEMBB1002427
 ESTs
 4.2e-83:400:98
 Hs.130783:AI263114
 10
 R-HEMBB1002465
 EST
 9.9e-38:231:90
 Hs.133443:AI061405
 15
 R-HEMBB1002661
 ESTs
 2.5e-101:472:99
 Hs.26878:AI421289
 20
 R-HEMBB1002663
 Small inducible cytokine A5 (RANTES)
 7.1e-43:268:88
 Hs.155464:AF088219
 25
 R-HEMBB1002693
 ESTs
 4.6e-84:435:96
 Hs.155522:AA829725
 30
 R-MAMMA1000046
 EST
 3.9e-06:196:65
 Hs.136664:AA707467
 35
 R-MAMMA1000102
 Human G protein-coupled receptor (STRL22) mRNA, complete cds
 1.1e-31:237:83
 Hs.46468:U45984
 40
 R-MAMMA1000106
 ESTs
 1.3e-65:333:95
 Hs.130749:AI284219
 45
 R-MAMMA1000118
 ESTs
 7.3e-95:465:97
 Hs.119286:AA126730
 50
 R-MAMMA1000141
 ESTs
 4.2e-94:515:93
 Hs.8116:H23508
 55
 R-MAMMA1000204
 Homo sapiens dysferlin mRNA, complete cds
 2.3e-108:542:96

Hs.143897:AF075575

R-MAMMA1000226
ESTs
5 2.1e-112:535:98
Hs.105761:AA903862

R-MAMMA1000403
ESTs
10 1.5e-36:162:83
Hs.152413:AA780515

R-MAMMA1000449
EST
15 1.5e-40:347:78
Hs.163333:AA879053

R-MAMMA1000457
Homo sapiens clone 638 unknown mRNA, complete sequence
20 2.6e-117:570:97
Hs.5825:AF091084

R-MAMMA1000473
ESTs
25 1.3e-62:308:99
Hs.53565:W02102

R-MAMMA1000496
Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)
30 0.051:125:68
Hs.189:AC005759

R-MAMMA1000528
ESTs
35 2.4e-12:216:71
Hs.134105:AI078038

R-MAMMA1000591
ESTs
40 5.0e-104:509:98
Hs.151678:AA032243

R-MAMMA1000614
Homo sapiens mRNA for KIAA0665 protein, complete cds
45 0.57:251:62
Hs.119004:AB014565

R-MAMMA1000652
ESTs
50 0.93:49:87
Hs.13248:R54144

R-MAMMA1000681
ESTs
55 1.3e-87:434:97
Hs.46668:N47089

R-MAMMA1000706

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Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds

3.7e-48:232:100

Hs.18953:AF067223

- 5 R-MAMMA1000788
ESTs
3.7e-108:559:94
Hs.38969:AA130220
- 10 R-MAMMA1000810
ESTs
1.2e-45:347:80
Hs.146811:AA410788
- 15 R-MAMMA1000814
ESTs
1.1e-18:288:70
Hs.140608:N53448
- 20 R-MAMMA1000881
ESTs
1.9e-107:557:96
Hs.141602:N63562
- 25 R-MAMMA1000986
ESTs
3.8e-46:342:83
Hs.132722:AA618531
- 30 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds
1.2e-109:552:96
Hs.102171:AB003184
- 35 R-MAMMA1001043
ESTs
2.3e-88:445:96
Hs.20450:AI094818
- 40 R-MAMMA1001066
Homo sapiens KIAA0414 mRNA, partial cds
1.5e-43:282:81
Hs.127649:AB007874
- 45 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
3.0e-116:566:97
Hs.20423:AF091094
- 50 R-MAMMA1001141
ESTs
1.2e-104:496:98
Hs.29669:AI285856
- 55 R-MAMMA1001150
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
1.9e-59:284:100
Hs.9915:AI300083

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R-MAMMA1001237
 ESTs
 0.45:206:62
 Hs.121366:AA758653
 5

R-MAMMA1001284
 ESTs
 6.3e-40:279:85
 Hs.109765:AI096738
 10

R-MAMMA1001310
 ESTs, Moderately similar to !!!! ALU SUBFAMTLY J WARNING ENTRY !!!! [H.sapiens]
 5.1e-98:498:96
 Hs.27264:AA159597
 15

R-MAMMA1001418
 Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds
 1.2e-41:302:85
 Hs.86188:D87845
 20

R-MAMMA1001532
 ESTs
 3.9e-22:331:71
 Hs.141840:AA028117
 25

R-MAMMA1001609
 Small inducible cytokine A5 (RANTES)
 1.5e-31:277:78
 Hs.155464:AF088219
 30

R-MAMMA1001615
 ESTs
 1.1e-72:376:95
 Hs.135569:AA923461
 35

R-MAMMA1001623
 ESTs
 7.9e-106:505:98
 Hs.22908:AI224910
 40

R-MAMMA1001634
 Homo sapiens PYRIN (MEFV) mRNA, complete cds
 1.9e-44:428:76
 Hs.113283:AF018080
 45

R-MAMMA1001893
 ESTs
 8.0e-67:367:92
 Hs.19210:W26097
 50

R-MAMMA1001901
 Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492
 4.7e-35:342:69
 Hs.127338:AB007961
 55

R-MAMMA1001957
 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
 5.5e-47:383:79

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Hs.1361:M55053

R-MAMMA1001978
ESTs
5 6.6e-108:560:95
Hs.8859:AA191552

R-MAMMA1002070

10 R-MAMMA1002080
ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]
9.8e-105:542:94
Hs.10092:AI189282

15 R-MAMMA1002087
ESTs
4.0e-19:153:84
Hs.136678:AA730474

20 R-MAMMA1002095
ESTs
6.8e-34:196:93
Hs.48119:AA454227

25 R-MAMMA1002128
ESTs, Highly similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]
9.0e-96:503:94
Hs.39088:AA194773

30 R-MAMMA1002142
ESTs
5.6e-21:145:90
Hs.62119:AA043299

35 R-MAMMA1002165
ESTs
1.6e-35:351:76
Hs.140413:N47721

40 R-MAMMA1002205
Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds
6.4e-42:217:79
Hs.133089:AF064019

45 R-MAMMA1002224
ESTs
0.50:170:64
Hs.144140:H04293

50 R-MAMMA1002234

R-MAMMA1002586
ESTs
5.0e-105:529:96
55 Hs.4814:AA631254

R-MAMMA1002633
ESTs

7.3e-97:470:98
Hs.38039:AI360128

5 R-MAMMA1003126
ESTs
6.1e-114:567:97
Hs.20733:AI417917

10 R-NT2RM4000100
ESTs
3.6e-71:343:99
Hs.92186:AI080282

15 R-NT2RM4000115
ESTs
1.5e-86:405:100
Hs.129151:AA988192

20 R-NT2RM4000198
ESTs
8.4e-83:462:93
Hs.96772:AI369496

25 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds
5.4e-95:440:100
Hs.110804:U12255

30 R-NT2RM4000295
ESTs
1.1e-112:544:97
Hs.21452:AA581881

35 R-NT2RM4000326
EST
4.0e-59:301:96
Hs.86264:AA206496

40 R-NT2RM4000417
ESTs
2.0e-88:489:93
Hs.29098:AA521439

45 R-NT2RM4000444
ESTs
6.4e-90:497:92
Hs.6129:U66676

50 R-NT2RM4000587
ESTs
1.0e-97:473:98
Hs.24947:AA039350

55 R-NT2RM4000593
ESTs
9.8e-109:554:95
Hs.7579:AA775865

R-NT2RM4000648
 ESTs, Moderately similar to GLYPICAN-1 PRECURSOR [Homo sapiens]
 7.6e-39:262:85
 Hs.118407:AA001322
 5

R-NT2RM4000761
 ESTs
 6.4e-86:433:95
 Hs.153428:AI246519
 10

R-NT2RM4000965
 ESTs
 2.8e-102:523:96
 Hs.61790:AA421156
 15

R-NT2RM4000997
 R-NT2RM4001321
 ESTs
 2.4e-66:315:100
 Hs.75425:AA149434
 20

R-NT2RM4001325
 ESTs
 0.99:104:62
 Hs.116257:AA628680
 25

R-NT2RM4001377
 Homo sapiens mRNA for KIAA0638 protein, partial cds
 9.3e-113:553:96
 Hs.77864:AB014538
 30

R-NT2RM4001735
 Homo sapiens clone 23904 mRNA sequence
 1.5e-107:553:94
 Hs.67364:AF052129
 35

R-NT2RM4001768
 EST
 1.6e-14:82:85
 Hs.140922:R51520
 40

R-NT2RM4001843
 ESTs
 2.1e-123:579:98
 Hs.3741:AI057614
 45

R-NT2RM4002352
 Homo sapiens hLRp105 mRNA for LI(L receptor related protein 105, complete cds
 1.8e-109:557:95
 Hs.143641:AB009462
 50

R-NT2RP2000092
 ESTs
 3.3e-08:286:65
 Hs.79881:AA401302
 55

R-NT2RP2000178

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ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]

2.3e-95:462:98

Hs.47305:AA195153

5 R-NT2RP2000240

ESTs

1.3e-55:272:98

Hs.125522:AI299693

10 R-NT2RP2000394

ESTs

2.4e-107:528:96

Hs.28555:W55892

15 R-NT2RP2000447

ESTs, Moderately similar to dynamin, internal form 2, short C-terminal form [H.sapiens]

1.6e-67:357:94

Hs.128788:AA424076

20 R-NT2RP2000479

ESTs

2.6e-48:312:86

Hs.146811:AA410788

25 R-NT2RP2000514

EST

3.2e-63:348:93

Hs.44542:N33966

30 R-NT2RP2000533

ESTs

0.017:307:57

Hs.97873:AA402799

35 R-NT2RP2000616

ESTs

1.0e-91:475:95

Hs.50344:AI300539

40 R-NT2RP2000649

Homo sapiens mRNA for Hs Ste24p, complete cds

1.4e-66:322:98

Hs.25846:AB016068

45 R-NT2RP2000663

ESTs

8.2e-59:311:96

Hs.9728:T98746

50 R-NT2RP2000712

EST

1.7e-27:239:76

Hs.161561:W60681

55 R-NT2RP2000739

ESTs, Weakly similar to zinc finger protein [H.sapiens]

6.3e-86:462:93

Hs.13323:AA897542

5 R-NT2RP2000818
ESTs
7.3e-99:485:97
Hs.100525:AI310204

10 R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.2e-100:505:96
Hs.82128:AJ012159

15 R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
6.6e-59:306:95
Hs.115763:AB014576

20 R-NT2RP2001223
ESTs
1.2e-94:475:95
Hs.27556:AA115361

25 R-NT2RP2001276
ESTs, Moderately similar to regulatory protein [M.musculus]
4.7e-65:354:92
Hs.105547:AI361036

30 R-NT2RP2001388
ESTs
5.5e-83:459:93
Hs.15713:AA485755

35 R-NT2RP2001469
ESTs, Weakly similar to teg292 protein [M.musculus]
2.0e-30:233:83
Hs.68791:AA527270

40 R-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.1e-84:426:95
Hs.82165:L38969

45 R-NT2RP2001495
ESTs, Weakly similar to transporter protein [H.sapiens]
1.7e-14:130:84
Hs.18272:N78499

50 R-NT2RP2001514
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
3.3e-45:242:95
Hs.9275:AA973284

55 R-NT2RP2001538
EST
1.4e-05:111:73
Hs.137268:T39311

R-NT2RP2001562
EST
0.50:35:91

Hs.140505:AA804211

R-NT2RP2001662
Homo sapiens clone 24615 mRNA sequence
5 1.0e-95:485:95
Hs.94785:AF055012

R-NT2RP2001755
Homo sapiens mRNA for KIAA0762 protein, partial cds
10 4.2e-105:576:92
Hs.5378:AB018305

R-NT2RP2001769
ESTs
15 4.2e-102:548:93
Hs.14014:AA745592

R-NT2RP2001817
ESTs
20 6.0e-97:472:97
Hs.31176:AI037953

R-NT2RP2001878
ESTs
25 3.3e-94:475:95
Hs.144655:AI279798

R-NT2RP2001903
ESTs
30 1.7e-88:461:95
Hs.112218:AI038601

R-NT2RP2001915
ESTs
35 7.8e-96:480:96
Hs.100890:AA779892

R-NT2RP2001921
ESTs
40 2.5e-88:466:94
Hs.104859:AA779101

R-NT2RP2001948
ESTs
45 1.9e-81:439:91
Hs.105463:AA583017

R-NT2RP2001956
ESTs
50 8.7e-85:477:91
Hs.12101:AA677423

R-NT2RP2002015
ESTs
55 3.5e-85:431:95
Hs.75425:AA149434

R-NT2RP2002063

EST
0.0083:199:62
Hs.48699:N63049

5 R-NT2RP2002188
ESTs
1.5e-108:559:94
Hs.47320:AA057440

10 R-NT2RP2002232
ESTs
2.5e-113:576:95
Hs.7099:AI089774

15 R-nnnnnnnnnnnn
Human mRNA for KIAA0383 gene, partial cds
8.0e-102:511:96
Hs.27590:AB002381

20 R-NT2RP2002409
ESTs
3.2e-84:432:95
Hs.128443:AI281991

25 R-NT2RP2002510
ESTs
1.3e-42:303:82
Hs.146811:AA410788

30 R-NT2RP2002527
Thromboxane A2 receptor
2.9e-23:164:88
Hs.89887:D38081

35 R-NT2RP2002533
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds
4.0e-117:580:96
Hs.127436:AF040709

40 R-NT2RP2002564
Human zinc-finger protein C2H2-150 mRNA, complete cds
4.0e-111:569:94
Hs.108139:U38864

45 R-NT2RP2002674
ESTs, Weakly similar to putative p150 [H.sapiens]
0.010:293:60
Hs.140964:AI214400

50 R-NT2RP2002721
ESTs
5.6e-10:165:69
Hs.108745:H95644

55 R-NT2RP2002824
EST
0.0055:209:58

Hs.136259:AA347883

R-NT2RP2002942
ESTs
5 9.2e-82:422:96
Hs.140952:R59211

R-NT2RP2002974
ESTs
10 5.6e-99:507:96
Hs.43314:AA160543

R-NT2RP2002976
ESTs
15 2.9e-78:397:91
Hs.83575:N28730

R-NT2RP2003042
ESTs
20 2.7e-107:526:97
Hs.6770:AA972732

R-NT2RP2003179
ESTs
25 2.9e-59:335:92
Hs.87019:AA760977

R-NT2RP2003210
ESTs
30 2.1e-80:419:94
Hs.25354:N28667

R-NT2RP2003302
ESTs, Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]
35 2.1e-92:443:98
Hs.112508:AA599140

R-NT2RP2003369
ESTs
40 9.7e-84:462:92
Hs.155116:C16874

R-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
45 1.3e-112:549:97
Hs.7414:AB007927

R-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
50 4.9e-56:286:96
Hs.31575:AF100141

R-NT2RP2003469
Human mRNA for KIAA0355 gene, complete cds
55 6.6e-40:302:83
Hs.153014:AB002353

R-NT2RP2003545

ESTs
8.0e-121:572:98
Hs.23643:AI299952

5 R-NT2RP2003593
EST
1.0:124:62
Hs.59890:AA001879

10 R-NT2RP2003599
EST
5.2e-06:319:60
Hs.147887:AI223203

15 R-NT2RP2003655
ESTs
9.3e-107:519:97
Hs.5831:AA176450

20 R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.3e-112:549:96
Hs.23581:Y12670

25 R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
1.7e-113:571:96
Hs.84123:AB002363

30 R-NT2RP2003940
EST
3.0e-71:385:93
Hs.162657:AA603590

35 R-NT2RP2003950
Homo sapiens clone 24778 unknown mRNA
5.0e-98:494:95
Hs.25306:AF070572

40 R-NT2RP2004069
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
6.3e-54:556:74
Hs.103948:K00627

45 R-NT2RP2004108
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
6.9e-92:442:98
Hs.14831:AI261191

50 R-NT2RP2004141
ESTs
8.3e-29:171:93
Hs.25700:AI338437

55 R-NT2RP2004179
ESTs
3.1e-71:461:88
Hs.6748:R68509

5 R-NT2RP2004205
ESTs
2.6e-44:397:78
Hs.95115:AA206594

10 R-NT2RP2004447
ESTs
4.0e-101:494:97
Hs.51655:AA523276

15 R-NT2RP2004495
ESTs, Weakly similar to transporter protein [H.sapiens]
6.1e-71:417:92
Hs.18272:N78499

20 R-NT2RP2004524
ESTs
1.8e-93:482:95
Hs.119285:AI225008

25 R-NT2RP2004556
Homo sapiens mRNA for KIAA0459 protein, partial cds
8.8e-48:353:82
Hs.28169:AB007928

30 R-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
3.5e-116:576:96
Hs.148726:X03124

35 R-NT2RP2004648
ESTs
5.9e-114:600:93
Hs.3741:AI057614

40 R-NT2RP2004670
ESTs
1.7e-92:488:94
Hs.6262:T89093

45 R-NT2RP2004794
EST
0.44:205:57
Hs.147759:AI220726

50 R-NT2RP2004837
ESTs
6.9e-111:576:94
Hs.12305:AA166889

55 R-NT2RP2004847
ESTs
8.3e-94:445:99
Hs.53996:AI268861

R-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
2.5e-104:508:97

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Hs.7594:M20681

R-NT2RP2005069
ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]
5 4.7e-111:541:97
Hs.26510:AA700425

R-NT2RP2005163
ESTs
10 6.8e-64:327:89
Hs.83575:N28730

R-NT2RP2005181
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
15 1.6e-106:527:97
Hs.86362:AA205485

R-NT2RP2005247
MHC class II transactivator
20 7.9e-35:465:69
Hs.3076:U18259

R-NT2RP2005378
ESTs
25 3.4e-110:566:94
Hs.23060:N64748

R-NT2RP2005391
ESTs
30 5.5e-82:463:92
Hs.118793:AA192438

R-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds
35 2.6e-101:526:94
Hs.58103:AB018346

R-NT2RP2005463
ESTs, Weakly similar to weakly similar to S. cerevisiae PTM1 precursor [C.elegans]
40 7.6e-111:554:97
Hs.16492:N95400

R-NT2RP2005514
ESTs
45 1.8e-97:490:95
Hs.109677:AA447864

R-NT2RP2005535
EST
50 5.1e-40:399:73
Hs.127142:AA937570

R-NT2RP2005541
ESTs
55 5.2e-114:573:96
Hs.70823:AI378619

R-NT2RP2005597

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- ESTs, Weakly similar to rotated abdomen protein [D.melanogaster]
3.7e-109:543:96
Hs.99654:AA670164
- 5 R-nnnnnnnnnnnnn
ESTs
1.1 e-100:501:97
Hs.112011:AA987961
- 10 R-NT2RP2005666
ESTs
2.7e-106:560:94
Hs.42814:AA205754
- 15 R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence
7.0e-96:440:96
Hs.139345:AF035364
- 20 R-NT2RP2005878
ESTs
2.8e-89:479:93
Hs.142305:R42591
- 25 R-NT2RP2005883
ESTs
1.0e-85:431:96
Hs.6909:AA928115
- 30 R-NT2RP2005887
ESTs
5.5e-109:566:94
Hs.12305:AA166889
- 35 R-nnnnnnnnnnnnn
Paired box homeotic gene 6 (aniridia, keratitis)
1.6e-116:578:96
Hs.89506:M93650
- 40 R-NT2RP2005994
EST
0.0061:129:68
Hs.160756:AI310589
- 45 R-NT2RP2006004
ESTs, Weakly similar to KIAA0405 [H.sapiens]
4.7e-45:303:86
Hs.14146:W92235
- 50 R-NT2RP2006042
EST
0.64:84:71
Hs.133275:AI053487
- 55 R-NT2RP2006092
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
1.1e-75:384:95
Hs.32822:AI194045

R-NT2RP2006099
ESTs
6.9e-35:224:82
Hs.139446:AA461080

5 R-NT2RP2006134
EST
1.3e-95:445:100
Hs.162033:AA514590

10 R-NT2RP2006269
Human mRNA for KIAA0315 gene, partial cds
0.96:343:60
Hs.3989:AB002313

15 R-NT2RP2006512
Homo sapiens clone 23904 mRNA sequence
1.5e-107:531:96
Hs.67364:AF052129

20 R-NT2RP3000011
ESTs
7.3e-92:508:91
Hs.112041:W26001

25 R-NT2RP3000022
EST
0.78:175:63
Hs.135650:AA902912

30 R-NT2RP3000059
ESTs
6.2e-99:475:98
Hs.123136:AA631067

35 R-NT2RP3000063
ESTs
9.7e-105:554:94
Hs.7542:AA121663

40 R-nnnnnnnnnnnn
Human mRNA for KIAA0314 gene, partial cds
5.0e-17:307:65
Hs.155045:AB002312

45 R-NT2RP3000148
ESTs
6.4e-101:527:94
Hs.58461:W80378

50 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds
1.4e-111:551:96
Hs.30985:AF093239

55 R-NT2RP3000171
EST
0.45:205:57

Hs.147759:AI220726

R-NT2RP3000172
ESTs
5 2.0e-89:494:93
Hs.6262:T89093

R-NT2RP3000201
Human mRNA for KIAA0355 gene, complete cds
10 1.1e-40:305:83
Hs.153014:AB002353

R-NT2RP3000232
ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]
15 5.7e-65:386:90
Hs.4841:AI279875

R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
20 1.1e-109:541:97
Hs.23672:AF074264

R-NT2RP3000378
EST
25 2.0e-05:112:74
Hs.137268:T39311

R-NT2RP3000436
EST
30 1.2e-08:347:62
Hs.158830:AI377454

R-NT2RP3000444
ESTs
35 3.3e-70:314:99
Hs.57973:AI263207

R-NT2RP3000460
EST
40 1.9e-50:294:92
Hs.7260:T23737

R-NT2RP3000481
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6
45 1.0:183:59
Hs.46332:U18549

R-NT2RP3000616
ESTs
50 3.0e-71:309:93
Hs.41296:N71923

R-NT2RP3000645
ESTs
55 1.5e-101:550:92
Hs.21910:AA020743

R-NT2RP3000652

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- ESTs
6.6e-88:411:100
Hs.43134:AA766138
- 5 R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
1.0e-104:542:94
Hs.158286:AB007915
- 10 R-NT2RP3000677
ESTs
0.33:307:59
Hs.133022:AI374739
- 15 R-NT2RP3000721
ESTs
1.6e-75:390:90
Hs.83575:N28730
- 20 R-NT2RP3000789
ESTs
1.5e-71:340:99
Hs.37776:H93038
- 25 R-NT2RP3000818
ESTs
1.9e-52:330:88
H.s.111052:H80504
- 30 R-NT2RP3000820
EST
9.1e-05:82:74
Hs.124352:AA830406
- 35 R-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
1.5e-100:522:94
Hs.77864:AB014538
- 40 R-NT2RP3000871
ESTs
3.9e-76:424:91
Hs.121642:AA772262
- 45 R-NT2RP3000907
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
4.5e-95:493:94
Hs.9275:AA973284
- 50 R-NT2RP3000921
ESTs
4.1e-52:283:94
Hs.49714:AA442453
- 55 R-NT2RP3001012
Homo sapiens mRNA for CMP-sialic acid transporter, complete cds
0.60:250:61
Hs.82921:D87969

5
R-NT2RP3001044
ESTs
3.5e-106:547:95
Hs.12305:AA166889

10
R-NT2RP3001061
ESTs
1.3e-96:453:99
Hs.4916:AI149707

15
R-NT2RP3001159
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.8e-47:302:90
Hs.6281:AA523081

20
R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
2.8e-118:561:98
Hs.3657:AB018327

25
R-NT2RP3001195
ESTs
1.5e-40:461:72
Hs.152438:AI334078

30
R-NT2RP3001240
EST
1.9e-50:294:92
Hs.7260:T23737

35
R-NT2RP3001271
ESTs
1.1e-77:432:92
Hs.12211:AA908631

40
R-NT2RP3001322
ESTs
0.25:331:60
Hs.44330:N32264

45
R-NT2RP3001542
EST
0.0032:432:58
Hs.148107:AA693476

50
R-NT2RP3001560
EST
3.5e-50:281:93
Hs.101727:H16171

55
R-NT2RP3001592
ESTs
3.2e-65:344:93
Hs.28964:AA715101

R-NT2RP3001685
EST
3.0e-37:165:81

Hs.160895:AI365871

R-NT2RP3001738
ESTs, Weakly similar to T13F2.1 [C.elegans]
5 3.8e-47:302:90
Hs.6281 :AA523081

R-NT2RP3001754
EST
10 0.00043:104:69
Hs.148331:AA911426

R-NT2RP3001858
ESTs
15 7.6e-93:502:93
Hs.153524:AA533582

R-NT2RP3001976
ESTs
20 5.0e-104:516:96
Hs.35461:AA777644

R-NT2RP3002015

25 R-NT2RP3002160
ESTs
1.4e-34:178:99
Hs.130783:AI263114

30 R-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds
3.5e-83:446:93
Hs.62318:AB018308

35 R-NT2RP3002286
ESTs
2.1e-103:513:97
Hs.58570:AA521423

40 R-NT2RP3002311
ESTs
1.4e-108:538:96
Hs.3741:AI057614

45 R-NT2RP3002324
ESTs
3.7e-102:483:99
Hs.99668:AA829521

50 R-NT2RP3002342
ESTs, Weakly similar to transporter protein [H.sapiens]
2.0e-60:339:95
Hs.18272:N78499

55 R-NT2RP3002353
ESTs
6.8e-98:484:97
Hs.9732:AA527784

NNNNNNNNNNNNNNNN
Homo sapiens mRNA for KIAA0788 protein, partial cds
2.7e-29:214:85
Hs.2397:Z70200

5

NNNNNNNNNNNNNNNN
ESTs
3.0e-72:389:94
Hs.32246:AA464020

10

R-NT2RP3002448
ESTs, Weakly similar to Y48E1B.t [C.elegans]
1.0e-19:131:75
Hs.8715:H58021

15

R-NT2RP3002571
ESTs
1.1e-78:407:95
Hs.27356:AA740928

20

R-NT2RP3002664
ESTs
1.2e-56:341:90
Hs.23308:AA115020

25

R-NT2RP3002721
EST
2.8e-41:302:82
Hs.124936:AA825548

30

R-NT2RP3002737
EST
1.7e-51:267:97
Hs.161348:AI422470

35

R-NT2RP3002738
ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]
1.7e-106:530:96
Hs.4894:AI191323

40

R-NT2RP3002790

R-NT2RP3002836
ESTs
4.6e-49:282:92
Hs.107979:AA146994

45

R-NT2RP3002887
ESTs
6.3e-98:516:94
Hs.11900:AA535065

50

R-NT2RP3002900
ESTs
2.0e-29:155:99
Hs.153329:AA112325

55

R-NT2RP3002958

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Homo sapiens clone 23851 mRNA sequence
6.6e-119:575:98
Hs.10065:AF035313

5 R-NT2RP3002983
ESTs
1.1e-61:374:90
Hs.17834:AA128246

10 R-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
4.1e-65:358:94
Hs.122359:AF051946

15 R-NT2RP3003076
ESTs
2.6e-95:507:93
Hs.21910:AA020743

20 R-NT2RP3003354
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
2.1e-78:385:96
Hs.92177:AI207792

25 R-NT2RP3003448
ESTs
6.7e-105:521:96
Hs.106833:AA470128

30 R-NT2RP3003469
ESTs
1.1e-91:461:96
Hs.75425:AA149434

35 R-NT2RP3003473

R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
1.6e-92:445:97

40 Hs.130988:Y17999

R-NT2RP3003532
ESTs
0.022:193:63

45 Hs.122593:Z99400

R-nnnnnnnnnnnnnnn
EST
0.036:279:59

50 Hs.158745:AI375513

R-NT2RP3003559
ESTs
9.8e-106:513:97

55 Hs.44970:AI061464

R-NT2RP3003614
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510

0.00016:113:69
Hs.92660:AB007979

5 R-NT2RP3003729
ESTs
1.2e-43:289:86
Hs.106401:R50967

10 R-NT2RP3003849
ESTs
5.4e-91:435:98
Hs.144840:AI221746

15 R-NT2RP3003874
ESTs
0.21:323:59
Hs.42919:AA805764

20 R-NT2RP3003963
ESTs
1.7e-90:438:97
Hs.105894:AA564110

25 R-NT2RP3004000
ESTs
2.9e-101:559:91
Hs.21910:AA020743

30 R-NT2RP3004025
ESTs
2.3e-108:517:98
Hs.15356:AA911109

35 R-NT2RP3004075
ESTs
7.4e-84:453:93
Hs.22412:AA523036

40 R-NT2RP3004083
ESTs, Weakly similar to R06B9.b [C.elegans]
4.2e-84:474:91
Hs.30432:W28988

45 R-NT2RP3004090
ESTs
1.0:207:61
Hs.92832:AA631027

50 R-NT2RP3004119
EST
1.8e-50:248:99
Hs.162023:AA506128

55 R-NT2RP3004130
ESTs
1.1e-103:520:96
Hs.10491:W28968

5 R-NT2RP3004133
ESTs
4.7e-104:545:93
Hs.15727:H98190

10 R-NT2RP3004202
ESTs
1.1e-98:471:98
Hs.61884:AI335985

15 R-NT2RP3004294
ESTs, Weakly similar to R06B9.b [C.elegans]
2.4e-96:500:94
Hs.30432:W28988

20 R-NT2RP3004309
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.5e-48:308:90
Hs.6281:AA523081

25 R-NT2RP3004321
ESTs
2.6e-99:494:97
Hs.19306:N53491

30 R-NT2RP3004345
ESTs
5.4e-95:444:99
Hs.107149:AI379497

35 R-NT2RP3004355
ESTs
3.9e-99:490:97
Hs.43410:N23651

40 R-NT2RP3004374
ESTs
1.2e-90:462:95
Hs.75425:AA149434

45 R-NT2RP3004406
ESTs
1.9e-100:502:96
Hs.24936:AA479402

50 R-NT2RP3004481
ESTs
1.6e-53:370:87
Hs.11953:AA194120

55 R-NT2RP3004552
ESTs, Weakly similar to gene SEZ-6 [M.musculus]
7.8e-92:488:93
Hs.6314:AA522619

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
2.6e-50:352:84

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Hs.26285:AF082516

R-NT2RP3004640
ESTs
5 1.1e-105:551:94
Hs.83348:AA527170

R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
10 4.9e-111:555:96
Hs.158286:AB007915

R-NT2RP4000108
ESTs
15 2.9e-94:479:96
Hs.6625:AA115182

R-NT2RP4000634
ESTs
20 3.0e-120:572:98
Hs.28827:AI125541

R-NT2RP4000962
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]
25 6.0e-17:98:98
Hs.4789:AI418298

R-NT2RP4001001
ESTs
30 3.1e-117:567:97
Hs.4931:AA523860

R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds
35 1.6e-83:404:98
Hs.25846:AB016068

R-NT2RP4001467
5' nucleotidase (CD73)
40 5.9e-113:545:97
Hs.153952:X55740

R-NT2RP4001877
ESTs, Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [*Rattus norvegicus*]
45 2.2e-67:375:93
Hs.16389:AA206356

R-NT2RP4001879

50 R-NT2RP4002187
EST
0.010:117:70
Hs.160416:AI394161

55 R-NT2RP4002451
EST
1.3e-62:386:87
Hs.57082:H25761

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5 R-NT2RP4002715
 ESTs
 6.9e-111:552:96
 Hs.12305:AA166889

10 R-NT2RP4002750
 ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
 7.0e-109:532:97
 Hs.86362:AA205485

15 R-OVARC1000003
 ESTs
 1.3e-74:391:95
 Hs.105039:AA477819

20 R-OVARC1000090
 Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
 9.9e-44:471:75
 Hs.129735:AF010144

25 R-OVARC1000105
 60S RIBOSOMAL PROTEIN L38
 8.8e-14:83:100
 Hs.2017:Z26876

30 R-OVARC1000137
 ESTs
 3.0e-84:387:95
 Hs.22028:AA167715

35 R-OVARC1000208
 Human mRNA for KIAA0392 gene, partial cds
 2.8e-51:313:89
 Hs.40100:AB002390

40 R-OVARC1000255
 Spleen tyrosine kinase
 2.8e-106:510:98
 Hs.74101:L28824

45 R-OVARC1000275
 ESTs, Highly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB [Saccharomyces cerevisiae]
 6.9e-105:556:94
 Hs.5748:AA608559

50 R-OVARC1000298
 ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
 2.4e-56:338:90
 Hs.108354:W19984

55 R-OVARC1000307
 ESTs
 2.4e-101:563:93
 Hs.24479:N25972

R-OVARC1000313
 Homo sapiens mRNA for KIAA0573 protein, partial cds

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5.0e-98:534:93
Hs.154023:AB011145

5 R-OVARC1000331
Homo sapiens chromosome 9, P1 clone 11659
1.0e-55:281:97
Hs.3439:AC004472

10 R-OVARC1000410
Homo sapiens clone 23767 and 23782 mRNA sequences
3.3e-90:462:94
Hs.8025:AF007150

15 R-OVARC1000439
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[Caenorhabditis elegans]
1.6e-99:510:95
Hs.7471:AI143226

20 R-OVARC1000467

R-OVARC1000529
ESTs
5.7e-93:461:96

25 Hs.21396:AA114834

R-OVARC1000553
ESTs
4.3e-51:351:87

30 Hs.42979:W31096

R-OVARC1000775

35 R-OVARC1000811
ESTs
1.3e-82:441:95
Hs.73452:AA581386

40 R-OVARC1000853
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3.1e-95:492:95
Hs.6853:AA401703

45 R-OVARC1000873
ESTs
2.4e-46:281:91
Hs.43857:R91358

50 R-OVARC1000916
H.sapiens PISSLRE mRNA
1.9e-112:588:94
Hs.77313:X78342

55 R-OVARC1000956
Homo sapiens mRNA for MDC3, complete cds
0.18:259:62
Hs.7164:AB009672

5 R-OVARC1000995
EST
6.6e-43:343:81
Hs.149580:AI281881

10 R-OVARC1001030
ESTs, Weakly similar to neuroendocrine-specific protein C [H.sapiens]
1.5e-21:116:100
Hs.65450:AA055913

15 R-OVARC1001049
ESTs
1.2e-70:369:95
Hs.42949:N21131

20 R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
1.3e-106:569:94
Hs.155478:AF048731

25 R-OVARC1001132
INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR
0.16:170:64
Hs.149894:L34600

30 R-OVARC1001163
ESTs
1.9e-39:219:94
Hs.126067:AI344351

35 R-OVARC1001222
ESTs
0.62:177:63
Hs.141162:H66213

40 R-OVARC1001260
ESTs
2.1e-79:425:94
Hs.105039:AA477819

45 R-OVARC1001336
ESTs
9.2e-75:439:91
Hs.105039:AA477819

50 R-OVARC1001338
ESTs
2.3e-19:139:92
Hs.7978:W05059

55 R-OVARC1001569
ESTs
2.4e-83:412:97
Hs.21396:AA114834

R-OVARC1001570
ESTs
2.6e-49:280:94

	Hs.3854:R12478
	R-OVARC1001596
	EST
5	8.2e-15:93:97
	Hs.136918:AA811543
	R-OVARC1001607
	ESTs
10	0.019:413:56
	Hs.24684:AA587245
	R-OVARC1001725
	ESTs
15	1.4e-96:504:95
	Hs.23754:N29716
	R-OVARC1001727
20	R-OVARC1001807
	Hormone receptor (growth factor-inducible nuclear protein N10)
	8.5e-78:425:94
	Hs.1119:D49728
25	R-OVARC1001833
	ESTs
	1.0e-63:325:96
	Hs.126912:AA469087
30	R-OVARC1001991
	ESTs
	1.3e-92:467:95
	Hs.26506:AI348000
35	R-OVARC1002058
	ESTs
	2.5e-89:512:91
	Hs.58093:W63576
40	R-OVARC1002178
	ESTs
	3.3e-99:487:96
	Hs.136527:AI419398
45	R-PLACE1000033
	ESTs
	0.012:202:59
	Hs.157400:AI370528
50	R-PLACE1000231
	ESTs
	2.9e-56:285:96
	Hs.36688:AA603479
55	R-PLACE1000258
	EST
	3.4e-50:353:83
	Hs.146794:AI149478

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R-PLACE1000442
 ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
 5.5e-91:437:98
 Hs.14831:AI261191
 5

R-PLACE1000560
 ESTs
 3.7e-60:317:94
 Hs.65713:AI269328
 10

R-PLACE1000740
 ESTs
 4.2e-67:362:94
 Hs.163434:T79849
 15

R-PLACE1000912
 ESTs
 3.4e-57:329:92
 Hs.121907:R66773
 20

R-PLACE1000914
 ESTs
 2.6e-71:419:89
 Hs.90809:AA010979
 25

R-PLACE1000927
 ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
 7.8e-111:545:97
 Hs.8661:AI189791
 30

R-PLACE1000986
 ESTs
 1.5e-91:431:99
 Hs.42458:AA452296
 35

R-PLACE1001016
 ESTs
 3.4e-45:231:97
 Hs.121013:AA324765
 40

R-PLACE1001100
 Homo sapiens nephrin (NPHS1) mRNA, complete cds
 3.5e-43:321:83
 Hs.128834:AF035835
 45

R-PLACE1001114
 Human clone 23732 mRNA, partial cds
 1.6e-42:305:83
 Hs.81281:U79258
 50

R-PLACE1001123
 ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]
 1.2e-51:310:90
 Hs.7773:AA127629
 55

R-PLACE1001183
 Human mRNA for KIAA0308 gene, partial cds

0.88:182:65
Hs.10351:AB002306

5 R-PLACE1001229
ESTs
5.2e-90:471:95
Hs.18271:N92774

10 R-PLACE1001231

R-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.6e-53:265:98
Hs.21198:AB018262

15 R-PLACE1001401
ESTs
1.9e-72:362:96
Hs.20161:AA056410

20 R-PLACE1001407
ESTs
2.1e-36:249:85
Hs.23579:W38893

25 R-PLACE1001464
5' nucleotidase (CD73)
1.0e-91:457:96
Hs.153952:X55740

30 R-PLACE1001500
ESTs, Weakly similar to DNA helicase Q1 [H.sapiens]
2.0e-19:150:87
Hs.154199:AA155882

35 R-PLACE1001516
EST
1.9e-11:109:82
Hs.137486:AA425225

40 R-PLACE1001536
Human BRCA2 region, mRNA sequence CG016
0.28:146:63
Hs.112434:U50529

45 R-PLACE1001564
ESTs
6.3e-14:109:88
Hs.26519:AA442703

50 R-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds
1.2e-118:578:97
Hs.47584:AF043472

55 R-PLACE1001788
ESTs
8.4e-38:205:95

Hs.23800:AA524095

R-PLACE1001795

ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [*S.cerevisiae*]

2.5e-77:392:96

Hs.7745:H92988

R-PLACE1001836

ESTs

1.5e-49:296:90

Hs.17691:H60366

R-PLACE1001918

ESTs, Weakly similar to multispinning membrane protein [*H.sapiens*]

2.0e-42:304:85

Hs.110439:N93209

R-PLACE1001949

R-PLACE1002080

Small inducible cytokine A5 (RANTES)

8.5e-41:296:82

Hs.155464:AF088219

R-PLACE1002095

ESTs

8.5e-25:227:81

Hs.110488:AA034235

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

1.5e-101:514:95

Hs.90415:AF095791

R-PLACE1002329

ESTs

8.7e-48:257:94

Hs.126062:AA411593

R-PLACE1002355

ESTs

7.7e-71:362:95

Hs.120866:AI076780

R-PLACE1002374

Cathepsin L

8.4e-103:501:97

Hs.78056:X12451

R-PLACE1002518

ESTs

6.9e-97:471:97

Hs.104893:AA576941

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds

6.5e-55:276:97

Hs.21198:AB018262

R-PLACE1002726
Human DNA-binding protein ABP/ZF mRNA, complete cds
5 3.8e-39:212:94
Hs.86185:U82613

R-PLACE1002905
Homo sapiens mRNA for KIAA0563 protein, complete cds
10 2.9e-41:330:81
Hs.15731:AB011135

R-PLACE1002911

15 R-PLACE1002967
ESTs
1.0e-43:384:77
Hs.132722:AA618531

20 R-PLACE1003135
ESTs
8.2e-94:462:97
Hs.23643:AI299952

25 R-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds
3.5e-110:541:96
Hs.15250:AF069301

30 R-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.
5.5e-49:287:91
Hs.30213:AF068227

35 R-PLACE1003428
ESTs, Moderately similar to BIOTINIDASE PRECURSOR [Homo sapiens].
6.8e-83:406:97
Hs.17586:AA461448

40 R-PLACE1003438
ESTs
2.9e-83:463:92
Hs.11067:H30385

45 R-PLACE1003460
ESTs
7.0e-27:187:87
Hs.18763:H56292

50 R-nnnnnnnnnnnnn
ESTs
1.7e-52:265:97
Hs.114049:AI091839

55 R-PLACE1003573
Human mRNA for KIAA0160 gene, partial cds
0.13:102:69
Hs.79880:D63881

R-PLACE1003598
 ESTs
 8.0e-39:210:95
 Hs.26286:AA040823
 5
 R-PLACE1003644
 EST
 0.47:84:73
 Hs.105856:AA551478
 10
 R-PLACE1003737
 ESTs
 1.1e-77:366:100
 Hs.62699:AA707766
 15
 R-PLACE1003772
 Human mRNA for KIAA0355 gene, complete cds
 6.1e-27:551:65
 Hs.153014:AB002353
 20
 R-PLACE1003839
 ESTs
 0.019:244:59
 Hs.137825:AA778400
 25
 R-PLACE1003845
 EST
 5.3e-79:416:93
 Hs.150153:AI300555
 30
 R-PLACE1003852
 Homo sapiens mRNA for KIAA0758 protein, partial cds
 2.2e-87:439:96
 Hs.22039:AB018301
 35
 R-PLACE1004028
 Sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)
 0.73:128:71
 Hs.60617:L13972
 40
 R-PLACE1004078
 ESTs
 1.7e-69:353:96
 Hs.142075:AA654529
 45
 R-PLACE1004166
 ESTs
 1.7e-64:362:92
 Hs.10177:AA191619
 50
 R-nnnnnnnnnnnnn
 EST
 0.98:59:71
 Hs.132255:AI027216
 55
 R-PLACE1004199
 ESTs
 1.3e-55:279:97

Hs.147585:AI217699

R-PLACE1004279
ESTs
5 3.7e-68:373:93
Hs.145531:H87181

R-PLACE1004282

10 R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds
6.4e-79:377:99
Hs.15099:AB018283

15 R-PLACE1004441
ESTs
1.8e-46:244:95
Hs.107082:R63714

20 R-PLACE1004450

R-PLACE1004482
ESTs
1.2e-92:491:93
25 Hs.17840:AI269915

R-PLACE1004492
ESTs
6.1e-54:278:95
30 Hs.55862:A1341676

R-PLACE1004519
ESTs
3.1e-25:133:100
35 Hs.47378:AI193598

R-PLACE1004520
Pregnancy-specific beta-1 glycoprotein 4
2.8e-66:390:89
40 Hs.108936:X17097

R-PLACE1004630
ESTs
7.3e-58:338:92
45 Hs.155506:AI281549

R-PLACE1004637
ESTs
1.1e-37:309:82
50 Hs.20102:AA150165

R-PLACE1004648
ESTs
2.3e-67:340:96
55 Hs.69321:AA633240

R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds

- 1.8e-104:586:90
Hs.9225:D88587
- 5 R-PLACE1004887
ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]
2.6e-30:222:86
Hs.18557:AA203416
- 10 R-PLACE1005003
ESTs
0.99:123:68
Hs.146244:AI276718
- 15 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
6.8e-58:299:95
Hs.151614:AF032456
- 20 R-PLACE1005031
ESTs
4.7e-57:325:92
Hs.31196:H13265
- 25 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-17
1.4e-86:450:93
Hs.26484:AJ223351
- 30 R-PLACE1005250
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
1.7e-106:521:97
Hs.36794:AI038407
- 35 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
6.3e-79:471:88
Hs.11494:AF093118
- 40 R-PLACE1005410
EST
2.3e-49:296:90
Hs.7260:T23737
- 45 R-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
8.0e-109:576:93
Hs.108936:X17097
- 50 R-PLACE1005519
ESTs
5.4e-108:569:93
Hs.23643:AI299952
- 55 R-PLACE1005539
ESTs, Weakly similar to p20 protein [R.norvegicus]
4.5e-05:107:77
Hs.56874:W61026

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R-PLACE1005544
 ESTs
 4.2e-57:280:98
 Hs.155391:AA451633
 5

R-PLACE1005569
 ESTs
 2.7e-90:470:94
 Hs.8904:AI129815
 10

R-PLACE1005601

 R-PLACE1005660
 ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
 [Caenorhabditis elegans]
 1.4e-91:483:93
 Hs.7471:AI143226
 15

R-PLACE1005669
 ESTs
 1.7e-84:438:95
 Hs.18271:N92774
 20

R-PLACE1005682
 ESTs
 6.3e-80:482:88
 Hs.128679:AI160081
 25

R-PLACE1005725
 ESTs
 1.5e-98:519:93
 Hs.11360:AI147467
 30

R-PLACE1005736
 ESTs
 3.1e-110:561:95
 Hs.24111:AI346026
 35

R-PLACE1005745
 ESTs
 2.4e-96:473:97
 Hs.126935:AA603217
 40

R-PLACE1005768
 Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
 4.0e-46:387:77
 Hs.1361:M55053
 45

R-PLACE1005815
 Homo sapiens PYRIN (MEFV) mRNA, complete cds
 7.1e-56:324:79
 Hs.113283:AF018080
 50

R-PLACE1005878
 ESTs
 3.1e-75:388:94
 Hs.153483:AA569128
 55

R-PLACE1005927
 ESTs
 4.3e-64:403:87
 Hs.126899:N50907
 5
 R-PLACE1006071
 ESTs
 5.3e-96:510:93
 Hs.24398:AI262946
 10
 R-PLACE1006073
 Homo sapiens mRNA for glucuronyltransferase I, complete cds
 3.0e-97:504:93
 Hs.26492:AB009598
 15
 R-PLACE1006079
 ESTs
 3.1e-79:453:90
 Hs.134194:AI142137
 20
 R-PLACE1006093
 ESTs
 1.3e-78:378:98
 Hs.129327:AI201040
 25
 R-nnnnnnnnnnnnn
 R-PLACE1006219
 EST
 1.6e-75:412:92
 Hs.150153:AI300555
 30
 R-PLACE1006277
 ESTs
 2.8e-92:493:93
 Hs.8904:AI129815
 35
 R-PLACE1006290
 ESTs
 2.8e-92:433:99
 Hs.23445:AA489015
 40
 R-PLACE1006443
 ESTs
 2.5e-73:419:91
 Hs.90809:AA010979
 45
 R-PLACE1006515
 Homo sapiens mRNA for KIAA0576 protein, partial cds
 6.9e-78:413:94
 Hs.14687:AB011148
 50
 R-PLACE1006716
 ESTs
 4.8e-44:262:88
 Hs.8503:AI393886
 55
 R-PLACE1006786

ESTs
6.3e-89:431:98
Hs.42458:AA452296

5 R-PLACE1006809
ESTs
1.6e-68:377:92
Hs.8956:AI146421

10 R-PLACE1006959
EST
0.00065:211:63
Hs.136605:AA665784

15 R-PLACE1007028
ESTs
7.4e-92:475:94
Hs.110222:AA532444

20 R-PLACE1007040
ESTs
5.1e-103:509:97
Hs.71190:AA524036

25 R-PLACE1007077
ESTs
1.0e-98:529:93
Hs.24398:AI262946

30 R-PLACE1007081
Human growth factor independence-1 (Gfi-1) mRNA, complete cds
0.57:238:61
Hs.73172:U67369

35 R-PLACE1007096
ESTs
1.2e-88:466:94
Hs.8268:N70144

40 R-PLACE1007296
EST
4.3e-53:338:86
Hs.147274:AI206582

45 R-PLACE1007591
EST
4.6e-76:384:97
Hs.94445:N90719

50 R-PLACE1007626
Homo sapiens unknown mRNA, complete cds
5.0e-30:179:91
Hs.11441:AF047439

55 R-PLACE1007702
ESTs
1.0e-52:341:87
Hs.103382:AA026923

5 R-PLACE1007845
ESTs
2.2e-102:541:93
Hs.15727:H98190

10 R-PLACE1007881
ESTs
4.1e-75:398:93
Hs.55560:AI142804

15 R-PLACE1007971
ESTs
2.8e-43:304:85
Hs.82933:AA058963

20 R-PLACE1008282
ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryc-
tolagus cuniculus]
2.2e-74:393:94
Hs.77613:AI367385

25 R-PLACE1008297
ESTs
6.5e-101:506:96
Hs.44274:AA523749

30 R-PLACE1008359
ESTs
1.8e-94:469:96
Hs.160551:AI281417

35 R-PLACE1008469
ESTs
7.0e-74:421:90
Hs.90809:AA010979

40 R-PLACE1008549
ESTs
2.0e-81:474:90
Hs.11713:T65960

45 R-PLACE1008657
ESTs
9.5e-89:512:89
Hs.142075:AA654529

50 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
5.6e-100:504:95
Hs.154844:U15128

55 R-PLACE1008744
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
2.3e-107:528:96
Hs.8963:AI379350

R-PLACE1008984
ESTs

- 2.0e-76:464:89
Hs.40094:D12041
- 5 R-PLACE1008985
EST, Highly similar to SYNAPTOTAGMIN B [Discopyge ommata]
2.2e-59:343:90
Hs.161031:H72014
- 10 R-PLACE1009067
ESTs
7.7e-90:503:92
Hs.55067:AA037664
- 15 R-PLACE1009196
EST
0.011:243:60
Hs.149839:AI287601
- 20 R-PLACE1009279
Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
5.4e-27:553:62
Hs.75111:D87258
- 25 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds
2.7e-92:497:91
Hs.86185:U82613
- 30 R-PLACE1009546
ESTs
5.9e-80:461:90
Hs.134292:AA603031
- 35 R-PLACE1009600
ESTs
5.5e-98:509:93
Hs.21015:AA428288
- 40 R-PLACE1009735
ESTs
1.1e-85:462:93
Hs.48563:AA526595
- 45 R-nnnnnnnnnnnnn
ESTs
6.8e-82:499:87
Hs.43498:AA570507
- 50 R-PLACE1010011
ESTs, Moderately similar to synaptonemal complex protein [M.musculus]
2.7e-15:171:78
Hs.31655:AI075991
- 55 R-PLACE1010078
ESTs
1.2e-48:267:92
Hs.12101:AA677423

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R-PLACE1010081.
 Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
 3.0e-106:560:93
 Hs.103755:AF027706
 5
 R-PLACE1010251
 ESTs
 0.00049:248:60
 Hs.154164:AI246893
 10
 R-PLACE1010445
 ESTs
 1.5e-90:496:92
 Hs.163999:AA778110
 15
 R-PLACE1010713
 Interleukin 1 receptor antagonist
 4.1e-07:307:59
 Hs.81134:U65590
 20
 R-PLACE1010784
 ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]
 1.5e-21:206:78
 Hs.29202:R71586
 25
 R-PLACE1010827
 R-PLACE 1010968
 ESTs
 2.6e-75:385:95
 Hs.109884:AA766018
 30
 R-PLACE1011045
 Homo sapiens E1-like protein mRNA, complete cds
 5.3e-92:453:96
 Hs.28190:AF094516
 35
 R-PLACE1011116
 Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds
 1.5e-73:385:94
 Hs.44053:AF006621
 40
 R-PLACE1011236
 R-PLACE1011364
 ESTs
 2.3e-47:289:89
 Hs.6163:W26652
 45
 R-PLACE1011407
 ESTs
 1.1e-09:191:64
 Hs.118620:T60326
 50
 R-PLACE1011516
 ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
 6.3e-75:441:88
 55

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Hs.110978:AA843431

R-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
5 7.7e-93:521:91
Hs.148318:AF034611

R-PLACE1011824
ESTs
10 0.013:199:62
Hs.44343:AA532514

R-PLACE1011978
EST
15 4.0e-97:462:98
Hs.116391:AA644085

R-PLACE2000118
ESTs
20 1.2e-83:468:92
Hs.110578:AA115763

R-PLACE2000219
Homo sapiens KIAA0414 mRNA, partial cds
25 2.0e-44:344:81
Hs.127649:AB007874

R-PLACE3000181
Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8
30 1.3e-82:441:94
Hs.115642:L11369

R-PLACE3000213
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
35 2.3e-114:557:97
Hs.8963:AI379350

R-PLACE4000354
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
40 3.4e-105:518:97
Hs.8963:AI379350

R-PLACE4000455
ESTs
45 9.0e-57:289:96
Hs.42458:AA452296

R-THYRO1000036
Collagen, type IX, alpha 3
50 1.3e-100:527:93
Hs.53563:L41162

R-THYRO1000061
ESTs
55 1.8e-87:460:94
Hs.124869:H98977

R-THYRO1000099

- ESTs
1.2e-34:193:94
Hs.149488:AI243816
- 5 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
3.7e-106:530:96
Hs.115418:AF016272
- 10 R-THYRO1000400
Human HU-K4 mRNA, complete cds
0.99:227:60
Hs.74573:U60644
- 15 R-THYRO1000580
Homo sapiens mRNA for KIAA0628 protein, complete cds
0.21:126:67
Hs.43133:AB014528
- 20 R-THYRO1000584
ESTs, Weakly similar to golgi alpha-mannosidase II [H.sapiens]
3.0e-106:529:96
Hs.12183:AA888145
- 25 R-THYRO1000678
EST
2.9e-62:304:99
Hs.48956:N64339
- 30 R-THYRO1000776
ESTs
1.3e-102:533:94
Hs.4866:AA582196
- 35 R-THYRO1000795
ESTs
3.3e-98:529:92
Hs.55263:AI344338
- 40 R-THYRO1000846
ESTs
1.6e-105:522:96
Hs.135106:AI335251
- 45 R-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds
1.3e-43:251:92
Hs.12912:AF015913
- 50 R-THYRO1000956
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
5.2e-106:548:94
Hs.9305:W84893
- 55 R-THYRO1000964

R-THYRO1000999
ESTs

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1.9e-18:150:84
Hs.111583:AA463590

5 R-THYRO1001063
ESTs
1.5e-95:464:97
Hs.142684:AA902402

10 R-THYRO1001071
ESTs
2.5e-104:496:98
Hs.6071:AA868544

15 R-THYRO1001102

R-THYRO1001113
ESTs, Weakly similar to FER-1 [C.elegans]
7.1e-90:446:97
Hs.8076:AA115644

20 R-THYRO1001128
ESTs
1.9e-16:270:68
Hs.140194:N35720

25 R-THYRO1001205
Small inducible cytokine A5 (RANTES)
1.9e-58:400:84
Hs.155464:AF088219

30 R-THYRO1001237
ESTs
1.5e-104:532:96
Hs.6603:AA772122

35 R-THYRO1001242
EST
1.7e-50:281:93
Hs.101727:H16171

40 R-THYRO1001266
Homo sapiens mRNA for KIAA0650 protein, partial cds
0.00037:403:60
Hs.8118:AB014550

45 R-THYRO1001327
ESTs
1.2e-96:530:93
Hs.28786:AA034412

50 R-THYRO1001456
ESTs, Weakly similar to Similar to phytoene desaturase [C.elegans]
3.3e-43:257:92
Hs.97031:AA773647

55 R-THYRO1001457
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
4.8e-59:284:99

	Hs.9915:AI300083
	R-THYRO1001471
	ESTs
5	1.1e-67:378:93
	Hs.52113:R40587
	R-THYRO1001478
10	R-THYRO1001495
	H.sapiens mRNA for Zinc-finger protein (ZNFpT17)
	1.6e-63:434:84
	Hs.32954:X65233
15	R-THYRO1001523
	ESTs
	5.8e-75:388:96
	Hs.6527:R21517
20	R-THYRO1001529
	ESTs
	1.1e-25:184:87
	Hs.18441:AA005104
25	R-THYRO1001593
	ESTs
	4.7e-34:182:98
	Hs.8312:AA813022
30	R-THYRO1001608
	ESTs
	2.8e-107:547:95
	Hs.23765:AA524283
35	R-THYRO1001641
	Homo sapiens clone 24448 unknown mRNA, partial cds
	1.1e-111:562:96
	Hs.4973:AF070638
40	R-THYRO1001700
	ESTs
	1.3e-78:407:95
	Hs.86987:N99896
45	R-THYRO1001702
	ESTs
	4.3e-98:566:92
	Hs.119447:AA524436
50	R-THYRO1001725
	ESTs
	1.3e-84:424:96
	Hs.38039:AI360128
55	R-THYRO1001770
	ESTs
	1.0e-62:325:97
	Hs.20137:R08273

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R-THYRO1001803
 ESTs
 6.8e-90:456:96
 Hs.134438:R42585
 5

R-Y79AA1000030
 ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
 2.4e-98:515:94
 Hs.32822:A1194045
 10

R-Y79AA1000127
 ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
 1.1e-57:307:95
 Hs.83513:W05849
 15

R-Y79AA1000207
 EST
 1.0e-97:411:96
 Hs.141431:N21286
 20

R-Y79AA1000226
 ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis
 elegans]
 7.2e-102:545:94
 Hs.11221:A1192291
 25

R-Y79AA1000270
 Human mRNA for ORF, Xq terminal portion
 3.3e-107:564:93
 Hs.6551:D16469
 30

R-Y79AA1000426
 H.sapiens mRNA for activin beta-C chain
 2.5e-10:217:66
 Hs.83267:X82540
 35

R-Y79AA1000521
 Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
 0.73:257:59
 Hs.113286:U77783
 40

R-Y79AA1000750
 ESTs
 4.3e-75:391:95
 Hs.157192:W84862
 45

R-Y79AA1000776
 ESTs
 3.5e-56:303:95
 Hs.118559:AA887084
 50

R-Y79AA1000777
 ESTs, Weakly similar to LIS-1 protein [H.sapiens]
 9.5e-98:515:95
 Hs.59461:W93217
 55

R-Y79AA1000876
 EST

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- 2.7e-23:173:84
Hs.135872:AI037885
- 5 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
3.4e-80:453:92
Hs.53066:AF093420
- 10 R-Y79AA1000967
ESTs
7.3e-86:461:93
Hs.6262:T89093
- 15 R-Y79AA1001013
ESTs
1.4e-115:566:97
Hs.108408:N31922
- 20 R-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus].
8.7e-111:557:95
Hs.36794:AI038407
- 25 R-Y79AA1001062
ESTs
0.0021:365:59
Hs.106129:AA292171
- 30 R-Y79AA1001090
ESTs
5.0e-52:255:99
Hs.106214:AI123831
- 35 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.8e-83:407:97
Hs.6710:AF038961
- 40 R-Y79AA1001264
ESTs, Highly similar to DNAJ PROTEIN HOMOLOG 2 [Homo sapiens]
2.8e-111:552:96
Hs.62489:AI057091
- 45 R-Y79AA1001272
Zinc finger protein, X-linked
0.019:317:59
Hs.2074:X59739
- 50 R-Y79AA1001328
ESTs
3.6e-67:385:92
Hs.127792:AI421472
- 55 R-Y79AA1001426
ESTs
2.0e-13:92:93
Hs.105607:AA478379

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R-Y79AA1001430
Homo sapiens mRNA for KIAA0469 protein, complete cds
2.0e-112:555:96
Hs.7764:AB007938

5

R-Y79AA1001523
EST
1.7e-07:120:73
Hs.130984:AI015430

10

R-Y79AA1001530
Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds
0.030:169:63
Hs.155489:AF037448

15

R-Y79AA1001592
ESTs
5.0e-60:340:91
Hs.87019:AA760977

20

R-Y79AA1001727
ESTs
6.1e-101:547:93
Hs.7404:W29012

25

R-Y79AA1001787
ESTs
8.8e-84:449:95
Hs.128866:AA977749

30

R-Y79AA1001795
Homo sapiens mRNA for GalT4 protein
9.9e-110:541:97
Hs.21495:AL031228

35

R-Y79AA1001799
ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]
1.6e-94:567:90
Hs.34401:AA447775

40

R-Y79AA1001803
ESTs, Highly similar to SECRETORANIN III PRECURSOR [Mus musculus]
1.2e-86:509:90
Hs.22215:AI371482

45

R-Y79AA1001863
ESTs
1.4e-23:268:73
Hs.131613:AI190576

50

R-Y79AA1002022
ESTs
8.9e-97:462:98
Hs.6140:D52151

55

R-nnnnnnnnnnnnn
R-nnnnnnnnnnnnn

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Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds
0.00075:456:59
Hs.153855:AF022778

- 5 R-Y79AA1002213
Human mRNA for KIAA0392 gene, partial cds
6.2e-45:304:85
Hs.40100:AB002390
- 10 R-Y79AA1002334
ESTs
7.7e-91:495:92
Hs.90804:W28091
- 15 R-Y79AA1002373
Human kpnI repeat mRNA (cdna clone pcd-kpnI-8), 3' end
5.2e-98:545:91
Hs.103948:K00627
- 20 R-Y79AA1002376
ESTs
2.0e-91:455:97
Hs.153375:AI287812
- 25 R-Y79AA1002378
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]
9.4e-15:131:83
Hs.20082:W89121
- 30 R-Y79AA1002381
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]
1.5e-104:531:95
Hs.26322:AA156858

35 Homology search result 10

[0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

- 45 C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762).//0//1230bp//92%//AB026894
C-nnnnnnnnnnnnn//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//2.30E-71//344aa//50%//P50636
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679
C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154
- 50 C-HEMBA1000275
C-HEMBA1000300
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
- 55 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS)//2.00E-07//445aa//27%/P02454
C-HEMBA1000907
C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44)//2.90E-39//362aa//31%/P41987
5 C-HEMBA1000962
C-HEMBA1001221//AGRIIN PRECURSOR//2.50E-25//294aa//29%/P31696
C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds//7.80E-286//1105bp//94%/L32137
C-HEMBA1001297
10 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds//2.50E-57//464bp//82%/AF036249
C-HEMBA1001563
C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ//3.50E-123//259aa//89%/P35414
C-HEMBA1001621//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)//2.40E-85//293aa//50%/P51523
15 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds//0//1488bp//99%/AF090988
C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%/P24802
20 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION//9.40E-28//309aa//30%/Q04651
C-HEMBA1002164
C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds//1.30E-305//1643bp//91%/U22952
C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1)//3.70E-10//140aa//30%/P24802
25 C-HEMBA1002195//Human glycyl-tRNA synthetase mRNA, complete cds//0//2380bp//99%/U09587
C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//8.80E-23//221aa//31%/Q00808
C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds//0//1324bp//98%/D10522
C-HEMBA1002239
30 C-HEMBA1002316
C-HEMBA1002420
C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end//0//2097bp//99%/J04621
C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds//0//1763bp//95%/U63336
35 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)//9.80E-08//110aa//37%/P49695
C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds//0//1497bp//99%/AF038660
C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2//2.00E-21//216aa//35%/P48510
40 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds//0//1768bp//99%/AF034611
C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds//3.30E-93//927bp//73%/U68380
C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds//0//1854bp//99%/AF049891
45 C-HEMBA1003230//Homo sapiens fibulin-5//5.60E-308//1398bp//99%/AJ133490
C-HEMBA1003294
C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds//6.30E-250//1426bp//88%/AB013912
C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds//0//1721bp//100%/AF074264
50 C-HEMBA1003399//MVP1 PROTEIN//2.30E-15//279aa//23%/P40959
C-HEMBA1003487
C-HEMBA1003530//S.scrofa mRNA for BM88 antigen//1.20E-60//900bp//66%/X82027
C-HEMBA1003602//Homo sapiens CGI-67 protein mRNA, complete cds//3.50E-70//732bp//66%/AF151825
55 C-HEMBA1003732//SFT2 PROTEIN//1.50E-06//162aa//30%/P38166
C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds//8.90E-287//757bp//97%/AF077030
C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds//0//2033bp//99%/AF064243

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C-HEMBB1001200
 C-HEMBB1001407
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158
 C-HEMBB1001573
 5 C-nnnnnnnnnnn//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//1.50E-251//
 1146bp//99%//AF118670
 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645
 C-HEMBB1001978
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AP062354
 10 C-HEMBB1002228
 C-HEMBB1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786
 C-HEMBB 1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC
 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-
 15 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-
 FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857
 C-HEMBB1002663
 C-HEMBB1002693
 20 C-MAMMA1000046
 C-MAMMA1000118
 C-nnnnnnnnnnn//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.50E-312//1594bp//93%//
 AF067420
 C-MAMMA1000449
 25 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-
 AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530
 30 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN)(BLAST-1)
 (CD48).//2.90E-12//239aa//28%//P10252
 C-MAMMA1001893
 C-NT2RM2000241
 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%//P91917
 35 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%//
 P48982
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%//P22516
 C-NT2RM2000514//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2381bp//99%//AB020682
 40 C-NT2RM2000622
 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%//AJ0001319
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312
 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482
 45 C-NT2RM4000198
 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 50 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 189aa//30%//P25234
 55 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001735

C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//
 2184bp//99%//AB009462
 C-NT2RP1000002
 C-NT2RP1000050
 5 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//
 AF126799
 C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082
 C-NT2RP1000325//H.sapiens gene for phosphate carmer.//0//439bp//98%//X77337
 10 C-NT2RP1000448
 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//
 99%//U09585
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//
 1951bp//94%//L21936
 15 C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
 3.40E-52//304aa//40%//P08060
 C-NT2RP1000903
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
 C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
 20 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
 VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
 AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
 C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//
 25 AF029071
 C-NT2RP2000479
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
 30 C-NT2RP2000663
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
 35 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//
 41%//P39986
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//
 O13310
 40 C-NT2RP2001878
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
 C-NT2RP2001915
 C-NT2RP2001956//ORM1 PROTEIN.//3.90E-19//137aa//37%//P53224
 45 C-NT2RP2002063//GNS1 PROTEIN.//3.60E-18//231aa//33%//P25358
 C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//1.90E-93//420aa//
 43%//Q09782
 C-NT2RP2002304//Human mRNA for KIAA0383 gene, partial cds.//0//1640bp//99%//AB002381
 50 C-NT2RP2002409
 C-NT2RP2002510
 C-NT2RP2002527//CYTOCHROME B5.//1.30E-11//92aa//38%//P40312
 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//
 2365bp//99%//AF042792
 55 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CY-
 TOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913
 C-NT2RP2002721//REGULATORY PROTEIN UHPC.//1.60E-23//153aa//30%//P27669

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C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
NENT) //3.50E-63//404aa//33%//P32802
C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
C-NT2RP2002974//HOMEODOMAIN PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HO-
MOLOG) (FRAGMENT) //8.20E-241//555aa//84%//P70178
C-NT2RP2002976
C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
(FRAGMENT) //2.10E-109//385aa//52%//P53760
C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-) //2.60E-67//256aa//
49%//Q05512
C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//
98%//AF055899
C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //5.90E-20//204aa//
34%//Q15404
C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER) //1.10E-45//324aa//
29%//P37021
C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//
AF024636
C-NT2RP2003593
C-NT2RP2003599
C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC //4.80E-15//93aa//47%//
P38869
C-NT2RP2003931
C-NT2RP2004141
C-NT2RP2004179
C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT) //1.60E-21//276aa//32%//Q62556
C-NT2RP2004447
C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//U49082
C-NT2RP2004524
C-NT2RP2004556
C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//
M12670
C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
C-NT2RP2004670//Rattus norvegicus vesicle-associated calmodulin-binding protein mRNA, complete cds.//0//
1250bp//86%//L22557
C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//
203aa//26%//P40857
C-NT2RP2004837
C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
C-ntnnnnnnnnnn//Homo sapiens SCG10-like-protein (SCLIP) mRNA, complete cds.//2.90E-170//813bp//98%//
AF069709
C-NT2RP2005027
C-NT2RP2005163
C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//
2126bp//81%//U70859
C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN) //5.00E-53//296aa//37%//Q62158
C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
C-NT2RP2005514
C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
COSAMINE-6-SULFATASE) //4.70E-24//78aa//51%//P15586
C-NT2RP2005632
C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-) //3.60E-55//238aa//50%//
O57314
C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-

HYDROXYLASE) (DBH).//6.70E-72//512aa//34%/P15101
C-NT2RP2005887
C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%/
M93650
5 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//
47%/P49191
C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//9.40E-15//501aa//25%/P08640
C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (E,C
10 2.4.1.109).//2.30E-78//679aa//32%/P31382
C-NT2RP2006512//GNS 1 PROTEIN.//2.00E-21//290aa//29%/P25358
C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//
3.70E-12//133aa//32%/Q01485
C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//
15 5.00E-29//596aa//30%/P19246
C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%/P29375
C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%/AF093239
C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-
NASE I).//1.30E-80//359aa//44%/Q14012
20 C-NT2RP3000201//Homo sapiens mRNA for KIAA0687 protein, partial cds.//2.00E-305//1224bp//99%/AB014587
C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//
90aa//42%/P38660
C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%/M96629
C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//
25 227aa//36%/Q06828
C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//
171aa//36%/P38800
C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//
33%/P49695
30 C-NT2RP3000871
C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//
42%/P39986
C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%/AB020636
C-NT2RP3001044
35 C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%/AB020660
C-NT2RP3001170//Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).//0//2421bp//
99%/AL080163
C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//
29%/P37021
40 C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%/M96629
C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-
ULUM CA2+-ATPASE).//1.70E-21//220aa//30%/P39524
C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%/P50232
C-nnnnnnnnnnnn//Human mRNA for KIAA0315 gene, partial cds.//0//2971bp//99%/AB002313
45 C-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//3243bp//99%/D87686
C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
0//2468bp//99%/AF037339
C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
2.1.1.32).//1.30E-18//279aa//27%/P15565
50 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%/P00169
C-NT2RP3001754
C-NT2RP3001858
C-NT2RP3002160//Canis familiaris forssman synthetase mRNA, complete cds.//5.00E-152//789bp//84%/U66140
C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//
55 43%/P48982
C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%/U49082
C-NT2RP3002448
C-NT2RP3002721//Porcine citrate synthase mRNA, complete cds.//9.10E-281//1454bp//93%/M21197

- C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//65%//L43821
C-NT2RP3002790
C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
5 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//8.00E-08//197aa//26%//P19814
C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//96%//AF051946
C-NT2RP3003076
10 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//O35609
C-NT2RP3003469
C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
15 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
C-NT2RP3003559
C-NT2RP3003614
C-NT2RP3003729
C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130
20 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381
C-NT2RP3003963
C-NT2RP3004000
25 C-NT2RP3004075
C-NT2RP3004083
C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
30 C-NT2RP3004202
C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118
C-NT2RP3004321
C-NT2RP3004355
35 C-NT2RP3004374
C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544
C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927
40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
C-NT2RP3004625//Homo sapiens mRNA for KIAA0975 protein, partial cds.//0//1339bp//99%//AB023192
C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//AF176680
45 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834
C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
C-OVARC1000090
50 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296
C-OVARC1000137
C-OVARC1000208
C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
55 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924
C-OVARC1000298
C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-

33//143aa//53%//P34280
 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//
 165aa//39%//P34244
 5 C-OVARC1000775
 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 157//1.00E-35//130aa//46%//P51786
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%//Q01177
 C-OVARC1000853
 C-OVARC1000916//H.sapiens PISSLRE mRNA//7.30E-280//1117bp//95%//X78342
 10 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.20E-09//250aa//
 28%//P17437
 C-OVARC1001030//Homo Sapiens mRNA for KIAA0886 protein, complete cds.//0//907bp//99%//AB020693
 C-OVARC1001049//TRANSCRIPTION FACTOR HES- (C-HAIRY1)//7.50E-14//96aa//36%//O57337
 C-OVARC1001086//Homo Sapiens cyclin T2a mRNA, complete cds.//0//1593bp//98%//AF048731
 15 C-OVARC10011321//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)
 (TCF-9)//2.30E-44//268aa//36%//P16383
 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I//2.30E-20//152aa//
 30%//Q09906
 C-OVARC1001222
 20 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//
 125aa//40%//P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//
 164aa//39%//P34244
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.//0//1766bp//99%//
 25 AF126062
 C-OVARC1001725
 C-OVARC1001727
 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)//8.30E-06//114aa//
 30 35%//Q01956
 C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR//3.80E-17//190aa//28%//Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//
 35 2.70E-101//947bp//74%//AF037272
 C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.70E-55//431aa//
 35%//Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.00E-88//213aa//67%//P16415
 C-PLACE1000560
 40 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X//6.30E-21//123aa//
 37%//Q11079
 45 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC
 PROTEIN)//6.80E-12//133aa//28%//P35500
 C-nnnnnnnnnnnn//Homo sapiens T245 protein (T245) mRNA, complete cds.//0//1801bp//99%//AF043906
 C-PLACE1001100
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN//9.20E-06//389aa//31%//P03181
 50 C-PLACE1001123
 C-PLACE1001183
 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds.//2.20E-137//918bp//80%//AF026554
 55 C-nnnnnnnnnnnn//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 7.60E-293//1631bp//90%//U18469
 C-PLACE1001340//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2868bp//99%//AB018262
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE

- FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//
 5 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//Q28181
 10 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.//0//1708bp//99%//AF043472
 C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//1776bp//99%//AF013759
 15 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.//3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P2OE].//5.00E-27//134aa//47%//P10269
 20 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//2.30E-53//339aa//33%//P32802
 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%//Q12697
 25 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%//AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%//AF095791
 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//213aa//45%//Q08509
 30 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//40%//P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%//X12451
 C-PLACE1002518
 35 C-PLACE1002547//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2985bp//99%//AB018262
 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//82%//AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%//P07106
 40 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%//P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%//Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%//P08458
 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%//
 45 AF069301
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%//AJ132099
 C-PLACE1003438
 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//1.30E-09//281aa//22%//P11414
 50 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).//3.70E-16//226aa//26%//P20937
 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%//P90917
 C-PLACE1003644
 55 C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%//P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//2.40E-12//124aa//38%//P 13983
 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//

771bp//58%//AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 GALACTOSE 4-EPIMERASE)//3.40E-37//302aa//30%//Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301
 5 C-PLACE1004028
 C-PLACE1004166//CREB-BINDING PROTEIN//1.80E-12//147aa//35%//P45481
 C-PLACE1004168//Homo sapiens mRNA for KIAA1007 protein, partial cds.//0//2637bp//99%//AB023224
 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III//1.40E-08//166aa//
 10 30%//P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL)//2.10E-11//
 189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//AC007383
 15 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 TIGEN CD13)//1.30E-91//562aa//35%//P15541
 C-PLACE 1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004519
 20 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%//M20881
 C-PLACE1004630
 C-PLACE1004637
 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 25 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//1.40E-18//395aa//25%//P08640
 C-nnnnnnnnnnn//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1825bp//99%//
 AF049891
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTEIN)//4.80E-33//179aa//47%//Q06003
 30 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-)//2.20E-52//269aa//41%//Q16651
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17)//1.80E-235//1010bp//84%//
 35 AJ223351
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 40 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 0//1629bp//95%//U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//
 AF024636
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 45 1237bp//76%//U89915
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III//1.90E-
 33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN)//4.90E-09//183aa//33%//
 50 P20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311
 C-PLACE1005768
 55 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AP047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-

GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 5 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 10 C-PLACE1007028
 C-PLACE1007040
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GETA.//2.70E-17//174aa//27%//O34368
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1373bp//99%//AJ224875
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 15 C-PLACE1007591
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 20 42%//Q19425
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-nnnnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1616bp//99%//AJ224875
 C-PLACE1008469
 25 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1888bp//99%//U15128
 30 C-PLACE1008984
 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 35 6.60E-86//1414bp//64%//E12965
 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 40 88%//D88315
 C-PLACE1009735
 C-PLACE1009982//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224
 C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//
 45 AF027706
 C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
 C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//
 1146bp//99%//AF008670
 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-
 50 19//163aa//34%//P49020
 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TY-
 ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
 C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 55 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
 C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
 C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//

139aa//34%//P53073
C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//
AF034611
C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424
5 C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//
57%//Q05481
C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//
P70315
C-PLACE2000219
10 C-SKNMC1000004
C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//
1376bp//93%//L41162
C-THYRO1000061
C-THYRO1000099
15 C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272
C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//
AL109665
C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
C-THYRO1000584//Homo sapiens mRNA for KIAA0935 protein, partial cds.//0//1338bp//99%//AB023152
20 C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585
C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114
C-THYRO1000846
C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963
C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642
25 C-THYRO1000999
C-THYRO1001063
C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN
ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
C-THYRO1001102
30 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//
99%//AL096713
C-THYRO1001128
C-THYRO1001205
C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1
35 PROTEIN).//3.10E-13//346aa//22%//P21334
C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
C-THYRO1001327
C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
40 C-THYRO1001471
C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEU-
TROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558)
BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//
35%//P04839
45 C-THYRO1001495
C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS
PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP)
50 (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//
73%//AJ001616
C-THYRO1001725
C-THYRO1001803
55 C-Y79AA1000127
C-Y79AA1000207
C-Y79AA1000226
C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//

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83%/U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%/U96386
 C-Y79AA1000521
 C-Y79AA1000776
 5 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%/Q00808
 C-nnnnnnnnnnnn//Homo sapiens intersectin long form mRNA, complete cds.//0//1519bp//99%/AF064244
 C-Y79AA1000876//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%/P13667
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%/AF093420
 10 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.00E-77//359aa//44%/Q14012
 C-Y79AA1001013
 C-Y79AA1001056
 15 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%/Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31%/Q63369
 20 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%/Q10005
 C-Y79AA1001272
 C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%/AB013440
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%/AB007938
 25 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%/P32507
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%/P03891
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%/Q02280
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%/U71267
 30 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%/P40085
 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%/Q99676
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%/Y13622
 35 C-HEMBA1000835
 C-HEMBA1000875
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822
 40 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997
 C-HEMBA1001296
 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803
 C-HEMBA1002985
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676
 45 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%/Q60821
 C-HEMBA1004007
 C-HEMBA1004085
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%/P30658
 50 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%/P52738
 C-HEMBA1005246
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//187aa//33%/Q01484
 55 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//57%/Q61967
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%/

O15127
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581
 5 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425
 C-HEMBA1006912
 C-HEMBA1007063
 C-HEMBB1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 C-HEMBB1000407
 10 C-HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//
 1452bp//85%//AF084259
 C-HEMBB1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937
 C-HEMBB1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 15 C-HEMBB1002039
 C-HEMBB1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//
 99%//AF179274
 C-HEMBB1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//
 AF115403
 20 C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
 C-HEMBB1002302
 C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//
 2174bp//99%//AF179274
 25 C-MAMMA1000106
 C-MAMMA1000141
 C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
 C-MAMMA1000226
 C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//
 1165bp//99%//AF117959
 30 C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//
 299aa//34%//P47088
 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258
 C-MAMMA1000528
 35 C-MAMMA1000614//Homo sapiens pseudouridine synthase 1 (PUS1) mRNA, partial cds.//2.10E-302//1370bp//
 99%//AF116238
 C-MAMMA1000652
 C-MAMMA1000706
 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
 40 C-MAMMA1000810
 C-MAMMA1000814
 C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
 C-MAMMA1000986
 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA,
 45 complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536
 C-MAMMA1001141
 C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
 C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
 C-MAMMA1001284
 50 C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-
 REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225
 C-MAMMA1001344
 C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%//P44742
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//
 55 P51523
 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%//Q13562
 C-MAMMA1001623//Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone DKFZp434J1027); partial cds.//
 1.30E-269//1222bp//99%//AL133084

C-MAMMA1001634
 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177
 5 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153
 C-MAMMA1002087
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-222//867aa//52%//O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338
 10 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.80E-17//146aa//35%//P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%//AF100780
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%//AL050119
 15 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509
 C-MAMMA1002633
 C-MAMMA1003126//Human Hpast (HPAST) mRNA, complete cds.//3.70E-162//1355bp//75%//AF001434
 20 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//9.40E-94//394aa//43%//Q09782
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976
 25 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%//Q03468
 C-NT2RM2000773//Homo sapiens KNLS4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335
 30 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%//AF093408
 C-NT2RM2001626//FLIGHTLESS-1 PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 35 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%//P23253
 C-NT2RM4000100//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2678bp//99%//AB023206
 40 C-NT2RM4000115//HYPOTHETICAL 68.8 KD PROTEIN B0464.6 IN CHROMOSOME III.//1.20E-16//204aa//30%//Q03564
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//24%//Q10297
 45 C-NT2RM4000761//H.sapiens mitochondrial genome (consensus sequence).//0//1931bp//99%//X62996
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//520aa//29%//O60100
 C-NT2RM4001377//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1346bp//99%//AB014538
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 50 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//P48982
 C-NT2RP1000239
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000679
 C-NT2RP1000740//Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone DKFZp586F1918).//4.60E-97//456bp//99%//AL050091

C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808
C-NT2RP2000178//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//
778aa//48%//P93647
C-NT2RP2000240
5 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379
C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210
C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
4.10E-12//323aa//30%//P13983
10 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742
C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZNNC FNNGER PROTENN HPF1).//7.50E-73//387aa//37%//
P51522
C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
cds.//0//2724bp//99%//AF089744
15 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576
C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615
C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322
C-NT2RP2001388//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
NUCLEASE).//5.90E-13//157aa//33%//P16658
20 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
C-NT2RP2001562//Homo Sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922
C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//
94aa//81%//Q90655
C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469
25 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106
C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2).//1.40E-08//191aa//27%//P53686
C-NT2RP2002015
C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779
C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//
Y12670
30 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//7.00E-111//401aa//43%//P28160
C-NT2RP2004069//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//3.00E-45//188aa//
52%//Q09297
C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.30E-171//474aa//62%//P16415
35 C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//99%//AF013759
C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//1792bp//87%//
U35245
C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-
28//183aa//47%//P10496
40 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor
Sp1.//0//1544bp//99%//AJ242978
C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//
97%//AF095136
C-NT2RP2005666
45 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//
227aa//36%//Q06828
C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247
C-NT2RP2006134
C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808
50 C-NT2RP3000022//Homo sapiens mRNA for KIAA0936 protein, complete cds.//0//2881bp//99%//AB023153
C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//
Z97207
C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//
AF074264
55 C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579
C-NT2RP3000444
C-NT2RP3000645
C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829

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C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%/P48378
 C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//
 100%//AF117106
 C-NT2RP3000818
 5 C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%/Q07283
 C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUP-
 PRESSOR).//4.00E-21//316aa//29%/P43146
 C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//
 99%//AL050118
 10 C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
 2.60E-09//334aa//22%/P52178
 C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 TEIN).//4.70E-11//132aa//37%/Q13829
 C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%/P77495
 15 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//
 P51523
 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
 C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
 C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE 1 mRNA, complete cds.//0//2719bp//
 20 99%//AF097645
 C-NT2RP3002324
 C-NT2RP3002353
 C-NT2RP3002571//Homo sapiens mRNA for KIAA1108 protein, partial cds.//4.40E-273//1311bp//97%//AB029031
 C-NT2RP3002664
 25 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//
 1552bp//99%//AF105202
 C-NT2RP3002887
 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
 C-NT2RP3002983
 30 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//
 99%//P41217
 C-NT2RP3004025
 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
 35 C-NT2RP3004119//PEREGRIN (BE140 PROTEIN).//7.30E-39//227aa//43%/P55201
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
 2.1.1.32).//3.90E-18//279aa//27%/P15565
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//
 40 0//1501bp//98%//AF111105
 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//
 AF131856
 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//
 AF127761
 45 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//
 AF078850
 C-NT2RP4002451
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//
 50 2084bp//81%//U70859
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000313//Homo sapiens mRNA for KIAA0573 protein, partial cds.//0//1833bp//99%//AB011145
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
 55 ASE).//9.40E-44//106aa//59%/P36959
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
 CULE) (THAM).//1.30E-23//169aa//40%/P28843
 C-OVARC1000873//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2178bp//99%//AB033073

C-OVARC1000995
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//0//1435bp//99%//AF111856
 5 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//
 100%//AF190725
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1836bp//96%//U15128
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
 10 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//
 99%//AF068227
 15 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%//D26549
 C-PLACE1004492//VERPROLIN.//3.30E-07//149aa//29%//P37370
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//
 3.10E-08//84aa//34%//Q00649
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 20 C-PLACE1005601
 C-PLACE1005745//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//
 P23508
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 25 33%//Q09875
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//
 P02469
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//
 AB009598
 30 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//
 AF028233
 C-PLACE1006786
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
 C-PLACE1007971
 35 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-)
 (HRI).//7.10E-274//627aa//82%//P33279
 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
 C-PLACE1008744//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114.//0//1757bp//99%//
 AL079279
 40 C-PLACE1010445
 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
 AF078850
 C-nnnnnnnnnnnn//Homo sapiens angiopoietin-2 mRNA, complete cds.//0//2227bp//99%//AF004327
 C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815
 45 C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE)
 (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
 C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//
 L11370
 C-SKNMC1000014
 50 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//30%//P29518
 C-THYRO1000964
 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
 0//2468bp//99%//AF037339
 C-THYRO1001608
 55 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-
 20//1169aa//35%//P53974
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247

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C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
6.20E-66//609aa//31%//P48751
5 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
AF169481
C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
99%//AF119042
C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
C-Y79AA1001592
10 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
Q12697
C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
C-Y79AA1001795//Homo sapiens mRNA for GaIT4 protein.//2.30E-250//1137bp//99%//Y15061
15 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
C-Y79AA1001863
C-Y79AA1002058//Mus musculus Gng31g mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
20 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
41%//Q03567
C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
304//1667bp//90%//U39045
25 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
AF155100
C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013
C-BNGH41000087//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2294bp//99%//AB033073
C-HEMBA1001886
30 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//8.30E-309//623bp//99%//
AB020666
C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//
1242bp//99%//AF192529
C-HEMBA1000309
35 C-HEMBA1000567
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
C-MAMMA1001066
C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
1394bp//93%//U71267
40 C-MAMMA1001609
C-MAMMA1001901
C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%//AF039916
C-NT2RM1000462
C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//
45 43%//P48982
C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%//Y11306
C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%//P23500
C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
50 C-NT2RP2001538//Homo sapiens mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235).//0//2139bp//
99%//AL117513
C-NT2RP2001921
C-NT2RP2003138//5'-TG-3'INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF).//2.10E-08//104aa//46%//
P70284
55 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
cds.//0//2891bp//99%//AB021644
C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//

62%/Q03923
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%/AB021644
 C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%/P51523
 5 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%/Q99676
 C-NT2RP3000427
 C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%/P28160
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//107aa//42%/P98063
 10 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%/AB018262
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%/AF078850
 C-NT2RP3003448
 15 C-NT2RP4002715
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%/Q50658
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%/P51522
 C-PLACE1007081
 20 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%/AF047431
 C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%/P19070
 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%/P17927
 25 C-PLACE4000455
 C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%/O74377
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%/P27448
 C-Y79AA1000750
 30 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%/P70973
 C-Y79AA1002129
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%/P14922
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%/P03891
 35 C-BNGH41000087//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//1.20E-17//83aa//40%/P50426
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%/Q02280
 C-HEMBA1000006//Homo sapiens mRNA for NESCA, complete cds.//0//1230bp//92%/AB026894
 40 C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%/P34679
 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%/P33154
 C-HEMBA1000275
 45 C-HEMBA1000300
 C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%/P41233
 C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%/AF151854
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%/U71267
 50 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%/P40085
 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%/AJ007581
 C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%/AF116272
 55 C-HEMBA1000671//ZINC FINGER. PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%/Q99676
 C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%/AF053470
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%/Y13622

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%/P02454
 C-HEMBA1000835//FIBRILLIN 2 PRECURSOR.//1.30E-42//214aa//45%/P35556
 C-HEMBA1000875
 C-HEMBA1000907
 5 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%/P41987
 C-HEMBA1000962
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822
 10 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%/P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//1105bp//94%/L32137
 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997
 C-HEMBA1001296
 15 C-HEMBA1001297//Homo sapiens putative transcription factor CA150 mRNA, complete cds.//4.60E-276//1081bp//99%/AF017789
 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//464bp//82%/AF036249
 C-HEMBA1001563
 20 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%/P35414
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%/AF090988
 C-HEMBA1001886//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-148//421aa//60%/Q03923
 25 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%/P24802
 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//309aa//30%/Q04651
 30 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%/U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%/P24802
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%/Q00808
 35 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%/D10522
 C-HEMBA1002239
 C-HEMBA1002316//GTP-BINDING PROTEIN HFLX.//5.80E-12//196aa//29%/P25519
 C-HEMBA1002420
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%/J04621
 40 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%/U63336
 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//37%/P49695
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//0//1497bp//99%/AF038660
 45 C-HEMBA1002985
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%/P48510
 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//99%/AF034611
 50 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//73%/U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%/AF049891
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676
 55 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%/AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%/AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//

100%//AF074264
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959
 C-HEMBA1003487
 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING
 5 PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%//Q60821
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027
 C-HEMBA1003602//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//2.80E-21//200aa//33%//Q50658
 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//
 10 AF077030
 C-HEMBA1004007
 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//0.00E+00//623bp//99%//
 AB020666
 C-HEMBA1004085
 15 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243
 C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//
 277aa//35%//P33450
 C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//F70211
 C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
 20 C-HEMBA1004454
 C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%//P30658
 C-HEMBA1004797
 25 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//
 Q07282
 C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//
 30 29%//P17437
 C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//1.20E-07//102aa//37%//P18160
 C-HEMBA1005145
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%//P52738
 35 C-HEMBA1005246//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4).//2.10E-15//
 230aa//28%//Q92949
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//
 187aa//33%//Q01484
 C-HEMBA1005430
 40 C-HEMBA1005449//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 5.40E-10//224aa//24%//P13983
 C-HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA,
 complete cds.//8.40E-255//924bp//80%//AF127084
 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
 45 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//590aa//100%//P20309
 C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//
 753bp//99%//AF039568
 C-HEMBA1005913
 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
 50 C-HEMBA1005945//BRITTLE-1 PROTEIN PRECURSOR.//1.70E-29//220aa//35%//P29518
 C-HEMBA1006016
 C-HEMBA1006171
 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//
 57%//Q61967
 55 C-HEMBA1006299
 C-HEMBA1006311
 C-HEMBA1006335
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%//

O15127
 C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//
 1108bp//65%//L38961
 C-HEMBA1006482//Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete
 5 cds.//0//1101bp//98%//AF026852
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803
 C-HEMBA1006658//Homo sapiens mRNA for NIK, partial cds.//0//1500bp//98%//AB013385
 10 C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581
 C-HEMBA1006724
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581
 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425
 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581
 15 C-HEMBA1006912
 C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687
 C-HEMBA1006960
 C-HEMBA1007013//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//1.10E-14//412bp//63%//
 AF068749
 20 C-HEMBA1007057
 C-HEMBA1007063
 C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//
 1242bp//99%//AF192529
 C-HEMBA1007241//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-14//
 25 106aa//42%//P40857
 C-HEMBA1007291
 C-HEMBA1007332//Homo sapiens mRNA for unr-interacting protein.//6.40E-83//266bp//98%//AJ010025
 C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 C-HEMBA1000276
 30 C-HEMBA1000309
 C-HEMBA1000407
 C-HEMBA1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523
 C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//
 1452bp//85%//AF084259
 35 C-HEMBA1000567
 C-HEMBA1000642
 C-HEMBA1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700
 C-HEMBA1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678
 C-HEMBA1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085
 40 C-HEMBA1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706
 C-HEMBA1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//5.30E-11//142aa//30%//P32802
 C-HEMBA1001048//SARCALUMENIN PRECURSOR.//6.50E-18//154aa//33%//P13666
 45 C-HEMBA1001200
 C-HEMBA1001407
 C-HEMBA1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158
 C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937
 C-HEMBA1001573
 50 C-HEMBA1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645
 C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 C-HEMBA1001978
 C-HEMBA1002039
 55 C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//
 99%//AF179274
 C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//
 AF115403

- C-HEM BB1002120//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%/P56558
C-HEM BB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%/AF062534
C-HEM BB1002228
5 C-HEM BB 1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%/Q62786
C-HEM BB1002302
C-HEM BB1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT).//1.80E-70//221aa//50%/P16442
10 C-HEM BB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%/P45857
C-HEM BB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//2174bp//99%/AF176422
15 C-HEM BB1002663
C-HEM BB1002693
C-MAMMA1000046
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%/O14791
C-MAMMA1000106
20 C-MAMMA1000118
C-MAMMA1000141
C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%/AF075575
C-MAMMA1000226
C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//1165bp//99%/AF117959
25 C-MAMMA1000449
C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%/M16462
C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//299aa//34%/P47088
30 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%/P53258
C-MAMMA1000528
C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%/Q07537
35 C-MAMMA10006141//Homo sapiens pseudouridine synthase I (PUS1) mRNA, partial cds.//2.10E-302//1370bp//99%/AF116238
C-MAMMA1000652
C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%/O08530
C-MAMMA1000706
40 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%/AF037349
C-MAMMA1000810
C-MAMMA1000814
C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%/AF169035
C-MAMMA1000986
45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%/AB024536
C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1) (CD48).//2.90E-12//239aa//28%/P10252
C-MAMMA1001066
50 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//1394bp//93%/U71267
C-MAMMA1001141
C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%/Q15139
C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%/P53988
55 C-MAMMA1001284
C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.//1.50E-67//441aa//37%/Q04225
C-MAMMA1001344

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C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%/P44742
C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%/P51523
C-MAMMA1001609//MYOSIN II HEAVY CHAIN, NON MUSCLE.//1.50E-26//204aa//38%/P05659
5 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%/Q13562
C-MAMMA1001623
C-MAMMA1001634
C-MAMMA1001893
C-MAMMA1001901
10 C-MAMMA1001957
C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%/AF085499
C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%/Q01177
C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%/P51153
C-MAMMA1002087
15 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%/AF039916
C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-222//867aa//52%/O43108
C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%/Q92338
C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
20 TEIN KINASE 1).//9.80E-17//146aa//35%/P18160
C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%/AF100780
C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%/AL050119
25 C-MAMMA1002224
C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%/Q00004
C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%/AF148509
C-MAMMA1002633
C-MAMMA1003126//SARCALUMENIN PRECURSOR.//1.10E-51//388aa//32%/P13666
30 C-NT2RM1000462//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//8.60E-14//104aa//40%/P15287
C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//43%/P48982
C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%/P43636
35 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%/Y11306
C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%/AF084458
C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%/S70011
C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%/P23500
C-NT2RM2000241
40 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%/P91917
C-NT2RM2000410
C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%/P48982
C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%/P22516
45 C-NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//4.40E-304//1374bp//99%/AF174601
C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//4.40E-304//394aa//43%/Q09782
C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%/AB028976
50 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%/U55042
C-NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.//3.00E-203//915bp//91%/AF176524
C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%/Q03468
C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%/AB017335
55 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%/AJ001319
C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%/AF093408

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C-NT2RM2001626//FLIGHTLESS-I PROTEIN HOMOLOG.//4.30E-19//362aa//26%/P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%/P33750
 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%/AF125175
 5 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%/P23253
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%/AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%/U55312
 10 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%/P08482
 C-NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//2678bp//99%/AF175966
 C-NT2RM4000115
 C-NT2RM4000198//BUTYROPHILIN PRECURSOR (BT).//5.10E-12//162aa//33%/Q13410
 15 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%/U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%/P51523
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%/P46097
 20 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%/P36370
 C-NT2RM4000587
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//24%/Q10297
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%/P51655
 25 C-NT2RM4000761//CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).//2.50E-245//306aa//91%/P00395
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//520aa//29%/O60100
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//189aa//30%/P25234
 30 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%/Q92179
 C-NT2RM4001377//R.norvegicus LL5 mRNA.//8.50E-236//990bp//87%/X74226
 35 C-NT2RM4001735
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%/AF151840
 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%/P48982
 C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//2184bp//99%/AB009462
 40 C-NT2RP1000002
 C-NT2RP1000050
 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%/AF126799
 45 C-NT2RP1000239
 C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%/P53224
 C-NT2RP1000271//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//4.70E-199//547aa//66%/Q03923
 C-NT2RP1000300//Human transporter protein (g17)-mRNA, complete cds.//3.80E-26//758bp//62%/U49082
 50 C-NT2RP1000325//H.sapiens gene for phosphate carrier.//0//439bp//98%/X77337
 C-NT2RP1000448
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%/P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%/P25210
 55 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//99%/U09585
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//1951bp//94%/L21936

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C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
 3.40E-52//304aa//40%//P08060
 C-NT2RP1000679
 C-NT2RP1000740
 5 C-NT2RP1000903
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
 C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
 VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
 10 C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
 AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
 C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
 C-NT2RP2000178//MITOCHONDRIAL ION PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//
 15 778aa//48%//P93647
 C-NT2RP2000240
 C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//
 AF029071
 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379
 20 C-NT2RP2000479
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210
 25 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 4.10E-12//323aa//30%//P13983
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
 C-NT2RP2000663
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
 30 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.50E-73//387aa//37%//
 P51522
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
 cds.//0//2724bp//99%//AF089744
 35 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322
 C-NT2RP2001388//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
 40 NUCLEASE).//5.90E-13//157aa//33%//P16658
 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//
 45 41%//P39986
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
 C-NT2RP2001538//Mus musculus mSin3A (sin3A) mRNA, complete cds.//7.60E-272//1480bp//84%//U22394
 C-NT2RP2001562//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922
 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//
 50 94aa//81%//Q90655
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//
 O13310
 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106
 55 C-NT2RP2001878
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
 C-NT2RP2001915

C-NT2RP2001921
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2)//1.40E-08//191aa//27%//P53686
 C-NT2RP2001956//ORM1 PROTEIN//3.90E-19//137aa//37%//P53224
 C-NT2RP2002015
 5 C-NT2RP2002063//GNS1 PROTEIN//3.60E-18//231aa//33%//P25358
 C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//1.90E-93//420aa//43%//Q09782
 C-NT2RP2002304//Homo sapiens histone acetyltransferase MORF mRNA, complete cds.//0//2737bp//99%//AF113514
 10 C-NT2RP2002409
 C-NT2RP2002510
 C-NT2RP2002527//CYTOCHROME B5//1.30E-11//92aa//38%//P40312
 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792
 15 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH)//5.50E-38//201aa//39%//P34913
 C-NT2RP2002721//REGULATORY PROTEIN UHPC//1.60E-23//153aa//30%//P27669
 20 C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)//3.50E-63//404aa//33%//P32802
 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
 C-NT2RP2002974//HOMEODOMAIN PROTEIN SIXS (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178
 25 C-NT2RP2002976//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION//1.30E-20//99aa//47%//P38800
 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT)//2.10E-109//385aa//52%//P53760
 30 C-NT2RP2003138//5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF)//2.10E-08//104aa//46%//P70284
 C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512
 35 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//0//2891bp//99%//AB021644
 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//5.90E-20//204aa//34%//Q15404
 40 C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779
 C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER)//1.10E-45//324aa//29%//P37021
 45 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636
 C-NT2RP2003593
 C-NT2RP2003599
 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869
 50 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//Y12670
 C-NT2RP2003931
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//7.00E-111//401aa//43%//P28160
 55 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
 C-NT2RP2004069
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.30E-171//474aa//62%//P16415
 C-NT2RP2004141

C-NT2RP2004179
 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT)//1.60E-21//276aa//32%//Q62556
 C-NT2RP2004447
 C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//L149082
 5 C-NT2RP2004524
 C-NT2RP2004556
 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670
 C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
 10 C-NT2RP2004670//Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.//0//1250bp//86%//L22557
 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%//P40857
 C-NT2RP2004837
 15 C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
 C-NT2RP2005027//GLUCOSE TRANSPORTER TYPE 3, BRAIN.//6.20E-67//130aa//100%//P11169
 C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//1792bp//87%//U35245
 C-NT2RP2005163
 20 C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//2126bp//81%//U70859
 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-28//183aa//47%//P10496
 25 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
 C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
 C-NT2RP2005514
 30 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//62%//Q03923
 C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//97%//AF095136
 35 C-NT2RP2005632
 C-NT2RP2005666
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 40 C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//O57314
 C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
 C-NT2RP2005887
 45 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//M93650
 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191
 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//227aa//36%//Q06828
 50 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247
 C-NT2RP2006099
 55 C-NT2RP2006134
 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109).//2.30E-78//679aa//32%//P31382
 C-NT2RP2006512//GNS1 PROTEIN.//2.00E-21//290aa//29%//P25358

- C-NT2RP2006580//Homo sapiens transitional epithelia response protein (TERE1) mRNA, complete cds.//0//1483bp//99%//AF117064
- C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808
- 5 C-NT2RP3000022//Rat heart mRNA serine/threonine protein kinase, complete cds.//4.80E-203//1496bp//78%//D26178
- C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.70E-12//133aa//32%//Q01485
- C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//5.00E-29//596aa//30%//P19246
- 10 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375
- C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523
- C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239
- 15 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//Z97207
- C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.30E-80//359aa//44%//Q14012
- C-NT2RP3000201//Homo sapiens HPK/GCK-like kinase HGK mRNA, complete cds.//1.30E-270//1231bp//99%//AF096300
- 20 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
- C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//AF074264
- C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579
- C-NT2RP3000427
- 25 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660
- C-NT2RP3000444
- C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629
- C-NT2RP3000481//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//0//2623bp//100%//AF098799
- 30 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//227aa//36%//Q06828
- C-NT2RP3000645
- C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
- C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829
- 35 C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378
- C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800
- C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%//AF117106
- 40 C-NT2RP3000818
- C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695
- C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283
- C-NT2RP3000871
- 45 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//42%//P39986
- C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%//P43146
- C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636
- 50 C-NT2RP3001044
- C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660
- C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%//AL050118
- 55 C-NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.//4.80E-240//850bp//88%//AF068198
- C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//29%//P37021
- C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629

C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
2.60E-09//34aa//22%//P52178
C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-
ULUM CA2+-ATPASE).//1.70E-21//220aa//30%//P39524
5 C-NT2RP3001388//SYNAPTOTAGMIN IV//2.00E-118//430aa//54%//P50232
C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
TEIN).//4.70E-11//132aa//37%//Q13829
C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
0//2468bp//99%//AF037339
10 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
2.1.1.32).//1.30E-18//279aa//27%//P15565
C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//
107aa//42%//P98063
C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
15 C-NT2RP3001738//CYTOCHROME B5//1.30E-11//133aa//33%//P00169
C-NT2RP3001754
C-NT2RP3001858
C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//
P51523
20 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
C-NT2RP3002160//HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [INCLUDES: GLYCO-
PROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40)
(FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP
A TRANSFERASE) (A TRANSFERASE); GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA- GALACTOSYL-
25 TRANSFERASE (EC 2.4.1.37) (FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE) (HISTO-
BLOOD GROUP B TRANSFERASE) (B TRANSFERASE)].//3.50E-72//231aa//49%//P16442
C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//0//2719bp//
99%//AF097645
30 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//
43%//P48982
C-NT2RP3002324
C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
C-NT2RP3002353
35 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
AF078850
C-NT2RP3002448
C-NT2RP3002571//Bos taurus mRNA for lyncein.//7.30E-169//1115bp//84%//Y17923
40 C-NT2RP3002664
C-NT2RP3002721//CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).//5.80E-249//466aa//
98%//O75390
C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//
1552bp//99%//AF105202
45 C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//
65%//L43821
C-NT2RP3002790
C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
C-NT2RP3002887
50 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//
8.00E-08//197aa//26%//P19814
C-NT2RP3002983
C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//
55 96%//AF051946
C-NT2RP3003076
C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//
O35609

C-NT2RP3003448
 C-NT2RP3003469
 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
 5 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%//P41217
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 10 C-NT2RP3003614
 C-NT2RP3003729//HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.//5.80E-17//204aa//30%//Q03151
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130
 15 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 C-NT2RP3004025
 20 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004119//PEREGRIN (BR140 PROTEIN).//7.30E-39//227aa//43%//P55201
 25 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 C-NT2RP3004202
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118
 30 C-NT2RP3004321
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%//P15565
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544
 C-NT2RP3004481//BUTYROPHILIN PRECURSOR (BT).//8.50E-22//276aa//32%//Q62556
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-GEN).//8.50E-24//263aa//33%//P17927
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1339bp//99%//AF082516
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
 45 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//X05608
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%//AF111105
 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 50 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//AF131856
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
 55 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//AF127761
 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//

AF078850
 C-NT2RP4002451
 C-NT2RP4002715
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//
 5 2084bp//81%//U70859
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000090
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 10 LIGASE) (UBIQUITIN CARRIER PROTEIN)//4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208//Human calcium-dependent group X phospholipase A2 mRNA, complete cds//1.50E-61//
 365bp//90%//U95301
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
 15 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT)//9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658
 C-OVARC1000313//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//3.00E-24//353aa//
 20 27%//Q12730
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
 ASE)//9.40E-44//106aa//59%//P36959
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-
 33//143aa//53%//P34280
 25 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.40E-23//
 165aa//39%//P34244
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
 CULE) (THAM)//1.30E-23//169aa//40%//P28843
 30 C-OVARC1000775
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%//Q01177
 C-OVARC1000853
 C-OVARC1000873//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 COSAMINE-6-SULFATASE)//1.00E-09//83aa//40%//P50426
 35 C-OVARC1000916//H.sapiens PISSLRE mRNA.//7.30E-280//1117bp//95%//X78342
 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG
 PROTEIN)//2.20E-09//250aa//28%//P17437
 C-OVARC1000995
 C-OVARC1001030//Homo sapiens mRNA for KIAA0886 protein, complete cds.//0//907bp//99%//AB020693
 40 C-OVARC1001049//TRANSCRIPTION FACTOR HES-1 (C-HAIRY1).//7.50E-14//96aa//36%//Q57337
 C-OVARC1001086//Homo sapiens cyclin T2a mRNA, complete cds.//0//1593bp//98%//AF048731
 C-OVARC1001132//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)(TCF-
 9).//2.30E-44//268aa//36%//P16383
 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.//2.30E-20//152aa//
 45 30%//Q09906
 C-OVARC1001222
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//0//1435bp//99%//AF111856
 50 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-).//8.80E-30//
 125aa//40%//P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-).//1.50E-22//
 164aa//39%//P34244
 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//
 55 100%//AF190725
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.//0//1766bp//99%//
 AF126062
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//

- 1836bp//96%//U15128
 C-OVARC1001725//Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.//0//
 1624bp//99%//AF064800
 C-OVARC1001727
- 5 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//
 35%//Q01956
- 10 C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR.//3.80E-17//190aa//28%//Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//
 2.70E-101//947bp//74%//AF037272
- 15 C-PLACE1000258//ZINC FINGER. PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//
 35%//Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415
 C-PLACE1000560
 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
- 20 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X.//6.30E-21//123aa//
 37%//Q11079
- 25 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).//6.80E-12//133aa//28%//
 P35500
- 30 C-PLACE1001100//Homo sapiens nephrin (NPHS1) mRNA, complete cds.//3.10E-46//323bp//84%//AF035835
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN.//9.20E-06//389aa//31%//P03181
 C-PLACE1001123//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).//
 5.00E-08//95aa//31%//Q04941
 C-PLACE1001183
- 35 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds.//2.20E-137//918bp//80%//AF026554
 C-PLACE1001340//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRI-
 AL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER)
- 40 (TRANSLOCASE OF OUTER MEMBRANE TOM70).//1.20E-23//231aa//31%//P23231
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
- 45 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//
 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//
- 50 Q28181
 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds.//0//1708bp//99%//AF043472
- 55 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR.//3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-

BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//5.00E-27//134aa//47%/P10269
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENOCYTIC INTERMEDIATE COMPO-
 NENT).//2.30E-53//339aa//33%/P32802
 5 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%/Q12697
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791
 10 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//213aa//45%/Q08509
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//40%/P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%/X12451
 15 C-PLACE1002518//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.50E-14//396bp//64%/AF064801
 C-PLACE1002547//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).//2.30E-28//277aa//31%/P23231
 20 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//82%/AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%/P07106
 25 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%/P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%/Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%/P08458
 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301
 30 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%/AF068227
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099
 C-PLACE1003438
 35 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//1.30E-09//281aa//22%/P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).//3.70E-16//226aa//26%/P20937
 40 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%/P90917
 C-PLACE1003644
 C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%/P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//2.40E-12//124aa//38%/P13983
 45 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//771bp//58%/AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.40E-37//302aa//30%/Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%/AB018301
 50 C-PLACE1004028
 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%/D26549
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%/P45481
 C-PLACE1004168//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.//9.10E-62//485aa//32%/P25655
 55 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//30%/P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.10E-11//

189aa//30%/P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1 //9.60E-29//197aa//41%/P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%/U13666
 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 5 TIGEN CD13) //1.30E-91//562aa//35%/P15541
 C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%/AF097723
 C-PLACE1004492//VERPROLIN//3.30E-07//149aa//29%/P37370
 C-PLACE1004519
 10 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%/M20881
 C-PLACE1004630//Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, com-
 plete cds.//1.00E-138//643bp//99%/AF072752
 C-PLACE1004637
 15 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //1.40E-18//395aa//25%/P08640
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%/D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTENN) //4.80E-33//179aa//47%/Q06003
 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-) //2.20E-52//269aa//41%/Q16651
 20 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%/AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64 //8.00E-92//205aa//87%/P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, PH4-17) //1.80E-235//1010bp//84%/AJ2233511
 25 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%/AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%/AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%/M96629
 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 30 0//1629bp//95%/U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%/AF024636
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP) //3.10E-08//84aa//34%/Q00649
 35 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 1237bp//76%/U89915
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%/AJ132502
 C-PLACE1005601
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 40 33//143aa//53%/P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN) //4.90E-09//183aa//33%/P20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 45 27%/Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%/E16311 C-PLACE1005745//ORM1
 PROTEIN.//2.40E-17//137aa//35%/P53224
 C-PLACE1005768
 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN) //1.50E-26//274aa//26%/P23508
 50 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%/L16547
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 33%/Q09875
 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN) //6.00E-08//215aa//26%/P02469
 55 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%/AB009598
 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%/

AF028233
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AF047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 5 GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 10 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006786
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 15 C-PLACE1007028//Homo sapiens TDAG51/lp1 homologue 1 (TIH1) mRNA, complete cds.//1.40E-307//1423bp//
 99%//AF151100
 C-PLACE1007040
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
 C-PLACE1007081//COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).//5.00E-
 20 20//247aa//34%//Q28107
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GUTA.//2.70E-17//174aa//27%//O34368
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 C-PLACE1007591
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 25 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 42%//Q19425
 C-PLACE1007971
 30 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-)
 (HRI).//7.10E-274//627aa//82%//P33279
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
 35 C-PLACE1008469
 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 40 1888bp//99%//U15128
 C-PLACE1008744//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//4.80E-32//338aa//30%//
 Q01102
 C-PLACE1008984
 45 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 6.60E-86//1414bp//64%//E12965
 50 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 88%//D88315
 55 C-PLACE1009735
 C-PLACE1009982//SALIVARY GILUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224

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C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//AF027706
C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
C-PLACE1010445
5 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850
C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//1146bp//99%//AF039686
C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-19//163aa//34%//P49020
10 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
15 C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815
C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
20 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//139aa//34%//P53073
C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611
25 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424
C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481
C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315
30 C-PLACE2000219
C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//L11370
C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070
35 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927
C-PLACE4000455
C-SKNMC1000004
C-SKNMC1000014
40 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//130%//P29518
C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162
C-THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//1.40E-117//1126bp//74%//AB030505
45 C-THYRO1000099
C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272
C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665
C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
50 C-THYRO1000584//EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE) (135 KD PROTEIN).//5.40E-127//335aa//71%//Q28949
C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585
C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377
C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114
55 C-THYRO1000846
C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963
C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642
C-THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//1.10E-

34//759bp//63%//AF091624
 C-THYRO1000999
 C-THYRO1001063
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN
 5 ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN)//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616)//0//1361bp//
 99%//AL096713
 C-THYRO1001128//Homo sapiens mRNA for hypothetical protein (C9orf9 gene)//6.40E-155//648bp//99%//
 10 AJ011375
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-) (PHYTOENE DESATURASE) (ALBINO-1
 PROTEIN)//3.10E-13//346aa//22%//P21334
 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds//
 15 0//2468bp//99%//AF037339
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C//9.40E-32//355aa//31%//Q10555
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu//2.30E-218//1183bp//73%//X75756
 20 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEU-
 TROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558)
 BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT)//8.90E-50//296aa//
 35%//P04839
 25 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS
 PROTEIN 2) (SPT 2)//5.50E-25//115aa//53%//Q09925
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-)//3.10E-203//550aa//
 30 62%//P27448
 C-THYRO1001608
 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds//0//1668bp//99%//AF151815
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP)
 (RECEPTOR INTERACTING PROTEIN)//9.70E-33//268aa//37%//Q60855
 35 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein//1.50E-128//1204bp//
 73%//AJ001616
 C-THYRO1001725
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-)//6.30E-20//
 169aa//35%//P53974
 40 C-THYRO1001803
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds//0//1828bp//100%//AB018247
 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 45 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds//1.00E-271//1490bp//
 83%//U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds//7.70E-200//1533bp//78%//U96386
 C-Y79AA1000521
 C-Y79AA1000750
 50 C-Y79AA1000776//Mus musculus mRNA for GSG1, complete cds//2.40E-161//820bp//85%//D87325
 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1//8.10E-48//283aa//38%//Q00808
 C-Y79AA1000876//PROTEIN DISULHDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72)//1.60E-
 44//210aa//38%//P13667
 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I)
 (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE)//1.50E-21//267aa//32%//P70973
 55 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds//4.80E-283//1405bp//
 95%//AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-

NASE I).//1.00E-77//359aa//44%//Q14012
 C-Y79AA1001013
 C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535
 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 5 TEIN).//8.90E-12//132aa//38%//Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1)
 (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT] (FRAG-
 MENT).//4.50E-09//144aa//31%//Q63369
 C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
 10 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-
 106//351aa//58%//Q10005
 C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//
 867bp//98%//AF172066
 C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440
 15 C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
 6.20E-66//609aa//31%//P48751
 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
 AF169481
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938
 20 C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
 99%//AF119042
 C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
 C-Y79AA1001592
 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
 25 C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
 Q12697
 C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
 C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061
 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
 30 C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
 C-Y79AA1001863
 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507
 C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
 C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
 35 C-Y79AA1002129
 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
 41%//Q03567
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
 40 C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
 304//1667bp//90%//U39045
 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
 AF155100
 45 C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set
 50 forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide
 is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucle-
 otides.
2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide
 55 complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth
 in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence, 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO:4 and SEQ ID NO:830
SEQ ID NO:5 and SEQ ID NO:831
SEQ ID NO:6 and SEQ ID NO:832
SEQ ID NO:7 and SEQ ID NO:833
SEQ ID NO:8 and SEQ ID NO:834
SEQ ID NO:9 and SEQ ID NO:835
SEQ ID NO:11 and SEQ ID NO:836
SEQ ID NO:12 and SEQ ID NO:837
SEQ ID NO:13 and SEQ ID NO:838
SEQ ID NO:14 and SEQ ID NO:839
SEQ ID NO:15 and SEQ ID NO:840
SEQ ID NO:16 and SEQ ID NO:841
SEQ ID NO:17 and SEQ ID NO:842
SEQ ID NO:18 and SEQ ID NO:843
SEQ ID NO:20 and SEQ ID NO:844
SEQ ID NO:22 and SEQ ID NO:845
SEQ ID NO:23 and SEQ ID NO:846
SEQ ID NO:24 and SEQ ID NO:847
SEQ ID NO:25 and SEQ ID NO:848
SEQ ID NO:26 and SEQ ID NO:849
SEQ ID NO:27 and SEQ ID NO:850
SEQ ID NO:28 and SEQ ID NO:851
SEQ ID NO:29 and SEQ ID NO:852
SEQ ID NO:30 and SEQ ID NO:853
SEQ ID NO:31 and SEQ ID NO:854
SEQ ID NO:32 and SEQ ID NO:855
SEQ ID NO:33 and SEQ ID NO:856
SEQ ID NO:34 and SEQ ID NO:857
SEQ ID NO:35 and SEQ ID NO:858
SEQ ID NO:36 and SEQ ID NO:859
SEQ ID NO:37 and SEQ ID NO:860
SEQ ID NO:39 and SEQ ID NO:861
SEQ ID NO:40 and SEQ ID NO:862
SEQ ID NO:41 and SEQ ID NO:863
SEQ ID NO:42 and SEQ ID NO:864
SEQ ID NO:44 and SEQ ID NO:865
SEQ ID NO:45 and SEQ ID NO:866
SEQ ID NO:46 and SEQ ID NO:867
SEQ ID NO:47 and SEQ ID NO:868

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4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
 5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
 6. A substantially pure protein encoded by polynucleotide of claim 4.
 7. A partial peptide of the protein of claim 6.
 8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following
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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

set forth in any one of the following SEQ ID NOs:

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 SEQ ID NO:4143, SEQ ID NO:4145, SEQ ID NO:4147, SEQ ID NO:4149, SEQ ID NO:4151,
 55 SEQ ID NO:4153, SEQ ID NO:4156, SEQ ID NO:4158, SEQ ID NO:4160, SEQ ID NO:4162,

SEQ ID NO:4164, SEQ ID NO:4166

SEQ ID NO:4169, SEQ ID NO:4171, SEQ ID NO:4173, SEQ ID NO:4175, SEQ ID NO:4177,
and SEQ ID NO:4179

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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and

b) recovering the synthesized product.

20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

22. A method for detecting the polynucleotide of claim 8, the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and

b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

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Figure 1

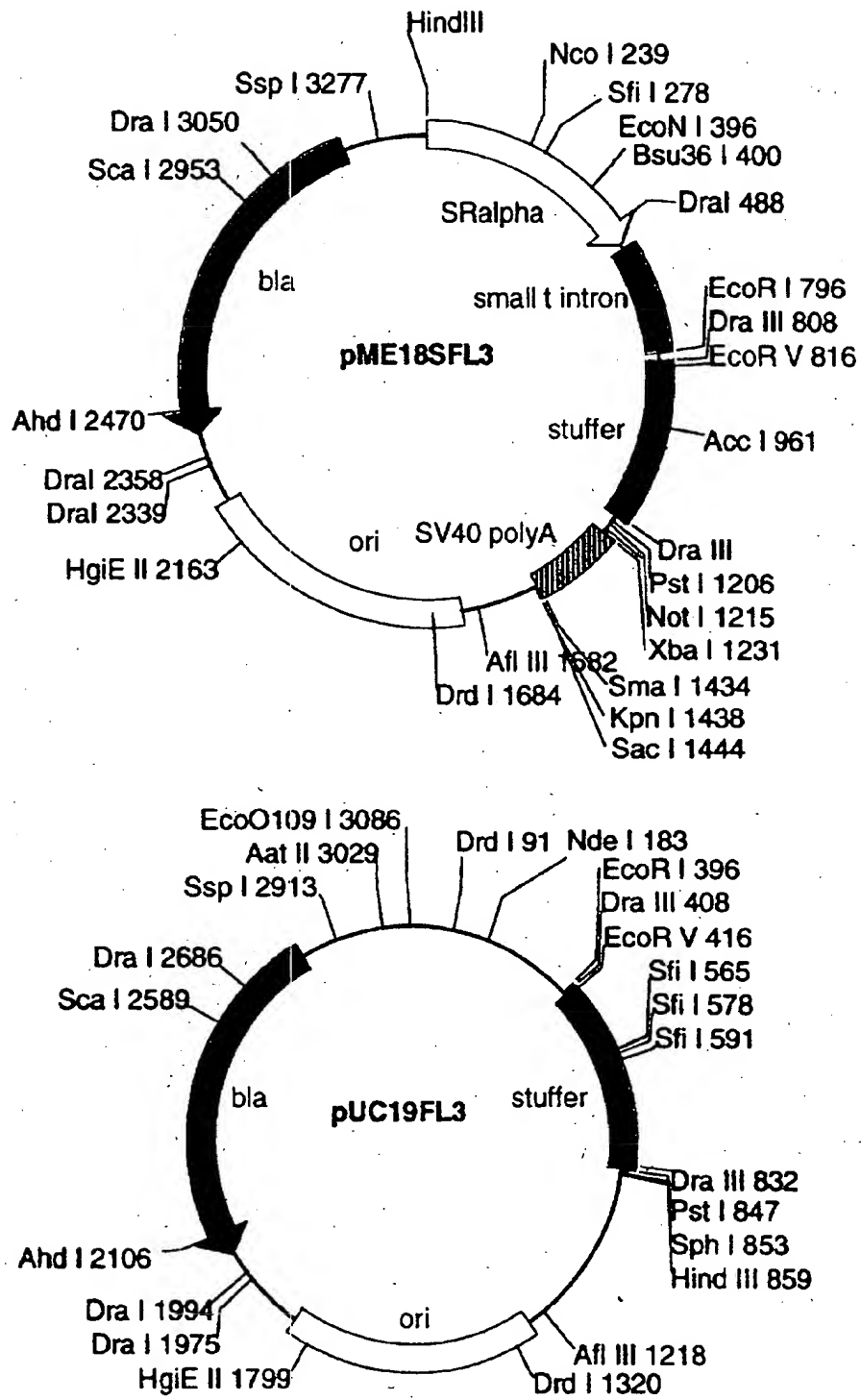


Figure 2

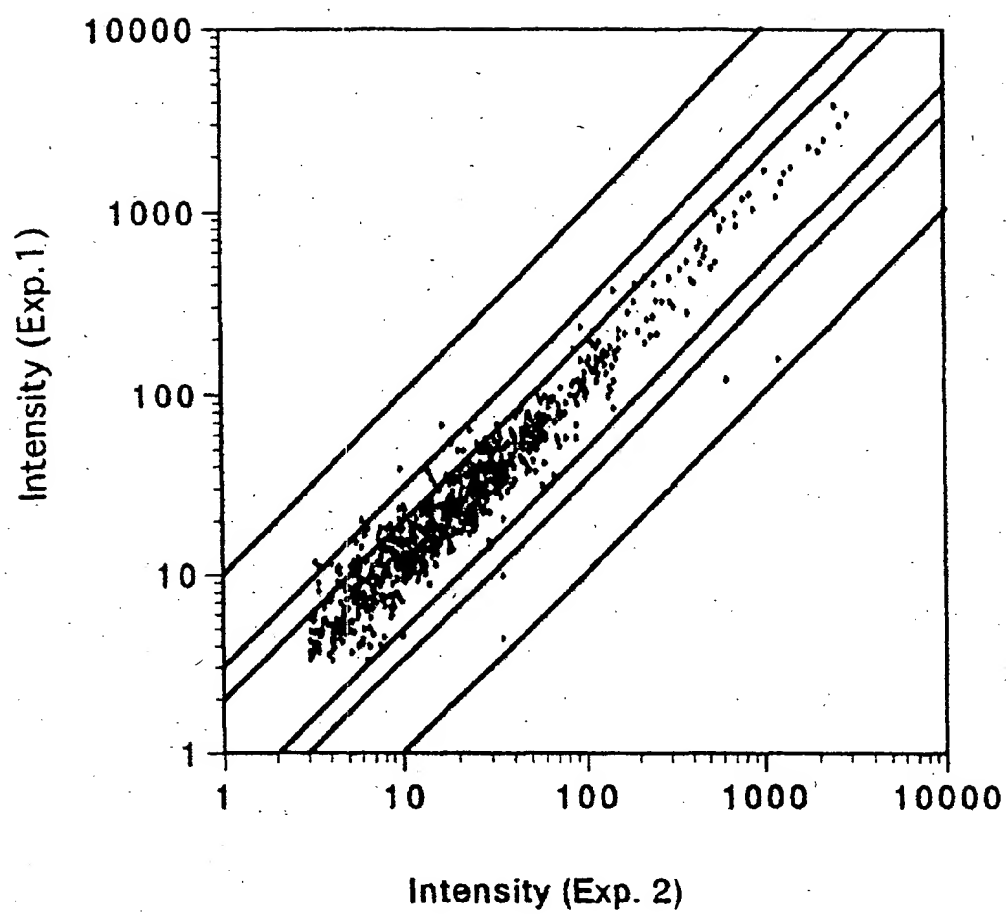


Figure 3

